SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 75%.

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 14, 2005, 16:23:19 ; Search time 3367 Seconds
(without alignments)
6206.500 Million cell updates/sec

Title: US-09-769-066-16
Perfect score: 2819
Sequence: 1 AVAPAHDTSPVPDVDSRGAI.....QSTVAELQRLKVKVGKTREL 549

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09769066/runat_13072005_133014_23069/app_query.fasta_1.1422
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09769066_@CGN_1_1_3556_@runat_13072005_133014_23069 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	137.5	4.9	2391	8	BH771003	BH771003 LLMGtag72
c	2	121.5	4.3	1778	3	BC054075	BC054075 Mus muscu
	3	121	4.3	2419	3	AK049595	AK049595 Mus muscu
	4	121	4.3	3612	3	AK050493	AK050493 Mus muscu
	5	121	4.3	3702	9	AY404468	AY404468 Mus muscu
	6	119	4.2	2707	9	CL953164	CL953164 OsJRUA000
c	7	117	4.2	3822	9	CL972913	CL972913 OsIFCC023
	8	115.5	4.1	759	7	CF870156	CF870156 tric021xl
	9	115.5	4.1	828	6	CB900324	CB900324 tric021xl
	10	114.5	4.1	2368	3	AK019649	AK019649 Mus muscu
	11	114.5	4.1	2907	3	AK080877	AK080877 Mus muscu
	12	114.5	4.1	3013	3	AK078246	AK078246 Mus muscu
	13	114	4.0	2313	9	CL976421	CL976421 OsIFCC028
	14	111	3.9	747	8	BZ156047	BZ156047 CH230-312
	15	110.5	3.9	2369	3	AK032985	AK032985 Mus muscu
	16	109.5	3.9	721	8	BZ494783	BZ494783 BONNL70TF
	17	109.5	3.9	805	6	CB644332	CB644332 OSJNEb05H
	18	109.5	3.9	866	5	BU906994	BU906994 AGENCOURT
	19	109.5	3.9	3177	3	AK004683	AK004683 Mus muscu
	20	108.5	3.8	759	7	CK803586	CK803586 AGENCOURT
	21	108.5	3.8	791	6	CD575859	CD575859 UCRPT01_0
c	22	108	3.8	927	5	BU174132	BU174132 AGENCOURT
	23	107.5	3.8	721	9	CG794911	CG794911 ZMMBBb032
	24	107.5	3.8	746	7	CF443648	CF443648 EST679993
	25	107.5	3.8	2225	3	AK043258	AK043258 Mus muscu
	26	107	3.8	769	7	CF869972	CF869972 tric021xb
	27	107	3.8	823	6	CB900129	CB900129 tric021xb
c	28	107	3.8	889	5	BQ681065	BQ681065 AGENCOURT
	29	107	3.8	1533	9	CL967750	CL967750 OsIFCC015
	30	107	3.8	3015	9	CL961191	CL961191 OsIFCC005
	31	107	3.8	4949	3	AK039390	AK039390 Mus muscu
	32	106.5	3.8	638	7	CN010297	CN010297 WHE3869_A
c	33	106.5	3.8	740	8	CC430070	CC430070 PUHGG47TB
	34	106.5	3.8	855	8	CC430073	CC430073 PUHGG47TD
c	35	106.5	3.8	939	9	CG131549	CG131549 PUJCL55TB
	36	106.5	3.8	977	9	CG131552	CG131552 PUJCL55TD
	37	106.5	3.8	1086	4	BM458331	BM458331 AGENCOURT
	38	106	3.8	2031	9	AY410823	AY410823 Homo sapi
	39	106	3.8	8526	9	CL969571	CL969571 OsIFCC018
	40	105.5	3.7	711	7	CF865933	CF865933 tric004xa
	41	105.5	3.7	765	6	CB895871	CB895871 tric004xa
c	42	105.5	3.7	1065	8	BZ549248	BZ549248 pacs1-60_
c	43	105.5	3.7	1437	9	CL970441	CL970441 OsIFCC019
	44	105.5	3.7	4212	3	AK031199	AK031199 Mus muscu
	45	105	3.7	784	7	CF743861	CF743861 UI-M-GI0-

ALIGNMENTS

RESULT 1
BH771003/c
LOCUS BH771003 2391 bp DNA linear GSS 01-MAY-2002
DEFINITION LLMGtag726 MG1363 Random Sequence Tag Library Lactococcus lactis subsp. cremoris genomic, genomic survey sequence.
ACCESSION BH771003
VERSION BH771003.1 GI:20373960
KEYWORDS GSS.
SOURCE Lactococcus lactis subsp. cremoris
ORGANISM Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
REFERENCE 1 (bases 1 to 2391)
AUTHORS Bolotin,A., Ehrlich,S.D. and Sorokin,A.
TITLE Studies of genomes of dairy bacteria Lactococcus lactis
JOURNAL Sci. Aliments (2002) In press
COMMENT Contact: Sorokin A
Genetique Microbienne
INRA
CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel:' 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
best homologue in strain IL1403 is yhgD (62%)
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 2361.
FEATURES Location/Qualifiers
source 1. .2391
/organism="Lactococcus lactis subsp. cremoris"
/mol_type="genomic DNA"
/strain="MG1363"
/sub_species="cremoris"

/db_xref="taxon:1359"
/clone_lib="MG1363 Random Sequence Tag Library"
/note="Vector: pSGMU2; Site_1: SmaI; Library of chromosomal fragments of L.lactis strain MG1363 was prepared by partial AluI digestion or by sonication."

ORIGIN

Alignment Scores:

Pred. No.:	0.00531	Length:	2391
Score:	137.50	Matches:	119
Percent Similarity:	31.99%	Conservative:	56
Best Local Similarity:	21.76%	Mismatches:	196
Query Match:	4.88%	Indels:	177
DB:	8	Gaps:	24

US-09-769-066-16 (1-549) x BH771003 (1-2391)

```
Qy          7 AspThrSerProValProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsn 26
              ||||||||||   |||   |||                ||||  :::   |||
Db       1579 GATACCTCAGTCGTAACTGACAATCCTTTCGCCTCGACGACCCTTCTTAAAAACTAT--- 1523

Qy         27 LeuSerThrSerProLeuThrSerSerValAlaSerGlyThrAsnLeuValLeuTyrAla 46
                 |||   ||||||:::::|||   :::|||   |||:::
Db       1522 ------GCCAGTGACTTGACAGCAGCTGTCCCTGCAGGCTACAACATTACG--------- 1478

Qy         47 AlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThr 66
                                     :::   :::||||||:::|||:::      ||||||
Db       1477 --------------------TCTATCACTAATGGCACGAGTACTTATACTGGTGCGACA 1439

Qy         67 GluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeu 86
              |||:::      |||   :::      |||      |||:::
Db       1438 ACTGCAGCGACACTGGCAACTTTCACAGCGGCCAACCCAACAGTTAGC------------ 1391

Qy         87 ValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThr 106
                 |||         |||   ::::::::::::      ||||||   |||
Db       1390 GCAACCCAAGCAAACAATAACTATACGGTCACGCTGACAGCAGCAGCACAAACGGCAACC 1331

Qy        107 ----------------------------------------ThrProThrSerValAsp 112
                                                      |||||||||:::
Db       1330 TTCAACTATGGCTACGTCTCAGGAGCACTCAACACGCCTGCTATACCTACTAGCCTGTCA 1271

Qy        113 MetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGlu 132
               :::      |||      :::|||                |||
Db       1270 GCGAGTGGGACGACAGGAGCAAATGTC---------ACACCACCA-------------- 1235

Qy        133 LeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThr 152
                                                 ||||||  :::      |||
Db       1234 ----------------------------------ACTGGCTGGAATACAGCATCCACA 1211

Qy        153 SerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySer 172
               :::  ||||||     :::          |||          :::     |||:::
Db       1210 GCGACAGTGGCT---AATAAAATCCCTTATGGATATTATATCTCTGCCATATATGCTGGA 1154

Qy        173 ProValAsnSerTyrThrAsnThrProTyr---------ThrGlyAlaLeuGly-LeuLe 189
              ||||||   |||   ||||||                ||||||      ||| |||
Db       1153 ------AACTCTGCGACAGGAACACCGATAGCCACAGGGACGGGAACAACCGGAACTGGC 1100

Qy        189 uAspPheAlaLeuGluLeuGluPheArgAsnLeuThr---------ThrCysAsnThrAs 206
                       |||:::         ||||||                |||||
Db       1099 GCAAATGCTGCCTTCCCTGCAACTGGTCAGACTTACGGTGCAACTGGTAATCAATACTAT 1040

Qy        206 nThrArgValSerArgTyrSer---SerThrAlaArgHisArgLeuArgArgGlyAlaAs 225
               ::::::|||   ||||||      |||:::  |||          |||  ||
Db       1039 -GTTCAACTCTCGCCATACTCAGTCAGAACTTCTTGGCACATTTCAGTATTAGGAACTGA 981

Qy        225 pGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheTh 245
              |
Db        980 CCCC------------------------------------------------------- 977

Qy        245 rGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAl 265
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Db        976 ----------------------------------------------------GATTACCT 969
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Qy        265 aAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPh 285
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Db        968 TGATACT---CTTGGAGGT---------CAGTATGCGGGTTATGTGGGAGGTCAAGCCAC 921

Qy        285 eTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerVa 305
                 :::                |||                        |||:::
Db        920 TCCTAATGCCCAAACCTTCATGATGAATGATGTTAATAATTCTACGCCTTTAACGACGAC 861

Qy        305 lGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeuGlyAspSe 325
               :::|||                |||      |||
Db        860 AGATAATATTGTCTATACAGATGGTGCAGGAATT------------------------- 827

Qy        325 rArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerPr 345
               |||   :::|||      |||                        :::      |||   :::
Db        826 -CGTTATATTATCACAGGCTATACCTATTCTTTGACCAGTAACTCGGCAACAGGAACGAC 768

Qy        345 oAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuTh 365
                ||:::      |||:::   |||                              |||
Db        767 TTATCCGACA------TTTACAGCTCTT--------------------------CTTGC 741

Qy        365 rAlaAlaGluTyr---AspGlnSerThrTyrGlySerSerThrGlyProVal-------- 381
               |||       |||             ||||||   ::   |||      |||
Db        740 CGCCAATCCTTATATGCCTGTCGGAACATACAATGCTCCGACGCAGTATGTCACGGTGAA 681

Qy        382 -TyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAla-------- 398
                |||||||||      ::::::  :::      |||  :::
Db        680 TATGATTTCTGATCAGACGAGTATAACGTCTAATTTGACAAGTAGCACAACACCGTTAAC 621

Qy        399 ------------------------------ValAlaArgSerLeuAspTrpSerLysVa 408
                                             :::      |||  |||      ||
Db        620 CCCAGCAACGAACTATATGCCTATCAACGATATCACGGCAAGTACAGATATTGATGGTGT 561

Qy        408 lThrLeuAspGlyArgPro---------------------------------------- 414
               |      ||||||   |||
Db        560 AGATGATGACGGTCTACCTTATGCTATCAATGGCTATAATGCCGTGACGAATATCGTAGG 501

Qy        415 ----------------------------------------LeuProThrValGluGl 420
                                                      ||||||   :::
Db        500 CGCCACGACTAACTACTGGGGAGATGCGACAAACTCTCTGAAACTTCCG---ATTGGCTC 444

Qy        420 nTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGl 440
               |||::::::   |||:::   |||          |||   |||      ::::::|||
Db        443 ATACACAGAAAATTTCTATGCGCTTAATTACTTGGGA---CTTCAGGCTTATCAAGCACA 387

Qy        440 yThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIl 460
               :::|||                |||   |||   ||||||                ::
Db        386 GTCAACA--------------------TACACGACAGTCGCTAGCTTTCTTCAAAGTCT 348

Qy        460 eGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGl 480
               :   :::|||         :::      :::|||:::   ||||||          |||
Db        347 GTCTAGTGCCAATCTGGCAAAATACACGGTAAGTTCAACAACCACACTAACCGTCGCTGA 288

Qy        480 yProValAlaIleSerAla 486
                     |||||||||
Db        287 TGCAACGACTATTTCGGCA 269
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RESULT 2
BC054075/c

LOCUS	BC054075 1778 bp mRNA linear HTC 03-JUL-2003
DEFINITION	Mus musculus cDNA clone IMAGE:5056392.
ACCESSION	BC054075
VERSION	BC054075.1 GI:32449938
KEYWORDS	HTC.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 1778)
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 1778)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (24-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 113 Row: k Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
This clone has the following problem: no 5' EST match.

FEATURES Location/Qualifiers

source 1. .1778
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5056392"
/tissue_type="Lung, 2 pooled mouse tumors."
/clone_lib="NCI_CGAP_Lu33"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac"

ORIGIN

Alignment Scores:

Pred. No.:	0.176	Length:	1778
Score:	121.50	Matches:	104
Percent Similarity:	36.32%	Conservative:	54
Best Local Similarity:	23.91%	Mismatches:	162
Query Match:	4.31%	Indels:	118
DB:	3	Gaps:	20

US-09-769-066-16 (1-549) x BC054075 (1-1778)

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Qy         10 ProValProAspValAspSerArgGlyAlaIleLeuArgArg---------GlnTyrAsn 26
              |||  |||         ||||||   ::::::|||
Db       1151 CCAACTCCT---------AGTAGGAATTCGGTGCTTCATCCTATAGAAATTCACAGCCAG 1101

Qy         27 LeuSerThrSerProLeuThrSerSerValAlaSer---------GlyThrAsnLeuVal 43
              ||||||:::      |||      :::||||||||||         |||         :::
```

```
Db       1100 TTATCAAGCAAGGCTTTGCCAGAGACAGTAGCTTCTGTAACAGAGGGCGCAGAAAACCTC 1041

Qy         44 LeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGly---Thr-AsnThrHi 62
              |||:::::::::  ::::::          |||      ::|||   ||| |||:::||
Db       1040 CTTTTTAGCTCCCGGATTTCAGTGTCTCAGCCATCAGGCAATGGCATGACTCAACAGCCA 981

Qy         62 sIleMetAlaThrGluAlaSerAsn---------TyrAlaGlnTyrArgValAlaArgAl 79
              |:::              |||:::     :::     :::         ||||||
Db        980 TCTGTCCCCCTGTGGGAGGTCTCACAGCCTCTAGTGGGTGTCCTGGCCACAAGCTCGGAC 921

Qy         79 aThrIleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSe 99
                     |||||||||:::  :::                 ||||||::::::
Db        920 AGATACCCTAATGAGACCACTGCTTGGATCGAACACCCA-GAGGAAGCCATCGCTCTAAG 862

Qy         99 rPheTrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSer-- 118
                 |||      ||||||:::||||||          :::|||      |||
Db        861 AGCACACCCTGGCATAACCACGTCACCCACAGACCCCACTTTTAGCAGTCAGCCTTCTGC 802

Qy        119 ------------------ThrAspValArgIleLeuValGln---ProGlyIleAlaSe 131
                               :::  |||           |||   ||||||::::::
Db        801 TCTATTTCAACCCCACTTTCATCTGTGTCTTTTGCTACCCAATTACCTGGTGTTTCGGA 742

Qy        131 rGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGl 151
               :::     :::  |||                                        ||
Db        741 GGACTCCTTCCTCTCTAGT-------------------------------------GA 721

Qy        151 uThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGl 171
               |  |||     |||                                        |||
Db        720 GGCCAGGGGAGCCTTAGAGTCA-----------------------------TGGCATAG 691

Qy        171 ySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPh 191
               |||||||||  |||:::|||:::  ||||||
Db        690 CTCCCCAGTCCCCAGTTTTACTGACCATCCTTATGTC---------------------CT 652

Qy        191 eAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerAr 211
               :::  |||          |||      |||  |||      :::      ||||||
Db        651 GAGCCCCGAGTCTTCCCTGAGACCACACACAGGGTGT---GTGTCTTGCGTTGTCTCATC 595

Qy        211 gTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuTh 231
               :::                |||                ||:::   :::
Db        594 ATTTCAACAAGAACTGGCCAGGAGCCTAACAGAGAAGGACATGGGGTCAGGCGACAGGCT 535

Qy        231 rThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGl 251
               |||  :::|||      ::::::      |||  :::   |||:::  |||||
Db        534 TGAGACTTTGTCTACTGCCTCGGTAGAGGCAAGTCATGTCTCTCCATTGAGCAGTGTGGG 475

Qy        251 yGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGl 271
               |                    |||      |||  :::
Db        474 C--------------------ACAGACCTCTCTGAACTTGAAGAG-------------;-- 450

Qy        271 yLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValVa 291
               |||  |||                          ||||||  ||||||||||||
Db        449 ----CCTCAAGAATTT--------------AATACGCTTTTCCCTTCCAGACCTGTGTT 409

Qy        291 lSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAs 311
               |||  :::      |||  |||  |||:::  :::     :::         ::
Db        408 TTCCTTTTCTTCCAGACCT---GTGGGGCTGTGGAAAGCCAGCATGGATGTGTCACCCGA 352

Qy        311 p---------LysGlyValAlaIle---------------------------------- 316
               :         |||:::||||||
Db        351 GGTGGATGTGAGTGGCATTGCCATCACTCAGGTGTACCCTTCCCATGGCCGCCTCTCCAC 292

Qy        317 -ProHisAspIleAsp------------------------------------------- 321
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Db        291 ACCAAGCTCACTGGATTCGACTTTTGGCTTCTCTGTCACCAGTGATCTAGTGATGTCATC 232

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Qy        334 ----------AsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgPr 350
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Db        171 CTTGACTGCAAATCAAAACAGTCCATCCTTTCCAGCTGGAAAGCCAAG-CCTTCTCA-CC 114
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Qy        350 oPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAs 370
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Qy        370 pGlnSerThrTyrGlySerSerThrGlyProValTyrIleSer 384
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```

RESULT 3
AK049595

```
LOCUS       AK049595               2419 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 7 days embryo whole body cDNA, RIKEN full-length
            enriched library, clone:C430049D20 product:hypothetical Serine-rich
            region containing protein, full insert sequence.
ACCESSION   AK049595
VERSION     AK049595.1  GI:26340339
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2419)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES                Location/Qualifiers
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                        /organism="Mus musculus"
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                        /db_xref="taxon:10090"
                        /clone="C430049D20"
                        /tissue_type="whole body"
                        /clone_lib="RIKEN full-length enriched mouse cDNA library"
                        /dev_stage="7 days embryo"
     CDS                40. .>2418
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                        InterPro)
                        putative"
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                        SMKPPISFLSSAASLGGYPLGKADLDHYTGRDSERSTRLSEKPPYSRYSSRNKSHDSV
                        YFLGGLEGRKTSGSLLTMWNGNSLSCTGSSPISRSGAASMPSSPKQVRKMNLQDHSTL
                        QPRLSRHKEPASENVSVRTRKYSGSSLSNMGAYSRSLPRLYKATDNQMSPLSLPPRSS
                        LGNSRRGQLGEKDLPHSLVDSDNYLNFSSLSSGASPYKTCLSEGNPYVSSALSVPASP
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                        SLRQSSETPQPVLRERKSSISSISGRDDLMDYHRRQREERLREQEMERLERQRLETIL
                        SLCAEYTKPEGRRLSAGTTVADVQKINKELEKLQLSDEESVFEDALVCPDARYRCHRK
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                        LPKTPEDIGEEQRTQELAAMEDARMVILNNLEELEQKIKDINDQMDESSRELDMECAL
                        LDGEQKSETAELMKEKEILDHLNRKITELEKNIVGEKTKEKVKLDAEREKLERLQELY
                        SEQKTQLDNCPESMREQLQQQLKRDADLLDVESKHFEDLEFQQLEHESRLDEEKENLT
                        QQLLREVAEYQRNIVARKEKISALKKQASHIVQQAQREQDHFVKEKNNLIMML"
ORIGIN
```

Alignment Scores:

Pred. No.:	0.318	Length:	2419
Score:	121.00	Matches:	94
Percent Similarity:	35.09%	Conservative:	66
Best Local Similarity:	20.61%	Mismatches:	177
Query Match:	4.29%	Indels:	119
DB:	3	Gaps:	17

US-09-769-066-16 (1-549) x AK049595 (1-2419)

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Qy          3 AlaProAlaHisAspThrSerProValPro--------------------AspValAsp 15
Db        129 GCCCCAAAACATGATGGAGAGCCTAAGCCCGAGGAAATACTCATCAAGTCTGAAGTTTAA 188

Qy         16 SerArgGlyAlaIleLeuArgArgGlnTyrAsn-Leu---------------------- 27
Db        189 AGCCAACGGGGACTATTCTGGCTCCTATTTAACCCTCTCCCAACCGGTGTCTGCCAAGAG 248

Qy         28 -SerThrSerProLeuThrSerSerValAlaSerGlyThrAsnLeuValLeuTyrAlaAl 47
Db        249 AAGCCCTTCTCCAATGGGCACCAGCGTCAGGAGCAGTCCCTCCTTG------------GC 296
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Qy        47 aProLeuAsnProProLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGl 67
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Qy        67 uAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuVa 87
Db       357 TCCTATTTCTTTCCTCAGTTCTGCAGCC------------------------------ 384

Qy        87 lProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrTh 107
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Qy       107 rProThrSerValAspMetAsnSerIleThrSerThrAsp------------ValArgIl 123
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Db       462 CTCAGAGAAGCCT----------------------CCCTATTCCAGATACAGCTCTAG 497

Qy       143 gAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaThrSerGl 163
Db       498 GAATAAATCTCATGACAGTGTCTACTTTCTAGGGGGGCTGGAAGGAAGAAAAACCTCTGG 557

Qy       163 yLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyr-- 182
Db       558 CTCGCTCCTGACCATGTGGAACGGAAATTCCTTGAGCTGCACTGGCTCGTCACCCATCAG 617

Qy       183 ----ThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuTh 201
Db       618 CAGGTCTGGGGCAGCGAGCATGCCTTCAAGTCCAAAGCAAGTCAGGAAGATGAACCTT-- 675

Qy       201 rThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuAr 221
Db       676 --------------------------CAGGACCACTCGACACTTCAGCCCAGGTTAAG 707

Qy       221 gArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAs 241
Db       708 CAGGCACAAGGAGCCGGCCTCAGAAAACGTCAGTGTGAGAACAAGGAAATACTCAGGG-- 765

Qy       241 pLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLe 261
Db       766 ----------AGCAGTCTGAGTAATATGGGTGCCTACAGCCGATCGCTTCCC---AGGTT 812

Qy       261 uLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGl 281
Db       813 GTATAAAGCCACAGACAACCAGATGTCGCCTCTCAGCCTGCCTCCAAGAAGTTCCCTGGG 872

Qy       281 y------------GlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPr 297
Db       873 CAATTCCAGAAGAGGTCAGTTA----------------------------------- 894

Qy       297 oThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIlePr 317
Db       895 ------------------------------GGAGAAAAGGAT------------CTACC 911

Qy       317 oHisAspIleAspLeuGlyAspSerArgValValIleGlnAsp---------------- 331
Db       912 TCATAGCCTAGTGGATAGTGACAATTACCTTAACTTTTCTTCTCTAAGCTCAGGGGCTTC 971

Qy       332 ----TyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgPr 350
Db       972 ACCCTATAAAACCTGTCTGTCAGAGGGAAATCCTTACGTAAGCTCCGCCCTCAGTGTTCC 1031

Qy       350 oPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAs 370
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Qy       370 pGlnSerThrTyr---GlySerSerThrGlyProValTyrIleSerAspSerValThrLe 389
Db      1092 TAGGGCTTCATACTCAGGGACCAGCCCAAGTCATTCCTTCATTTCTGGAGAGCCAGACCG 1151

Qy       389 uValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValTh 409
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Db      1152 AGTGCTTGTGGCC----------------AGGAGGAACTTCTCTTGTGGATCAATGGA 1193

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RESULT 4
AK050493
LOCUS       AK050493               3612 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult pancreas islet cells cDNA, RIKEN full-length
            enriched library, clone:C820004H04 product:hypothetical Serine-rich
            region containing protein, full insert sequence.
ACCESSION   AK050493
VERSION     AK050493.1  GI:26093966
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3612)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
```

Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Cells were provided by Hiroo Iwata (Department of Reparative Materials Field of Tissue Engineering Institute for Frontier Medical Sciences,Sakyo-ku,Kyoto,606-8507,Japan) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1. .3612
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ORIGIN

Alignment Scores:

Pred. No.:	0.588	Length:	3612
Score:	121.00	Matches:	94
Percent Similarity:	35.09%	Conservative:	66
Best Local Similarity:	20.61%	Mismatches:	177
Query Match:	4.29%	Indels:	119
DB:	3	Gaps:	17

US-09-769-066-16 (1-549) x AK050493 (1-3612)

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Qy         16 SerArgGlyAlaIleLeuArgArgGlnTyrAsn-Leu---------------------- 27
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Db        502 AGCCAACGGGGACTATTCTGGCTCCTATTTAACCCTCTCCCAACCGGTGTCTGCCAAGAG 561

Qy         28 -SerThrSerProLeuThrSerSerValAlaSerGlyThrAsnLeuValLeuTyrAlaAl 47
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Db        562 AAGCCCTTCTCCAATGGGCACCAGCGTCAGGAGCAGTCCCTCCTTG------------GC 609

Qy         47 aProLeuAsnProProLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGl 67
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Qy         87 lProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrTh 107
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Qy        107 rProThrSerValAspMetAsnSerIleThrSerThrAsp------------ValArgIl 123
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Qy        123 eLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeuHisTyrAr 143
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Qy        163 yLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyr-- 182
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Qy        201 rThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuAr 221
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Db        989 --------------------------CAGGACCACTCGACACTTCAGCCCAGGTTAAG 1020

Qy        221 gArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAs 241
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Db       1021 CAGGCACAAGGAGCCGGCCTCAGAAAACGTCAGTGTGAGAACAAGGAAATACTCAGGG-- 1078

Qy        241 pLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLe 261
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Db       1079 ----------AGCAGTCTGAGTAATATGGGTGCCTACAGCCGATCGCTTCCC---AGGTT 1125

Qy        261 uLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGl 281
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Db       1126 GTATAAAGCCACAGACAACCAGATGTCGCCTCTCAGCCTGCCTCCAAGAAGTTCCCTGGG 1185

Qy        281 y----------GlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPr 297
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Qy        297 oThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIlePr 317
                                              ::::::|||           :::||
Db       1208 ------------------------------GGAGAAAAGGAT-----------CTACC 1224

Qy        317 oHisAspIleAspLeuGlyAspSerArgValValIleGlnAsp---------------- 331
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Qy        332 ----TyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgPr 350
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Qy        350 oPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAs 370
              |   |||          |||      :::|||      |||   ::::::   :::::::||
Db       1345 TGCCAGTCCTCGTGTGGCTCGGAAGATGCTCCTGGCCTCCACCTCCTCTGATGACTTTGA 1404

Qy        370 pGlnSerThrTyr---GlySerSerThrGlyProValTyrIleSerAspSerValThrLe 389
              |:::::::::|||   |||:::|||            :::||||||
Db       1405 TAGGGCTTCATACTCAGGGACCAGCCCAAGTCATTCCTTCATTTCTGGAGAGCCAGACCG 1464

Qy        389 uValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValTh 409
              |||   ||||||                ||:::          :::
Db       1465 AGTGCTTGTGGCC-----------------AGGAGGAACTTCTCTTGTGGATCAATGGA 1506

Qy        409 rLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThr 424
              ||||||      |||   ::::::   |||   |||:::|||
Db       1507 GCTTGATGACTCTGATCTGGAAAGCCTAAGACAGTCGTCAGAAACT 1552
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RESULT 5
AY404468
LOCUS AY404468 3702 bp DNA linear GSS 12-DEC-2003
DEFINITION Mus musculus HCM1900 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY404468
VERSION AY404468.1 GI:39760445
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

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  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3702)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 3702)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .3702
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1. .>3702
                     /locus_tag="HCM1900"
ORIGIN

Alignment Scores:
Pred. No.:                0.61          Length:          3702
Score:                    121.00        Matches:         94
Percent Similarity:       35.09%        Conservative:    66
Best Local Similarity:    20.61%        Mismatches:      177
Query Match:              4.29%         Indels:          119
DB:                       9             Gaps:            17

US-09-769-066-16 (1-549) x AY404468 (1-3702)

Qy          3 AlaProAlaHisAspThrSerProValPro--------------------AspValAsp 15
              |||||| ||||||       |||  |||                      :::|||
Db        171 GCCCCAAAACATGATGGAGAGCCTAAGCCCGAGGAAATACTCATCAAGTCTGAAGTTTAA 230

Qy         16 SerArgGlyAlaIleLeuArgArgGlnTyrAsn-Leu---------------------- 27
              |||:::     :::          :::||| |||
Db        231 AGCCAACGGGGACTATTCTGGCTCCTATTTAACCCTCTCCCAACCGGTGTCTGCCAAGAG 290

Qy         28 -SerThrSerProLeuThrSerSerValAlaSerGlyThrAsnLeuValLeuTyrAlaAl 47
               |||   ||||||:::   :::||||||   |||      :::|||             ||
Db        291 AAGCCCTTCTCCAATGGGCACCAGCGTCAGGAGCAGTCCCTCCTTG-----------GC 338

Qy         47 aProLeuAsnProProLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGl 67
              |   :::                        ||||||   :::   :::|||
Db        339 CAAAATCCAGGGAAGCAAACAGTTCTGCGATGGAATTGATAAAAATATTTCCATGAAACC 398

Qy         67 uAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuVa 87
                  ::::::
Db        399 TCCTATTTCTTTCCTCAGTTCTGCAGCC------------------------------ 426

Qy         87 lProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrTh 107
                ::::::|||||||||   :::
Db        427 -------TCTCTTGGCGGCTATCCTCTTGGG---------------------------- 450

Qy        107 rProThrSerValAspMetAsnSerIleThrSerThrAsp------------ValArgIl 123
                          |||:::::      |||      |||                |||::
Db        451 -------AAAGCAGATTTGGATCATTATACTGGTCGAGACAGTGAGAGGTCCACCAGGCT 503

Qy        123 eLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeuHisTyrAr 143
              :    :::|||                          |||      |||       ||
Db        504 CTCAGAGAAGCCT----------------------CCCTATTCCAGATACAGCTCTAG 539

Qy        143 gAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaThrSerGl 163
              ||||:::          ||||||       |||      |||          ||||||||
Db        540 GAATAAATCTCATGACAGTGTCTACTTTCTAGGGGGGCTGGAAGGAAGAAAAACCTCTGG 599

Qy        163 yLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyr-- 182
              |   ::::::          :::|||:::   ::::::          :::::::|||
Db        600 CTCGCTCCTGACCATGTGGAACGGAAATTCCTTGAGCTGCACTGGCTCGTCACCCATCAG 659

Qy        183 ----ThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuTh 201
                  :::||||||      :::                 ::::::          ||||||
Db        660 CAGGTCTGGGGCAGCGAGCATGCCTTCAAGTCCAAAGCAAGTCAGGAAGATGAACCTT-- 717

Qy        201 rThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuAr 221
                                                 :::      ||||||   :::   ||||||
Db        718 --------------------------CAGGACCACTCGACACTTCAGCCCAGGTTAAG 749

Qy        221 gArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAs 241
              |||      :::      :::|||      :::              ::::::
Db        750 CAGGCACAAGGAGCCGGCCTCAGAAAACGTCAGTGTGAGAACAAGGAAATACTCAGGG-- 807

Qy        241 pLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLe 261
                  :::   |||:::  :::|||          |||  :::          ||
Db        808 ----------AGCAGTCTGAGTAATATGGGTGCCTACAGCCGATCGCTTCCC---AGGTT 854

Qy        261 uLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGl 281
              |          |||      :::      |||                ||||||  ||
Db        855 GTATAAAGCCACAGACAACCAGATGTCGCCTCTCAGCCTGCCTCCAAGAAGTTCCCTGGG 914

Qy        281 y------------GlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPr 297
              |            |||||||||
Db        915 CAATTCCAGAAGAGGTCAGTTA------------------------------------ 936

Qy        297 oThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIlePr 317
                                                  ::::::|||          :::||
Db        937 ----------------------------GGAGAAAAGGAT------------CTACC 953

Qy        317 oHisAspIleAspLeuGlyAspSerArgValValIleGlnAsp---------------- 331
              ||||   :::        |||:::  :::
Db        954 TCATAGCCTAGTGGATAGTGACAATTACCTTAACTTTTCTTCTCTAAGCTCAGGGGCTTC 1013

Qy        332 ----TyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgPr 350
                  |||                ::      |||      |||  |||  |||  ||
Db       1014 ACCCTATAAAACCTGTCTGTCAGAGGGAAATCCTTACGTAAGCTCCGCCCTCAGTGTTCC 1073

Qy        350 oPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAs 370
              |   |||          |||      :::|||      |||   ::::::  ::::::||
Db       1074 TGCCAGTCCTCGTGTGGCTCGGAAGATGCTCCTGGCCTCCACCTCCTCTGATGACTTTGA 1133

Qy        370 pGlnSerThrTyr---GlySerSerThrGlyProValTyrIleSerAspSerValThrLe 389
              |:::::::::|||   |||:::|||          :::||||||
Db       1134 TAGGGCTTCATACTCAGGGACCAGCCCAAGTCATTCCTTCATTTCTGGAGAGCCAGACCG 1193

Qy        389 uValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValTh 409
                |||   ||||||                    |||:::                 :::
Db       1194 AGTGCTTGTGGCC-----------------AGGAGGAACTTCTCTTGTGGATCAATGGA 1235

Qy        409 rLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThr 424
                ||||||          |||   ::::::   |||   |||:::|||
Db       1236 GCTTGATGACTCTGATCTGGAAAGCCTAAGACAGTCGTCAGAAACT 1281

RESULT 6
CL953164
LOCUS       CL953164               2707 bp    DNA     linear   GSS 21-SEP-2004
DEFINITION  OsJRUA000119 Oryza sativa Express Library Oryza sativa (indica
            cultivar-group) genomic, genomic survey sequence.
ACCESSION   CL953164
VERSION     CL953164.1  GI:52365173
KEYWORDS    GSS.
SOURCE      Oryza sativa (indica cultivar-group)
  ORGANISM  Oryza sativa (indica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
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REFERENCE   1  (bases 1 to 2707)
  AUTHORS   Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
            Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
            Wong,G.K.S., Deng,X.W. and Wang,J.
  TITLE     An analysis of transcriptional regulation of the rice genome and
            its comparison to Arabidopsis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Chen Chen
            Department of Bioinformatic
            Beijing Institute of Genomics
            Chinese Academy of Sciences, Beijing 101300, China
            Tel: 86-10-80481559
            Fax: 86-10-80488676
            Email: chenchen@genomics.org.cn
            Rice genomic sequence.
            Class: exon-trapped.
FEATURES             Location/Qualifiers
     source          1. .2707
                     /organism="Oryza sativa (indica cultivar-group)"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:39946"
                     /clone_lib="Oryza sativa Express Library"
                     /note="Oryza sativa exon trapped genomic sequences "
ORIGIN

Alignment Scores:
Pred. No.:                0.62          Length:          2707
Score:                    119.00        Matches:         124
Percent Similarity:       32.45%        Conservative:    71
Best Local Similarity:    20.63%        Mismatches:      208
Query Match:              4.22%         Indels:          199
DB:                       9             Gaps:            27

US-09-769-066-16 (1-549) x CL953164 (1-2707)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              |||  |||           :::  |||  |||       :::|||  |||:::
Db        215 GCCAGCGCCGCCTGCCGTCCCTCCGTCCCTCCTCCTCCGGCGGGCGCGCGGCCTGCCGTC 274

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||                        |||:::|||   |||
Db        275 CCTCGCCGC----------------------GCGACCGCCAGCGCCGCCTGCCGTCCG 310

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
                 :::|||          |||      ||||||
Db        311 CCGTCCCTCCTCCGCCAGCCTCCGTCGCCGCCTCCC---------------------- 346

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
                    |||  |||      |||      |||      |||||||||
Db        347 --------------ACCAGCGCCGGCCCGTCGGCGTCCCCCAGGCCCCAGCGCGCGACC 391

Qy         81 IleArgTyrArg--------------ProLeuValProAsnAlaValGlyGlyTyrAla 95
              |||  |||                 |||:::  |||  :::  |||  :::|||
Db        392 ACCAGAGCTCGCCGCTGCCGGAGCTCGCCCGTCTGCCCTGTGTCAGCAGGATGCCACGCA 451

Qy         96 ---IleSerIleSerPheTrpProGlnThrThrThrThrProThrSerValAspMetAsn 114
                 :::|||:::                |||:::||||||  |||  :::   |||
Db        452 AGGTTGTCTCTGGGCCTGACTACGATGACGAGTACAACGATGACTATGATGAGTATGATG 511

Qy        115 SerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGluLeuVal 134
              |||                 |||  |||:::||||||     :::
Db        512 AAGACTACG-----------ATGATTACGGTGAGACCGGGCACAGTGACGACATTCAGC 559

Qy        135 IleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGly 154
              |||      |||       |||           ||||||  :::
Db        560 ACCCCGTGAAGAAGG---------AGAAAGAGTCATCGAAGAAGTCCTCAAGTACGGTGC 610

Qy        155 ValAlaGluGluGluAla----------------------ThrSerGlyLeuValMet 166
              :::      :::|||                  :::     ::::::
Db        611 CTGTGCTTTGGAGATGCTCCATGTGCATGTTCGATAATCATGAAAGCATGGTGTATTGTG 670

Qy        167 LeuCysIleHisGlySerProValAsnSerTyrThrAsnThrPro-------------- 181
                |||:::  |||         |||         |||  |||
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Db        671 AGATGTGTG---GGGTTTTTCGAGAATCCTTTATGAAATCTGCCAAGGATGGTTCAATAA 727

Qy        182 -----------TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPhe 197
                        |||       ||||||                 |||
Db        728 AAGTCCATGGGATACCAAGTGATTTTGGGA----------------CACCTTCGATGC 769

Qy        198 ArgAsnLeuThr------ThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||      |||      |||||||||   :::   :::
Db        770 CGAAATCTGACTCTACAAAGATGCCA-GTGAATACTCGTACTACAGACTTT--------- 819

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
                                          ||||||     |||:::        :::
Db        820 --------------------------GATGGTGACCCTGAGATAAAGAATGCTAGCATA 852

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              :::                                                 :::||||||
Db        853 TCTCAT-------------------------------------GAGAAAGTTGGT--- 870

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                                                                  :::
Db        871 ----------------------------------------------------TCCACA 876

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGly 295
                  :::|||||||||                          |||:::::|||
Db        877 CAGTACACATCTGCTGGT--------------------------AGCTCATCAGGC 906

Qy        296 GluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAla 315
                                                  ::::::   |||   :::|||
Db        907 GCT--------------------------------GGGAAAAAGGTGAAACACATTGCA 933

Qy        316 IleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAsp---TyrAspAsn 334
              :::|||   |||:::  :::     :::     :::|||   |||   :::
Db        934 CTTCCTGAAGATGTGCCTGTCGAGAGGACAGCTCAATTGATTTCTGATCATTTTCAGCTG 993

Qy        335 GlnHisGluGlnAspArgProThrProSerProAlaProSerArgProProheSerValLeu 354
              :::   :::|||                |||  |||  :::      :::
Db        994 AAGGAGGACCAGAGTAGTAGGGCTACCAGTTCTGCACAGAATGAGGATGTGGCCCAGAAA 1053

Qy        355 ArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyr 374
                  ::::::|||:::     |||  |||       |||  |||
Db       1054 CTTTCTTCTGACATACAGAAGCTAGGTTTAGAAAAGAATGAAGTAGAT------------ 1101

Qy        375 GlySerSerThrGlyProValTyrIleSerAspSerVal---------------ThrLeu 389
                       |||       |||:::  :::
Db       1102 ---------ACTGCAAAACCTTATTTACCTGAAGAATATAAGCCTGAGAAGTGGATGTTC 1152

Qy        390 ValAsnValAlaThrGlyAla--------------GlnAlaValAlaArgSerLeuAsp 404
                 |||      :::|||                  |||:::         :::|||
Db       1153 GCTAATGAGGAATCAGGAGTGCTGAGCCAACTAAACCTTGCAATAGTAGGTCATGTTGAT 1212

Qy        405 TrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThr 424
                  |||  ||||||  ||||||  |||      :::  :::  ||||||
Db       1213 TCTGGCAAGTCAACACTCTCTGGGAGACTGCTACATCTGTTAGGAAGGATATCGAAAAAA 1272

Qy        425 PhePhe---------------ValLeuProLeuArgGlyLysLeuSerPhe--------- 436
                                    :::|||||   ||||||
Db       1273 GATATGCACAAGAATGAGAAGGAGGCTAAAGAAAAAGGAAAAGGATCATTTGCTTATGCG 1332

Qy        437 Trp--------------------------GluAlaGlyThrThrLysAlaGlyTyrPro 447
                 |||                     |||  |||  |||
Db       1333 TGGGCTATGGATGAAAGCAGTGAAGAAAGAGAAAGAGGCGTGACAATGACT---GTGGCC 1389

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArg 467
                  |||      |||          ::::::::::   ::::::   ||||||:::
Db       1390 GTGGCTTATTTGGAGACCAAGAAGTACCGTGTAGTTTTGCTTGACTCTCCAGGCCATAAA 1449

Qy        468 ValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAla 487
                       :::      :::  :::|||                 ||||||
Db       1450 -----------GATTTTGTACCAAATATGATATCTGGCGCAACGCAAGCTGATGCAGCT 1497

Qy        488 AlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGly 507
                 ::::::
Db       1498 ATTCTTGTTGTT---------------------------------------------- 1509
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Qy        508 ArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCys 527
Db       1510 -----------------GATGCTTGCACTGGTTCATTTGAAGCTGGCATGGACGGTGAA 1551

Qy        528 AlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLysValGlyLysThrArg 547
Db       1552 GGAGGGAAAAGT-------------------------------GTTGGCCAGACAAAA 1578

Qy        548 Glu 548
Db       1579 GAA 1581

RESULT 7
CL972913/c
LOCUS       CL972913               3822 bp    DNA     linear   GSS 21-SEP-2004
DEFINITION  OsIFCC023739 Oryza sativa Express Library Oryza sativa (indica
            cultivar-group) genomic, genomic survey sequence.
ACCESSION   CL972913
VERSION     CL972913.1  GI:52400355
KEYWORDS    GSS.
SOURCE      Oryza sativa (indica cultivar-group)
  ORGANISM  Oryza sativa (indica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 3822)
  AUTHORS   Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
            Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
            Wong,G.K.S., Deng,X.W. and Wang,J.
  TITLE     An analysis of transcriptional regulation of the rice genome and
            its comparison to Arabidopsis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Chen Chen
            Department of Bioinformatic
            Beijing Institute of Genomics
            Chinese Academy of Sciences, Beijing 101300, China
            Tel: 86-10-80481559
            Fax: 86-10-80488676
            Email: chenchen@genomics.org.cn
            Rice genomic sequence.
            Class: exon-trapped.
FEATURES             Location/Qualifiers
     source          1. .3822
                     /organism="Oryza sativa (indica cultivar-group)"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:39946"
                     /clone_lib="Oryza sativa Express Library"
                     /note="Oryza sativa exon trapped genomic sequences "
ORIGIN

Alignment Scores:
Pred. No.:              1.72          Length:         3822
Score:                  117.00        Matches:        119
Percent Similarity:     31.26%        Conservative:   77
Best Local Similarity:  18.98%        Mismatches:     239
Query Match:            4.15%         Indels:         192
DB:                     9             Gaps:           25

US-09-769-066-16 (1-549) x CL972913 (1-3822)

Qy         10 ProValProAspValAspSerArgGlyAlaIleLeu---------------ArgArgGln 24
Db       2789 CCACCGCCGAGGCTCGACGAGAACGCCGTGCAGTTCACCTCCCCGGACCGCCGCCGCCGC 2730

Qy         25 TyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThrAsnLeuValLeu 44
Db       2729 ACCGCGATCAGCACGAGCACGATCACCAGCAGC-------------------------- 2697

Qy         45 TyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsnThrHisIleMet 64
Db       2696 ----------------------------------------ACCACCGACAGCGTCACC 2679

Qy         65 AlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArg 84
Db       2678 GCCGCCGACACCAGCGCGATCGTC---------GCCGACCGCAGCGCCGACCGGCCGCCG 2628

Qy         85 ProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThr 104
Db       2627 CCGCCGACGCCGCAGCTCACCAGCGGG--------------------TGGCCGCAGAGC 2589

Qy        105 ThrThrThrProThrSerValAspMet------------AsnSerIleThrSerThrAsp 120
Db       2588 CGCGCGTTGCCGGCGAACGCGCCACGCGGCCACCGCGAGAACTCGCTCCCCAGCCTCCCC 2529

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
Db       2528 TGCAGCTGGTTGCTGGACAAATCCAGCTGCACCAAGCTGCTCATCCCGGCG--------- 2478

Qy        141 HisTyrArgAsnGlnGly-----------------------TrpArgSerValGluThr 152
Db       2477 ---------AGCTGCGGCGGCACAGCTCCGGCGAGCGCGTTGTGGGAGAGATTCAAGCTC 2427

Qy        153 SerGlyValAlaGluGluGluAlaThrSerGlyLeuVal---------MetLeuCysIle 169
Db       2426 TCCAGCTTGGAGAGCGACCCGAGCGACGCCGGGATGCTGCCGCTGAGATCGTTGCTGCTC 2367

Qy        170 HisGlySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGly------ 187
Db       2366 AAATCCAGCAAGCTCTGCAGCTCTTGCAGCTGGCCAATGTCGGGAGGGATCGGGCCGGAC 2307

Qy        188 -------------------------------LeuLeuAspPheAlaLeuGlu------ 194
Db       2306 AAGAGATTCCGCGACAGGTTCAGCTCGTACAGGTTGATCAGCTTCGCGAGGGTAGCCGGA 2247

Qy        195 ------------------LeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArg 208
Db       2246 ATCTCGCCGGAGAGCTGGTTGCCGGCCAGGTTGAGCACGTTGAGCGAGACCAAGCTGCCG 2187

Qy        209 ValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAla 228
Db       2186 ATCTCC-----------------------------------------GATGGCACTGTT 2169

Qy        229 GluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHis------------Phe 244
Db       2168 CCATTGATCTGGTTGCCGTCGAGCGAGAGCTTGATGAGCTTGGAGCAGTTGCTGAGCTGG 2109

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
Db       2108 ACGGGCACCGGCCCGGTGAGCTCGTTGCCGGAGAGCGCCAGCTCACCGAGCTCCGGCAGC 2049

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeu 284
Db       2048 GCGCCGACCCACGCCGGCACGGGGCCGGACAGCCGGTTGCCGCTGAGGGCG------ATG 1995

Qy        285 PheTyrSerArgPro---ValValSerAlaAsnGlyGluProThrValLysLeuTyr--- 302
Db       1994 TGGCTGAGCCGCGCGCACCGCGCGAGGGCGTCCGGGATGCCGCCGGTGAGCGCGTTCCCC 1935

Qy        303 ------ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
Db       1934 GACGCGTCGAGCATCGTCAGCGCG--------------GCGGCGTTGCCGAGCGCCGCC 1890

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
Db       1889 GGGATCGGGCCGGACAGCGCGTTGCTCCCGAAGCGGACGCGCTGGAGCGACCGCGACCGG 1830

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAsp------ 358
Db       1829 CCGAGCTGCGCCGGGATGCCGCCGGAGAAGGAGTTGTTGGTGGCGTCGAACGACAGGAGC 1770

Qy        359 ------------------------------------ValLeuTrpLeuSerLeuThr 365
Db       1769 CTCGCCGAGCCGCAGAGCGGCAGGAGGCTGCCGGCGAGCCGGTTGTGCGCGATGTTGACG 1710

Qy        366 AlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro-------------- 380
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Db       1709 CGGGTGATGTTCCGGCACTCGAACATGCCGTCGGGGACGTCGCCGGCGAGCGAGTTGTTG 1650

Qy        381 ------ValTyrIleSerAspSerValThrLeuValAsnValAla---------------- 393

Db       1649 TACAGCATGAGCTGCTCCAGCGACCGGAGCCTCCCGAACGTCGCCGGGATCTCGCCGGAG 1590

Qy        393 ------------------------------------------------------------ 393

Db       1589 AGCGCGTTGTCGGCTAGGTCGAGGACGGCGAGGTTCACGCAGTCGCCGAGCTCCGGCGGG 1530

Qy        394 --------------------------------ThrGlyAlaGlnAlaValAlaArgSer 402

Db       1529 ATCCGGCCGGACAGCTCGTTCTGCCGGAGATGGAGGAACGCCAGCTCGGAGAGCTTCCCG 1470

Qy        403 LeuAspTrpSerLysValThrLeuAspGlyArgPro----------------------- 414

Db       1469 ATGGACGCCGGCAAGCTGCCGTTGAACCGGTTCCCGAAGAAATCAACCATCTGCAAGCTC 1410

Qy        415 ------LeuProThrValGluGlnTyrSer------LysThrPhePheValLeuProLeu 430

Db       1409 GAGCACTCCCCGATCGTCTCCGGTATCTCGCCGGAGAAGTCGTTC---------TCGTAC 1359

Qy        431 ArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGly------------Tyr 446

Db       1358 AGGAAGAGCACCTCGAGGTTCACGAGGCGGCCGACGGCGTCCGGCAGCCGGCCGGTGAGC 1299

Qy        447 ProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHis 466

Db       1298 CCGTTGTGATACAATGCGAGGACCTTGAGCTCGGTGAGGTTGAAGAGCTCCGGCGGGAGC 1239

Qy        467 Arg------------ValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482

Db       1238 TCGCCGGAGAGGGTGTTGTTGTTGAGCAGCAGGTCCGTCAGGTTGCCGAGCTCGCCGAGC 1179

Qy        483 AlaIleSerAlaAlaAlaVal------LeuAlaProArgSerAlaLeuAlaLeuGluGlu 500

Db       1178 GCCGCCGGGATCGCGCCGGTGAGGCTGTTGTTCGCCAGGTCGAGCTGCGTCAGCGCCCGG 1119

Qy        501 AspThrPheAspTyrProGly 507

Db       1118 CACCGCGAGAGCCCCCCCGGT 1098
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RESULT 8
CF870156
LOCUS CF870156 759 bp mRNA linear EST 31-OCT-2003
DEFINITION tric021xl12.b1 T.reesei mycelial culture, Version 6 October 2003 Hypocrea jecorina cDNA clone tric021xl12, mRNA sequence.
ACCESSION CF870156
VERSION CF870156.1 GI:38124838
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE 1 (bases 1 to 759)
AUTHORS Diener,S.E., Dunn-Coleman,N., Foreman,P., Houfek,T.D., Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K., Ward,M. and Dean,R.A.
TITLE Characterization of the protein processing and secretion pathways in a comprehensive set of expressed sequence tags from Trichoderma reesei
JOURNAL FEMS Microbiol. Lett. 230 (2), 275-282 (2004)
COMMENT Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph_dean@ncsu.edu
Seq primer: LT-F1 primer.
FEATURES Location/Qualifiers
source 1. .759
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="tric021xl12"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October 2003"
/note="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."
ORIGIN

Alignment Scores:

Pred. No.:	0.211	Length:	759
Score:	115.50	Matches:	74
Percent Similarity:	37.66%	Conservative:	42
Best Local Similarity:	24.03%	Mismatches:	104
Query Match:	4.10%	Indels:	89
DB:	7	Gaps:	11

US-09-769-066-16 (1-549) x CF870156 (1-759)

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Qy         12 ProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThrSerPro 31

Db         15 CCTGATATAGCTTCAAAATGGCCATTACCAAGGTTCACGCTCGCTCTGTCTACGACTCCC 74

Qy         32 LeuThrSerSerValAlaSerGlyThrAsnLeuValLeuTyrAla------AlaProLeu 49

Db         75 GTGGCAACCCCACCGTGGAGGTCGACCTCGTCACTGACACTGGCCTGCACCGCGCCATTG 134

Qy         50 AsnProProLeuProLeuGlnAspGlyThr------AsnThrHisIleMetAlaThrGlu 67

Db        135 TCCCCTCCGGTGCCTCTACCGGCCAGCACGAGGCTGTCGAGCTTCGAGATGGCGACAAGG 194

Qy         68 AlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuVal 87

Db        195 CCAAGTGGG--------------GTGGCAAGGGTGTCACCAAGG--------------- 224

Qy         88 ProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThr 107

Db        225 ----------------------------------------CCGTCGAGAACGTCAACA 242

Qy        108 ProThrSerValAspMetAsnSer--------------------------------Ile 116

Db        243 CCATCATCGGCCCCGCTCTCATCAAGGAGAACCTTGATGTCAAGGACCAGTCCAAGGTCG 302

Qy        117 ThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIlePro 136

Db        303 ACGAGTTCCTGAACAGCCTTGACGGCACCCCCAACAAGGGCAAGCTCGGTGCCAACGCCA 362

Qy        137 SerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAla 156

Db        363 TCC--------------------------------TCGGTGTCAGCTTG-GCTGTTGCC 388

Qy        157 GluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSer 176

Db        389 AAGGCCGGTGCCGCTGAGAAGAACGTCCCCCTGTACGCCCACATCTCCGACCTT---GCC 445

Qy        177 TyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGlu 196

Db        446 GGAACCAAGAAGCCCTAC-------------------------GTCCTCCCCGTTCCC 478

Qy        197 PheArgAsnLeuThrThrCysAsnThrAsnThrArg---------------------- 208

Db        479 TTCATGAACGTCCTCAACGGCGGTTCCCACGCCGGTGGCCGTCTTGCCTTCCAGGAGTTC 538

Qy        209 ------ValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGly 226

Db        539 ATGATTGTTCCTTCAGAGGCTCCCAGCTTCTCCGAGGCCCTTCGCCAGGGCTCCGAGGTC 598

Qy        227 ThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGly 246
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Db        599 TACCAGAAGCTGAAGACCCTGGCCAAGAAGAAGTAC---------------------- 634

Qy        247 LeuAsnGlyValGlyGluValGlyArgGly-IleAlaLeuThrLeuLeuAsnLeuAlaAs 266
                                 |||:::    :::|||   :::         :::
Db        635 --------------------GGCCAGTCCGCTGGCAACGTCGGCGACGAGGGTGGTGTC 673

Qy        266 pThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTy 286
                 :::     |||||||||   |||:::||||||:::         |||
Db        674 GCTCCCGATATCCAGACTGCCGACGAGGCTCTTGAGCTCATCACCGACGCCATTG----- 728

Qy        286 rSerArgProValValSerAla 293
               |||||||||         |||
Db        729 -AGCAGGCCGGCTACACTGGCA 749

RESULT 9
CB900324
LOCUS       CB900324                828 bp    mRNA    linear   EST 02-JUL-2003
DEFINITION  tric021xl12 T.reesei mycelial culture, Version 3 april Hypocrea
            jecorina cDNA clone tric021xl12, mRNA sequence.
ACCESSION   CB900324
VERSION     CB900324.1  GI:30114982
KEYWORDS    EST.
SOURCE      Hypocrea jecorina (anamorph: Trichoderma reesei)
  ORGANISM  Hypocrea jecorina
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE   1  (bases 1 to 828)
  AUTHORS   Foreman,P.K., Brown,D.E., Dankmeyer,L., Dean,R., Diener,S.,
            Dunn-Coleman,N.S., Goedegebuur,F., Houfek,T.D., England,G.J.,
            Kelley,A.S., Meerman,H.J., Mitchell,T., Mitchinson,C.,
            Olivares,H.A., Teunissen,P.J., Yao,J. and Ward,M.
  TITLE     Transcriptional regulation of biomass-degrading enzymes in the
            filamentous fungus Trichoderma reesei
  JOURNAL   J. Biol. Chem. 278 (34), 31988-31997 (2003)
  MEDLINE   22803314
   PUBMED   12788920
COMMENT     Contact: Pamela K. Foreman
            Genencor Intl.
            925 Page Mill Road, Palo Alto, CA 94304, USA
            Tel: (650) 846-7635
            Fax: (650) 621-7817
            Email: Pforeman@genencor.com
            Seq primer: LT-F1 primer.
FEATURES             Location/Qualifiers
     source          1. .828
                     /organism="Hypocrea jecorina"
                     /mol_type="mRNA"
                     /strain="QM6a"
                     /db_xref="taxon:51453"
                     /clone="tric021xl12"
                     /dev_stage="mycelia"
                     /clone_lib="T.reesei mycelial culture, Version 3 april"
                     /note="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial
                     culture grown from 24 hrs to 6 days with varying Carbon
                     and Nitrogen sources and concentrations."
ORIGIN

Alignment Scores:
Pred. No.:              0.241          Length:         828
Score:                  115.50         Matches:        74
Percent Similarity:     37.66%         Conservative:   42
Best Local Similarity:  24.03%         Mismatches:     104
Query Match:            4.10%          Indels:         89
DB:                     6              Gaps:           11

US-09-769-066-16 (1-549) x CB900324 (1-828)

Qy         12 ProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThrSerPro 31
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Db         84 CCTGATATAGCTTCAAAATGGCCATTACCAAGGTTCACGCTCGCTCTGTCTACGACTCCC 143

Qy         32 LeuThrSerSerValAlaSerGlyThrAsnLeuValLeuTyrAla------AlaProLeu 49
              :::   :::              |||:::   :::      |||      |||||||||

Db        144 GTGGCAACCCCACCGTGGAGGTCGACCTCGTCACTGACACTGGCCTGCACCGCGCCATTG 203

Qy         50 AsnProProLeuProLeuGlnAspGlyThr------AsnThrHisIleMetAlaThrGlu 67
              :::||||||:::||||||          |||      ::::::      |||||||||
Db        204 TCCCCTCCGGTGCCTCTACCGGCCAGCACGAGGCTGTCGAGCTTCGAGATGGCGACAAGG 263

Qy         68 AlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuVal 87
              |||           |||||||||   :::   |||
Db        264 CCAAGTGGG--------------GTGGCAAGGGTGTCACCAAGG---------------- 293

Qy         88 ProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThr 107
                                                     |||      |||:::|||
Db        294 ----------------------------------------CCGTCGAGAACGTCAACA 311

Qy        108 ProThrSerValAspMetAsnSer--------------------------------Ile 116
              |||:::|||     ::::::|||
Db        312 CCATCATCGGCCCCGCTCTCATCAAGGAGAACCTTGATGTCAAGGACCAGTCCAAGGTCG 371

Qy        117 ThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIlePro 136
              ||||||:::         :::       |||      ||||||   :::         |||
Db        372 ACGAGTTCCTGAACAGCCTTGACGGCACCCCCAACAAGGGCAAGCTCGGTGCCAACGCCA 431

Qy        137 SerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAla 156
              |||                                  ||||||              ||||||
Db        432 TCC--------------------------------TCGGTGTCAGCTTG-GCTGTTGCC 457

Qy        157 GluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSer 176
              :::       |||         |||  |||      |||   |||   :::   :::
Db        458 AAGGCCGGTGCCGCTGAGAAGAACGTCCCCCTGTACGCCCACATCTCCGACCTT---GCC 514

Qy        177 TyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGlu 196
              |||      ||||||                                |||   :::
Db        515 GGAACCAAGAAGCCCTAC--------------------------GTCCTCCCCGTTCCC 547

Qy        197 PheArgAsnLeuThrThrCysAsnThrAsnThrArg---------------------- 208
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Db        548 TTCATGAACGTCCTCAACGGCGGTTCCCACGCCGGTGGCCGTCTTGCCTTCCAGGAGTTC 607

Qy        209 ------ValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGly 226
                    |||       :::   :::          ||||||:::|||::::::
Db        608 ATGATTGTTCCTTCAGAGGCTCCCAGCTTCTCCGAGGCCCTTCGCCAGGGCTCCGAGGTC 667

Qy        227 ThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGly 246
                 :::|||   |||   |||       ::::::
Db        668 TACCAGAAGCTGAAGACCCTGGCCAAGAAGAAGTAC---------------------- 703

Qy        247 LeuAsnGlyValGlyGluValGlyArgGly-IleAlaLeuThrLeuLeuAsnLeuAlaAs 266
                                 |||:::    :::|||   :::         :::
Db        704 --------------------GGCCAGTCCGCTGGCAACGTCGGCGACGAGGGTGGTGTC 742

Qy        266 pThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTy 286
                 :::     |||||||||   |||:::||||||:::         |||
Db        743 GCTCCCGATATCCAGACTGCCGACGAGGCTCTTGAGCTCATCACCGACGCCATTG----- 797

Qy        286 rSerArgProValValSerAla 293
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Db        798 -AGCAGGCCGGCTACACTGGCA 818

RESULT 10
AK019649
LOCUS       AK019649                2368 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male testis cDNA, RIKEN full-length enriched
            library, clone:4930480I16 product:unknown EST, full insert
            sequence.
ACCESSION   AK019649
VERSION     AK019649.2  GI:26386767
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
```

TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2368)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT On Dec 10, 2002 this sequence version replaced gi:12859956.
Please visit our web site (http://genome.gsc.riken.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

FEATURES Location/Qualifiers
source 1. .2368
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:4930480I16"
/db_xref="taxon:10090"
/clone="4930480I16"
/sex="male"
/tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
CDS 299. .2116
/note="unnamed protein product; putative unknown EST (GB|BF468166, evidence: BLASTN, 99%, match=778)"
/codon_start=1
/protein_id="BAB31823.1"
/db_xref="GI:12859957"
/translation="MAATAAVSPSDYLQPAAATTQDSQPSPLALLAATCSKIGPPAVE AAVTPPAPPQPTPRKLVPIKPAPLPLSPCKNSFSILSSKGNILQIQGSQLSTSYPGGQ FVFAIQNPTLINKGSRSNASIQYQVPQIQGNSSQTIQVQPSLTNQIQVIPGTNQAITT PSTSGHKPVPIKPAPVQKSSTTTPVQSGANVVKLTGGGSNMTLTLPLNNLVNTSDIG GPAQLLTESPPTPLSKTNKKARKKSLPVSQPSVAVAEQVETVLIETTADNIIQAGNNL LIVQSPGGGQPAVVQQVVVPPKAEQQQVVQIPQQALRVVQAASATLPTVPQKPSQNF QIQTTEPTPTQVYIRTPSGEVQTVLVQDSPPATAATTSTVTCNSPALRAPHLSGTSKK HSAAILRKERPLPKIAPAGSIISLNAAQLAAAAQAMQTININGVQVQGVPVTITNTGG QQQLTVQNVSGNNLTISGLSPTQIQLQMEQALAGEAQPGEKRRRMACTCPNCKDGEKR SGEQGKKKHVCHIPDCGKTFRKTSLLRAHVRLHTGERPFVCNWFFCGKRFTRSDELQR HARTHTGDKRFECAQCQKRFMRSDHLTKHYKTHLGTKGL"

ORIGIN

Alignment Scores:

Pred. No.:	1.54	Length:	2368
Score:	114.50	Matches:	116
Percent Similarity:	30.85%	Conservative:	58
Best Local Similarity:	20.57%	Mismatches:	177
Query Match:	4.06%	Indels:	213
DB:	3	Gaps:	30

US-09-769-066-16 (1-549) x AK019649 (1-2368)

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Qy        48 ProLeuAsnPro---ProLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThr 66
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Db       482 CCTATCAAACCCGCTCCTCTCCCTCTCAGTCCCTGCAAGAATAGCTTTAGCATCTTATCA 541

Qy        67 GluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeu 86
                |||      |||  :::  ::::::  :::     |||
Db       542 TCTAAAGGAAATATACTTCAGATTCAGGGCTCCCAGCTGAGTACCTCCTAC--------- 592

Qy        87 ValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThr 106
               |||             :::||||||
Db       593 ---CCTGGAGGGCAGTTTGTGTTTGCAATCCAG------------------------- 622

Qy       107 ThrProThrSerValAspMetAsnSerIleThrSerThrAspValArg----------- 122
             ||||||   ::::::      |||   ::::::      ::::::
Db       623 AACCCCACCCTGATCAACAAAGGGAGCCGATCAAATGCAAGTATCCAGTACCAAGTCCCT 682

Qy       123 -------------------------IleLeuValGlnProGlyIleAlaSerGluLeu 133
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Db       683 CAGATCCAAGGGAACAGTTCCCAGACCATCCAGGTGCAGCCCAGTCTCACCAACCAGATC 742

Qy       134 ---ValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThr 152
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Db       743 CAGGTCATCCCAGGC-----------------------------------------ACC 760

Qy       153 SerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySer 172
             :::                ::::|||||||||          :::   |||     :::
Db       761 AACCAAGCCATCACCACCCCGTCAACATCTGGTCATAAGCCTGTCCCCATCAAGCCAGCT 820

Qy       173 ProVal------AsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeu--- 189
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Db        821 CCTGTCCAGAAGTCAAGTACGACTACCACCCCTGTGCAGAGCGGGGCCAACGTGGTGAAG 880
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Qy        204 AsnThrAsn-----------------------------------------ThrArgVal 209
Db        935 AACACCAGCGATATTGGGGGCCCTGCTCAGCTCCTCACTGAGAGCCCCCCCACCCCACTG 994
Qy        210 SerArgTyrSerSerThrAlaArgHisArg---------LeuArgArgGlyAlaAspGly 226
Db        995 TCTAAGACTAACAAGAAAGCTAGGAAGAAGAGCCTCCCTGTGTCACAGCCATCCGTAGCT 1054
Qy        227 ThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGly 246
Db       1055 GTGGCTGAGCAGGTGGAGACGGTGCTGATAGAGACCACGGCAGAC--------------- 1099
Qy        247 LeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAsp 266
Db       1100 -------------------------------------AACATCATCCAGGCAGGAAAC 1120
Qy        267 ThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyr 286
Db       1121 AACCTGCTG-----------------ATCGTCCAGAGCCCTGGCGGG------------ 1150
Qy        287 SerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerVal--- 305
Db       1151 ----------------------GGCCAGCCAGCTGTGGTCCAGCAAGTCCAGGTGGTG 1186
Qy        306 ---GluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeuGlyAsp 324
Db       1187 CCACCCAAGGCTGAGCAGCAGCAGGTGGTCCAGATCCCCCAGCAGGCA------------ 1234
Qy        325 SerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSer 344
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Qy        345 ProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeu 364
Db       1280 CAGAAGCCCTCTCAGAACTTTCAGATC------------------------------- 1306
Qy        365 ThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrIle--- 383
Db       1307 -----------------CAGACAACTGAACCAACACCAACC---CAGGTTTATATCCGT 1345
Qy        384 ------SerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArg 401
Db       1346 ACACCTTCTGGTGAGGTACAGACAGTCCTTGTCCAGGACAGCCCCCCAGCAACAGCTGCA 1405
Qy        402 SerLeuAspTrpSerLysValThr-----------------------------LeuAsp 411
Db       1406 ACCACA------TCAACCGTCACCTGTAACAGCCCTGCACTCCGAGCTCCCCATCTGAGT 1459
Qy        412 Gly-------------------------------------ArgProLeuProThrVal 418
Db       1460 GGCACCAGCAAAAAACATTCAGCTGCCATTCTCCGAAAAGAGCGGCCCCTGCCAAAG--- 1516
Qy        419 GluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
Db       1517 ----------------------ATTGCACCTGCTGGGAGCATCATCAGCCTGAACGCC 1552
Qy        439 Ala-----------------------------------------GlyThrThrLys 443
Db       1553 GCACAGCTGGCAGCAGCTGCTCAGGCCATGCAGACCATCAACATCAATGGTGTCCAAGTC 1612
Qy        444 AlaGlyTyrProTyrAsnTyr---AsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
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RESULT 11
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LOCUS AK080877 2907 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length enriched library, clone:B430115A06 product:unknown EST, full insert sequence.
ACCESSION AK080877
VERSION AK080877.1 GI:26348834
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2907)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,

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            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
  COMMENT   cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
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  Best Local Similarity:    20.57%       Mismatches:      177
  Query Match:              4.06%        Indels:          213
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  Qy       173 ProVal------AsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeu--- 189
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  Db       916 AACCTGCTG-----------------ATCGTCCAGAGCCCTGGCGGG------------ 945

  Qy       287 SerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerVal--- 305
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  Db       946 ----------------------GGCCAGCCAGCTGTGGTCCAGCAAGTCCAGGTGGTG 981

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RESULT 12
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DEFINITION  Mus musculus adult male olfactory brain cDNA, RIKEN full-length
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ACCESSION   AK078246
VERSION     AK078246.1  GI:26347082
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3013)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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ORIGIN

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Best Local Similarity:    20.57%        Mismatches:      177
Query Match:              4.06%         Indels:          213
DB:                       3             Gaps:            30

US-09-769-066-16 (1-549) x AK078246 (1-3013)

Qy         48 ProLeuAsnPro---ProLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThr 66
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Db        309 TCTAAAGGAAATATACTTCAGATTCAGGGCTCCCAGCTGAGTACCTCCTAC--------- 359

Qy         87 ValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThr 106
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Qy        107 ThrProThrSerValAspMetAsnSerIleThrSerThrAspValArg----------- 122
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Qy        153 SerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySer 172
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Qy        173 ProVal------AsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeu--- 189
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Qy        210 SerArgTyrSerSerThrAlaArgHisArg---------LeuArgArgGlyAlaAspGly 226
              |||:::   :::       ||||||   :::          :::   :::   :::
Db        762 TCTAAGACTAACAAGAAAGCTAGGAAGAAGAGCCTCCCTGTGTCACAGCCATCCGTAGCT 821

Qy        227 ThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGly 246
                 ||||||      |||                 |||
Db        822 GTGGCTGAGCAGGTGGAGACGGTGCTGATAGAGACCACGGCAGAC--------------- 866

Qy        247 LeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAsp 266
                                                  ::::::          :::
Db        867 -----------------------------------AACATCATCCAGGCAGGAAAC 887

Qy        267 ThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyr 286
              ||||||                  ::::::   |||   ||||||
Db        888 AACCTGCTG-----------------ATCGTCCAGAGCCCTGGCGGG------------ 917

Qy        287 SerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerVal--- 305
                                                  |||:::|||   |||              |||
Db        918 -----------------------GGCCAGCCAGCTGTGGTCCAGCAAGTCCAGGTGGTG 953

Qy        306 ---GluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeuGlyAsp 324
                    |||:::|||   :::   |||   ||||||
Db        954 CCACCCAAGGCTGAGCAGCAGCAGGTGGTCCAGATCCCCCAGCAGGCA----------- 1001

Qy        325 SerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSer 344
                 |||||||||                                      ||||||
Db       1002 CTGCGGGTGGTG--------------CAAGCTGCCTCTGCCACCCTCCCCACCGTCCCC 1046

Qy        345 ProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeu 364
                    ||||||:::   |||  :::
Db       1047 CAGAAGCCCTCTCAGAACTTTCAGATC------------------------------- 1073

Qy        365 ThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrIle--- 383
                             |||:::|||      :::   |||      ||||||||
Db       1074 -----------------CAGACAACTGAACCAACACCAACC---CAGGTTTATATCCGT 1112

Qy        384 ------SerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArg 401
                    |||      |||      |||   |||                |||   |||
Db       1113 ACACCTTCTGGTGAGGTACAGACAGTCCTTGTCCAGGACAGCCCCCCAGCAACAGCTGCA 1172

Qy        402 SerLeuAspTrpSerLysValThr----------------------------LeuAsp 411
              :::      |||   ||||||                              |||
Db       1173 ACCACA------TCAACCGTCACCTGTAACAGCCCTGCACTCCGAGCTCCCCATCTGAGT 1226

Qy        412 Gly-------------------------------------ArgProLeuProThrVal 418
              |||                                    ||||||||||||
Db       1227 GGCACCAGCAAAAAACATTCAGCTGCCATTCTCCGAAAAGAGCGGCCCCTGCCAAAG--- 1283

Qy        419 GluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
                                       :::   |||          :::|||
Db       1284 -----------------------ATTGCACCTGCTGGGAGCATCATCAGCCTGAACGCC 1319

Qy        439 Ala-----------------------------------------------GlyThrThrLys 443
              |||                                              |||
Db       1320 GCACAGCTGGCAGCAGCTGCTCAGGCCATGCAGACCATCAACATCAATGGTGTCCAAGTC 1379

Qy        444 AlaGlyTyrProTyrAsnTyr---AsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
              |||   |||             ||||||          ||:::   ::::::|||
Db       1380 CAGGGTGTGCCTGTCACCATCACCAACACTGGCGGGCAGCAGCAGCTGACCGTGCAGAAC 1439

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482
                 :::|||:::   :::   ||||||                ||||   |||
Db       1440 GTTTCTGGAAACAACCTGACTATCAGT-----------------GGGCTGAGCCCCACC 1481

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502
              |||                 |||                 |||||||||
Db       1482 CAGATCCAG-----------CTGCAGATGGAGCAGGCTCTAGCC--------------- 1514

Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAsp-----------------PheCys 516
                       |||   |||          :::                      |||
Db       1515 -----------GGAGAGGCCCAGCCTGGGGAGAAACGGCGGCGCATGGCCTGCACGTGT 1562

Qy        517 ProGluCysArg 520
              |||   |||:::
Db       1563 CCCAACTGCAAG 1574 .

RESULT 13
CL976421
LOCUS       CL976421               2313 bp    DNA     linear   GSS 21-SEP-2004
DEFINITION  OsIFCC028897 Oryza sativa Express Library Oryza sativa (indica
            cultivar-group) genomic, genomic survey sequence.
ACCESSION   CL976421
VERSION     CL976421.1  GI:52407355
KEYWORDS    GSS.
SOURCE      Oryza sativa (indica cultivar-group)
  ORGANISM  Oryza sativa (indica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 2313)
```

```
  AUTHORS   Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
            Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
            Wong,G.K.S., Deng,X.W. and Wang,J.
  TITLE     An analysis of transcriptional regulation of the rice genome and
            its comparison to Arabidopsis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Chen Chen
            Department of Bioinformatic
            Beijing Institute of Genomics
            Chinese Academy of Sciences, Beijing 101300, China
            Tel: 86-10-80481559
            Fax: 86-10-80488676
            Email: chenchen@genomics.org.cn
            Rice genomic sequence.
            Class: exon-trapped.
FEATURES             Location/Qualifiers
     source          1. .2313
                     /organism="Oryza sativa (indica cultivar-group)"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:39946"
                     /clone_lib="Oryza sativa Express Library"
                     /note="Oryza sativa exon trapped genomic sequences "
ORIGIN

Alignment Scores:
Pred. No.:                1.68          Length:          2313
Score:                    114.00        Matches:         133
Percent Similarity:       31.79%        Conservative:    66
Best Local Similarity:    21.25%        Mismatches:      245
Query Match:              4.04%         Indels:          182
DB:                       9             Gaps:            30

US-09-769-066-16 (1-549) x CL976421 (1-2313)

Qy          3 AlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIleLeuArg 22
              |||   |||      ::::::|||   |||                |||
Db        536 GCAACCGCAAGCTCATCGGCGCCCGCGCCTTCTTCCGGGGATATGGGGCCGGCGGCGGCG 595

Qy         23 ArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThrAsnLeu 42
                        |||   |||         ||||||         ||||||
Db        596 GGAACGGTTCCCACGTCAGCCTCG---------AGTTCTCCTCGCCGAGGGACCACGACG 646

Qy         43 ValLeuTyrAlaAlaProLeuAsn-----------ProProLeuProLeuGlnAspGly 58
              |||                               |||      |||   :::|||
Db        647 GTCACGGCACGCACACGGCGTCGACGGCGGCCGGCGCCGTCGTGGCCGACGCGGGACTCC 706

Qy         59 ThrAsnThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArg 78
              :::              ||||||     :::      |||   :::|||      |||
Db        707 TCG--------------GCTACGCGGAAGGCACGGCCCGCGGCATGGCGCCCGGTGCGC 751

Qy         79 AlaThrIleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIle 98
              |||:::   |||   |||                  ||||||      :::|||
Db        752 GCGTCGCGGCGTACAAGG--------------TGTGCTGGAGGCAGGGGTGTTTCAGCT 796

Qy         99 SerPheTrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSer 118
                 :::                  |||:::                          |||
Db        797 CCGACATACTAGCCGGCATGGAGAAGGCCATCGATGACG--------------GCGTCG 841

Qy        119 ThrAspValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGlu 138
              |||      |||   |||:::          :::         |||   ||||||
Db        842 ACGTTCTCTCGCTGTCTCTTGGCGGCGGCGCGTTCCCGCTCTCGCGTGACCCCATCGCGG 901

Qy        139 ArgLeuHisTyrArg------------AsnGlnGlyTrpArgSer--------------- 149
                       |||                ||||||:::
Db        902 TCGGCGCGCTCGCGGCCACTCGCCGCGGCATCGTCGTGGCGTGCTCCGCGGGGAACAGTG 961

Qy        150 ----------------------------------------------------------Val 150

Db        962 GTCCTTCTCCGTCGTCGCTGGTGAACACTGCTCCGTGGGTGATCACCGTCGGTGCAGGCA 1021

Qy        151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
              ::::::|||   :::          :::||||||
Db       1022 CGCTCGACAGGAACTTCCCGGCGTACGCCGAGCTCGGGAACG----------------- 1063

Qy        171 GlySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
                    |||      :::      :::||||||  ||||||
Db       1064 GCGAGACCCACGCCGGCATGTCGCTCTACTCCGGCGACGGGC----------------- 1105

Qy        191 PheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSer 210
                 :::                ||||:::   ||||||      :::
Db       1106 ---TCGGCGACGAGAAGCTCCCGGTCGTGTACAACAAAGGCATCCGCGCCGGCAGCAATG 1162

Qy        211 ArgTyrSerSerThrAlaArg-HisArgLeuArgArgGlyAlaAspGlyThrAlaGluLe 230
              |||   ||||||       ||| |||      |||   |||   :::|||
Db       1163 CGAGCAAGCTCTGCATGGAGGGCACGCTGGACGCGGCGGCGGTGAAGGGCAAGGT----- 1217

Qy        230 uThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyVa 250
                                  |||      :::   |||         |||
Db       1218 ----------GGTCCTGTGCGACCGCGGCGGCAACTCGAG---GGTGGAGAAGGGGCTGG 1264

Qy        250 lGlyGluValGlyArg-GlyIleAlaLeuThrLeuLeuAsn------------------ 263
              ||||||   ||||| |||:::   :::   |||   |||
Db       1265 TGGTGAAGCAGGCCGGCGGCGTCGGTATGGTGCTCGCGAACACCGCGCAGAGCGGCGAGG 1324

Qy        264 -----LeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyG 282
                  :::||||||:::   |||      ||||||         :::   :::      |
Db       1325 AGGTCGTGGCCGACAGCCACCTT------CTCCCCGCGGTGGCCGTCGGCGCCAAGAGCG 1378

Qy        282 lyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuT 302
              ||                ||       |||   ::::::   :::       |||   |||
Db       1379 GCGACGCCATA------AGGAGGTACGTGGAGTCGGACGCCGACGCCGAGGTGGGGCTAA 1432

Qy        302 yrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspL 322
                 :::                        |||   |||:::       |||:::
Db       1433 CCTTCGCC----------------------GGCACGGCGCTC------GACGTG---- 1458

Qy        322 euGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProT 342
                                                                  ||||||
Db       1459 ----------------------------------------------------CGGCCGG 1465

Qy        342 hrPro-----------------SerProAlaProSerArgProPheSerValLeuArgA 356
                 |||                  |||      |||:::|||      :::   |||
Db       1466 CGCCGGTGGTGGCCGCGTTCAGCTCGCGTGGGCCGAACAGGCAGGTGGCGCAGCTGCTCA 1525

Qy        356 laAsnAspValLeu---------------------------Trp---------------- 361
                 ||||||:::                            |||
Db       1526 AGCCGGACGTGATCGGGCCGGGGGTGAACATCCTCGCCGGCTGGACGGGGTCCGTCGGGC 1585

Qy        362 --LeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyr-----------GlySerS 377
                    ||||||      |||      :::|||   :::             |||:::|
Db       1586 CGACCGGACTCACCGTTGACGAG---CGGCGGTCGCCGTTCAACATCTTGTCAGGAACAT 1642

Qy        377 erThrGlyProValTyrIleSerAspSerValThrLeuValAsnValAla---------T 394
              ||           :::||||||                |||      |||
Db       1643 CCATGTCATGCCCGCACATCAGCGGCCTCGCCGCCTTCGTCAAGGCGGCACACCCGGACT 1702

Qy        394 hrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArgP 414
                    |||:::      :::|||      :::      |||:::|||
Db       1703 GGAGCCCCAGCGCAATCAAGTCGGCGCTCATGACCACCGCATACACCGTCGACAACACCG 1762

Qy        414 roLeuProThrValGluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysL 434
                 |||   |||:::      |||   |||
Db       1763 GCTCGCCGATCGTCGACGCCGCCAGCAACACC-----------------------ACGG 1798

Qy        434 euSerPheTrpGluAlaGlyThr---------------ThrLysAlaGlyTyrPro---T 448
                 :::   |||          |||                ||||||     |||
Db       1799 CGACGCCGTGGTCCATCGGCGCCGGCCACGTGGACCCCGTCAAGGCCCTCTCCCCGGGCC 1858

Qy        448 yrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgV 468
                 |||:::|||:::      |||   :::
Db       1859 TCGTCTACGACACCTCCGTCGACGACTACGTC-------------------------- 1890

Qy        468 alAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyPro---------ValAlaIleS 485
                          :::      :::|||      |||             ||||||:
Db       1891 -----------GCCTTCCTGTGCTCCGTCGGCACGTCGCCGCCGCAGGTCCAGGCCATCA 1939
```

```
Qy        485 erAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspT 505
              ::||||||      :::      :::      |||:::         |||      :::|
Db       1940 CGGCGGCGCCCAACGTGACGTGCCAGCGGAAGCTGTCCAGCCCCGGGGAC---CTCAACT 1996

Qy        505 yrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuG 525
              |||||      ::      |||                                |||   :
Db       1997 ACCCGTCGTTCTCCGTCGTGTTC----------------------------GGCCGGC 2026

Qy        525 lnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLysValGlyL 545
              ::      :::   :::||||||      :::   :::|||                |||||
Db       2027 GGTCGTCGTCGTCGCGCAGCACCACCGTCAAGTACCGGCGCGAGCTGACCAACGTCGGCG 2086

Qy        545 ysThrArgGluLeu 549
                 |||   :::
Db       2087 ACGGCAGGTCGGTG 2100
```

RESULT 14
BZ156047
LOCUS BZ156047 747 bp DNA linear GSS 11-OCT-2002
DEFINITION CH230-312A15.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone CH230-312A15, genomic survey sequence.
ACCESSION BZ156047
VERSION BZ156047.1 GI:23797001
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 747)
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M.
TITLE Rat BAC End Sequences from Library CHORI-230 MboI segment
JOURNAL Unpublished (1999)
COMMENT Other_GSSs: CH230-312A15.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 312 row: A column: 15
Seq primer: SP6
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .747
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-312A15"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI; CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by Pieter de Jong"
ORIGIN

Alignment Scores:

Pred. No.:	0.626	Length:	747
Score:	111.00	Matches:	73
Percent Similarity:	32.80%	Conservative:	29
Best Local Similarity:	23.47%	Mismatches:	113
Query Match:	3.94%	Indels:	97

```
DB:                    8              Gaps:         11

US-09-769-066-16 (1-549) x BZ156047 (1-747)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGly------ 18
              |||::::::||||||      |||:::          :::      :::||||||
Db         23 GCCCTGAGCCCCGCCTCCGG-ACAACTTATTACACAAACACGGGCGCGCGCGGACACGCA 81

Qy         19 ---AlaIleLeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAla 37
                 |||::::::|||   :::          :::       |||
Db         82 TGCGCACTCATACGTACCAGAAGCCCCTGAGCCCCGCCTCCGTACAACAGAGACACAAAC 141

Qy         38 SerGlyThrAsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGln--- 56
              :::||||||              |||      ||||||   ||||||         |||
Db        142 ACCGGCACACGCACTCACTCCTACCAGAAGCCTCTGAGGCCACCCTCCGGACCACAGAGA 201

Qy         57 --------------------AspGlyThrAsnThrHisIleMetAlaThrGluAlaSer 69
                                   |||:::||||||:::          |||||||||
Db        202 TACAAACACGGGCACGCGCACACGCACACGCATACACACTTACACGTACCGGAAGCCTCT 261

Qy         70 AsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsn 89
                 |||      |||   |||||||||                        ||||||
Db        262 GAG---GCCGCCCTCCGGACCGCACGCGCGCACCAGCACACGCACTCACACGTACCAGGA 318

Qy         90 AlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThr 109
              |||      |||      :::::::::|||
Db        319 GCCCGTGACGGCCCCCTTCTGACGTTATCG---------------------------- 348

Qy        110 SerValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIle 129
                                                                  |||
Db        349 ------------------------------------------------CCGCCAGCA 357

Qy        130 AlaSerGluLeuValIleProSer--------------------GluArgLeuHisTyr 142
                 |||:::   |||                             |||||||||
Db        358 ACGCATAGCCTACTTTCTCCACAACTACCCCAGATGTGGTTGTAAACAACCCTTCATTAC 417

Qy        143 ArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaThrSer 162

Db        417 ------------------------------------------------------------ 417

Qy        163 GlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyr 182
                           |||   ||||||          :::|||   ||||||
Db        418 --------------ATCATCCAGGGCTCGACCACCCGCGACCACACTAAAACTCCAAAG 462

Qy        183 ThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThr 202
                                    :::|||      :::   |||   :::
Db        463 CCC-----------------CAGCGTTCACTCACAAACAAAACACGCAGAATCCTTGGC 504

Qy        203 CysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArg 222
                    |||   |||              :::   |||:::   |||   |||:::|||
Db        505 GACTGTTTCAACCTGCGCAGATGCGAATTCCCCAGCTCGCCGCGCACACGCATGCGC--- 561

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
                                  ::|||      ||||||      |||         |||
Db        562 --------------ACTCCAATCACACTGGCGGCCGCTTGGTTTTTTCAGTTTGGTTTG 606

Qy        243 HisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeu 262
                                  |||:::   ||||||   :::|||
Db        607 TTTTGTTTTGCTCCACTAACTAAGGGACAGGCAGGCCGGGCCTTAGCC------------ 654

Qy        263 AsnLeuAla--------------------AspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||                      :::||||||      ||||||
Db        655 AACCTCCTCCCAGGTCGTCACAGCAACTAGGAAACTTTGGCTGCTCCTCTTCCCATGTCC 714

Qy        276 LeuIle------SerSerAlaGlyGlyGlnLeu 284
              |||:::      |||      ||||||:::|||
Db        715 CTAATGGGTTTTTCTGGGGTAGGGGGAAAACTG 747
```

RESULT 15
AK032985
LOCUS AK032985 2369 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:6720484N02

```
            product:CDNA FLJ13589 FIS, CLONE PLACE1009308, WEAKLY SIMILAR TO
            GLUCOSE REPRESSION MEDIATOR PROTEIN homolog [Homo sapiens], full
            insert sequence.
ACCESSION   AK032985
VERSION     AK032985.1  GI:26328748
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2369)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .2369
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                     /db_xref="taxon:10090"
                     /clone="6720484N02"
                     /sex="male"
                     /tissue_type="wolffian duct includes surrounding region"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="12 days embryo"
     CDS             163. .>2367
                     /note="unnamed protein product; CDNA FLJ13589 FIS, CLONE
                     PLACE1009308, WEAKLY SIMILAR TO GLUCOSE REPRESSION
                     MEDIATOR PROTEIN homolog [Homo sapiens] (SPTR|Q9H8I9,
                     evidence: FASTY, 91.2%ID, 100%length, match=1243)
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                     /translation="MPVVWPTLLDLSRDECKRILRKLELEAYAGVISALRAQGDLTKE
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ORIGIN

Alignment Scores:
Pred. No.:                4.13          Length:          2369
Score:                    110.50        Matches:         119
Percent Similarity:       33.52%        Conservative:    63
Best Local Similarity:    21.92%        Mismatches:      220
Query Match:              3.92%         Indels:          141
DB:                       3             Gaps:            26

US-09-769-066-16 (1-549) x AK032985 (1-2369)

Qy          1 AlaValAlaProAla---------HisAspThrSer---ProValPro------------ 12
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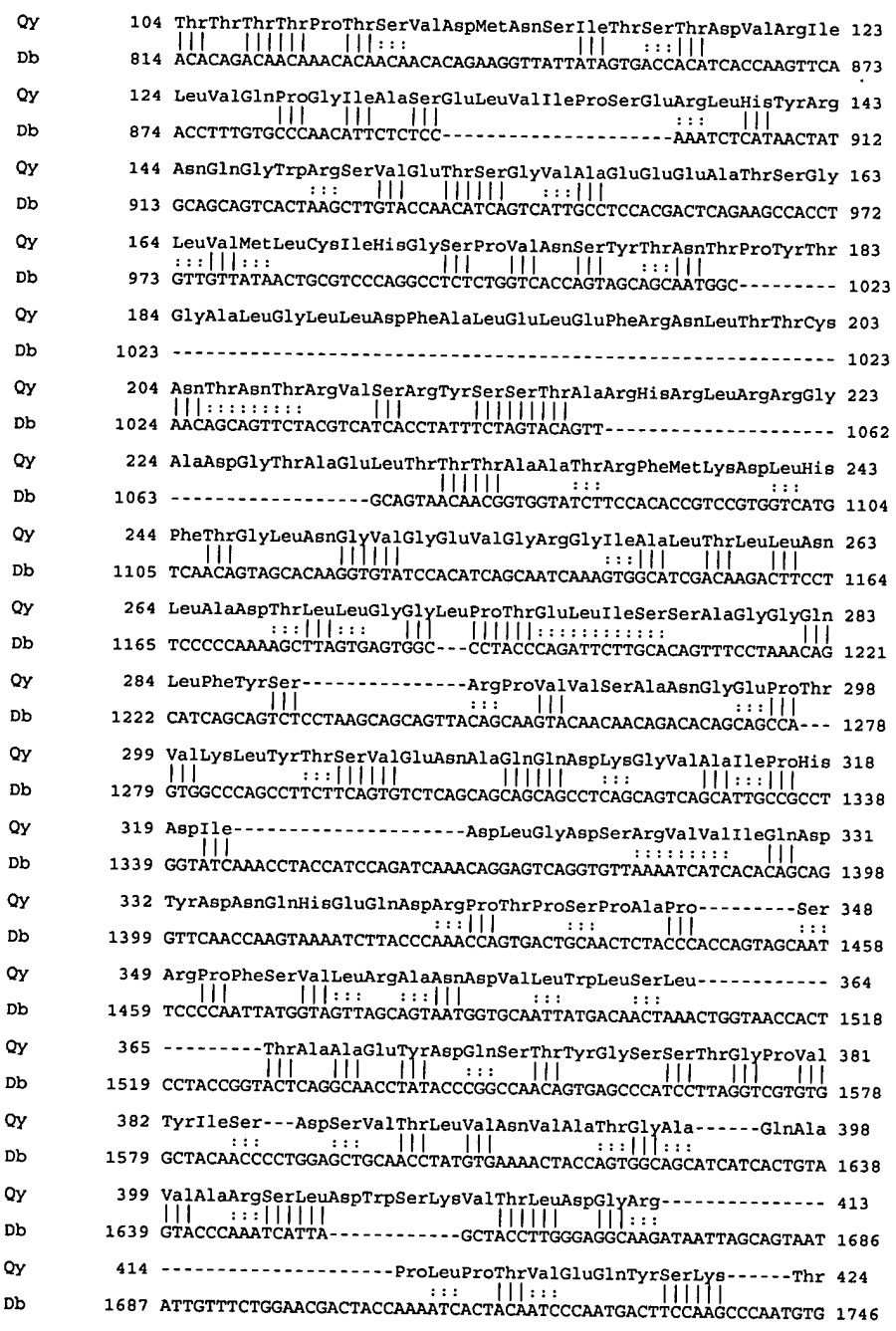
Qy         13 ------------------------AspValAspSerArgGlyAlaIleLeuArgArgGln 24
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Db        574 AGCAAAGACGGCGTTAGCTGCTCAGATGAAGATGAAAAACCCAGAAAACGCAGGCGAACA 633

Qy         25 TyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThrAsnLeuValLeu 44
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Db        634 AACTCCTCTAGCTCCTCCCCT----------------------------GTTGTCCTC 663

Qy         45 TyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsnThrHisIleMet 64
                      |||           :::|||:::                       :::
Db        664 AAGGAAGTTCCA---AAGGCTGTTGTTCCGGTCTCAAAGACGATCACTGTGCCTGTGAGT 720

Qy         65 AlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArg 84
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Db        721 GGAAGTCCCAAGATGAGCAACATTATGCAGAGCATTGCCAACTCC-------------- 765

Qy         85 ProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrp---ProGln 103
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Search completed: July 14, 2005, 21:23:23
Job time : 3402 secs

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Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Db       1411 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1470

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1471 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1530

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
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Db       1531 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1590

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Db       1591 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1650

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db       1651 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1710

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
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Db       1711 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1770

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuGluGlu 500
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Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        541 MetLysValGlyLysThrArgGluLeu 549
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RESULT 19
AAQ27436
ID AAQ27436 standard; DNA; 1643 BP.
XX
AC AAQ27436;
XX
DT 27-AUG-2003 (revised)
DT 05-FEB-1993 (first entry)
XX
DE DNA encoding epidemic NANBH virus antigen peptide.
XX
KW NANBH; non-A non-B hepatitis; immunoassay; ss.
XX
OS Non-A.
OS non-B hepatitis virus.
XX
FH Key Location/Qualifiers
FT CDS 3. .1643
FT /*tag= a
XX
PN JP04200388-A.
XX
PD 21-JUL-1992.
XX
PF 29-NOV-1990; 90JP-00334835.
XX
PR 29-NOV-1990; 90JP-00334835.
XX
PA (KAGA) KAGAKU OYOBI KESSEI RYOHO.
XX
DR WPI; 1992-290153/35.
DR P-PSDB; AAR26189.
XX
PT Epidemic non-A, non-B hepatitis virus antigen peptide (I) - and a nucleic
PT acid (II) fragment coding it.
XX
PS Claim 3; Fig 1; 15pp; Japanese.
XX
CC The sequence is that encoding an epidemic non-A, non-B hepatitis (NANBH)
CC virus antigen peptide. The peptide is useful for the detection of NANBH
CC virus by immunoassay of the antibody relates to epidemic NANBH virus in
CC which the peptide is used as an antigen. (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 1643 BP; 297 A; 522 C; 382 G; 439 T; 0 U; 3 Other;

Alignment Scores:

Pred. No.:	1.07	Length:	1643
Score:	482.50	Matches:	506
Percent Similarity:	95.83%	Conservative:	0
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Query Match:	87.89%	Indels:	2
DB:	1	Gaps:	1

US-09-769-066-15 (1-549) x AAQ27436 (1-1643)

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Db          3 CGCCGGCAGTATAATCTATCAACATCTCCCCTCACTTCTTCCGTGGCCACCGGCACTAAC 62

Qy         42 LeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsnThr 61
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Qy         62 HisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIle 81
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Db        123 CATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGTCCGTGCCACAATC 182

Qy         82 ArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrp 101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 CGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTCTGG 242

Qy        102 ProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAspVal 121
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Db        243 CCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGATGTT 302

Qy        122 ArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeuHis 141
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Qy        142 TyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaThr 161
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Db        363 TATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCTACC 422

Qy        162 SerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrPro 181
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Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
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Db        483 TATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTTACC 542

Qy        202 ProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
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Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
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Db        603 CGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAGGAC 662

Qy        242 LeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeu 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        663 CTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTG 722

Qy        262 PheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGly 281
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Db        723 TTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGT 782

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Db        783 GGCCAGCTGTTCTACTCCCGTCCCGTCGTCTCGGCCCATGGCGAGCCGACTGTTAAGTTG 842

Qy        302 TyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAsp 321

Db        843 TATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGAC 902

Qy        322 LeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgPro 341

Db        903 CTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGGCCG 962

Qy        342 ThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrp 361

Db        963 ACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGG 1022

Qy        362 LeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProVal 381

Db       1023 CTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTT 1082

Qy        382 TyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArg 401

Db       1083 TATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGG 1142

Qy        402 SerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyr 421

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Qy        422 SerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThr 441

Db       1200 ACCCGAAGACCTTCTTTGTCCTGCGCTCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACA 1259

Qy        442 ThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGlu 461

Db       1260 ACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAG 1319

Qy        462 AsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyPro 481

Db       1320 AATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCC 1379

Qy        482 ValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAsp 501

Db       1380 GTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGAT 1439

Qy        502 ThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgPro 521

Db       1440 ACCTTGGACTACCCTGCCTGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCT 1499

Qy        522 LeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMet 541

Db       1500 CTTGGCCTCCA-GGGTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGANN 1558

Qy        542 LysValGlyLysThrArgGluLeu 549

Db       1559 NAGGTGGGTAAAACTCGGGAGTTA 1582
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RESULT 20
AAT27111
ID AAT27111 standard; DNA; 984 BP.
XX
AC AAT27111;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Burma strain) SG3 antigen DNA.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; ds.
XX
OS Hepatitis E virus; Burma strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
DR P-PSDB; AAR96093.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Disclosure; Page 74-75; 125pp; English.
XX
CC A DNA sequence (AAT27111) codes for SG3 antigen (AAR96093) comprising the
CC C-terminal 327 amino acids of hepatitis E virus (HEV) Burma strain capsid
CC protein (AAR96089). It is obtd. by PCR amplification of pBET1 contg. the
CC HEV ORF-2 (AAT27107) and ORF-3 (AAT27115). The amplified fragment is
CC inserted into pBluescript and the cloned insert is ligated into vector
CC pGEX for prodn. of SG3 in E. coli cells SG3 shows low antigenicity
CC compared with 62K antigen (see also AAR96091-92 and AAR96101-04) from HEV
CC Burma and Mexico strain capsid proteins, produced using a baculovirus
CC expression system. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 984 BP; 180 A; 300 C; 246 G; 258 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.81	Length:	984
Score:	327.00	Matches:	327
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	59.56%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AAT27111 (1-984)

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Qy        243 TyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPhe 262

Db         61 TATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTC 120

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282

Db        121 AACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGC 180

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302

Db        181 CAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTAT 240

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322

Db        241 ACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTC 300

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342

Db        301 GGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGGCCGACG 360

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362

Db        361 CCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTC 420
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Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
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Db        421 TCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTTAT 480

Qy        383 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCG 540

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAGTACTCG 600

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACAACT 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTC 780

Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThr 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACC 840

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCCTT 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||
Db        961 GTGGGTAAAACTCGGGAGTTG 981
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RESULT 21
AAT96965
ID AAT96965 standard; DNA; 984 BP.
XX
AC AAT96965;
XX
DT 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 26-FEB-1998 (first entry)
XX
DE Hepatitis E virus Burma strain peptide antigen SG3 encoding DNA.
XX
KW Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
KW diagnosis; HEV; ds.
XX
OS Hepatitis E virus; - Burma strain.
XX
FH Key   Location/Qualifiers
FT CDS   1. .984
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FT   /product= "Peptide_antigen_SG3"
XX
PN US5686239-A.
XX
PD 11-NOV-1997.
XX
PF 09-MAY-1994; 94US-00240049.
XX
PR 17-JUN-1988; 88US-00208997.
PR 11-APR-1989; 89US-00336672.
PR 16-JUN-1989; 89US-00367486.
PR 13-OCT-1989; 89US-00420921.
PR 05-APR-1990; 90US-00505888.
PR 05-APR-1991; 91US-00681078.
PR 17-JAN-1992; 92US-00822335.
PR 20-APR-1992; 92US-00870985.
PR 01-MAY-1992; 92US-00876941.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Tam AW, Reyes GR, Yarbough PO;
XX
DR WPI; 1997-558132/51.
DR P-PSDB; AAW35820.
XX
PT Diagnosis of hepatitis E virus Burma and Mexico strain infection - by
PT immunoassay with hepatitis E virus peptide antigens.
XX
PS Disclosure; Col 29-32; 36pp; English.
XX
CC A method has been developed for detecting hepatitis E virus (HEV)
CC antibodies (Ab). The method comprises: (a) reacting a serum sample with a
CC HEV peptide antigen; and (b) examining the peptide for the presence of
CC bound Ab, where the presence of bound Ab indicates the presence of HEV
CC Ab. The present sequence encodes a specifically claimed HEV peptide
CC antigen. The method can be used to diagnose infection with the
CC enterically transmitted non-A/non-B viral hepatitis agent HEV,
CC specifically the HEV Burma and Mexico strains. (Updated on 25-MAR-2003 to
CC correct PF field.) (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 984 BP; 180 A; 300 C; 246 G; 258 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.81	Length:	984
Score:	327.00	Matches:	327
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	59.56%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AAT96965 (1-984)

```
Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTC 60

Qy        243 TyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPhe 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTC 120

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGC 180

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTAT 240

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTC 300

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGGCCGACG 360

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTC 420

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTTAT 480

Qy        383 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        481 GTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCG 540

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAGTACTCG 600

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACAACT 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTC 780

Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThr 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACC 840

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCCTT 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||
Db        961 GTGGGTAAAACTCGGGAGTTG 981
```

RESULT 22
AAZ00231
ID AAZ00231 standard; DNA; 1020 BP.
XX
AC AAZ00231;
XX
DT 12-OCT-1999 (first entry)
XX
DE Nucleic acid sequence of HEV clone us2-1019.
XX
KW Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW vaccine; passive immunisation; ss.
XX
OS Hepatitis E virus.
XX
PN WO9919732-A1.
XX
PD 22-APR-1999.
XX
PF 15-OCT-1998; 98WO-US021941.
XX
PR 15-OCT-1997; 97US-0061199P.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Schlauder GG, Erker JC, Desai SM, Dawson GJ, Mushahwar IK;
XX
DR WPI; 1999-288017/24.
XX
PT Detection of United States isolates of hepatitis E virus.
XX
PS Example 5; Page 192; 260pp; English.
XX
CC The invention provides a method for detecting a US (sub)type hepatitis E
CC virus (US-HEV), or its naturally occurring variants in a sample by
CC treatment with a binding partner specific for a marker of the virus, and
CC then detecting any complex formed. The method is used to diagnose
CC infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC are useful in vaccines or for passive immunisation. The polypeptides are
CC also used to raise specific antibodies (useful as immunoassay reagents).
CC Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC usual hybridisation and amplification assays for detecting infection. The
CC present sequence represents a HEV US subtype specific sequence obtained
CC by PCR amplification
XX
SQ Sequence 1020 BP; 204 A; 292 C; 246 G; 276 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.:	5.31	Length:	1020
Score:	322.00	Matches:	322
Percent Similarity:	95.55%	Conservative:	0
Best Local Similarity:	95.55%	Mismatches:	15
Query Match:	58.65%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AAZ00231 (1-1020)

```
Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              |||||| |||||| |||||| ||||||||||||||||||||||||||||||||||||||
Db          9 GCCGTGTCACCGGCTCCTGACACAGCCCCTGTACCTGATGTTGACTCACGTGGTGCTATT 68

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         69 CTGCGCCGGCAGTACAATTTGTCCACGTCCCCGCTCACGTCATCTGTCGCTTCGGGTACT 128

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        129 AATTTGGTCCTCTATGCTGCCCCGCTGAATCCCCTCTTGCCTCTCCAGGATGGTACCAAC 188

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        189 ACTCATATTATGGCTACTGAGGCATCCAATTATGCCCAGTATCGGGTTGTTCGAGCTACA 248

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 ATCCGTTATCGCCCGCTGGTGCCGAATGCCGTTGGTGGCTATGCCATTTCCATTTCTTTC 308

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TGGCCCCAAACTACAACTACCCCTACTTCTGTCGATATGAATTCTATTACTTCCACYGAT 368

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GTTAGGATTTTGGTTCAGCCCGGTATTGCCTCCGAGCTAGTCATCCCCAGTGAGCGCCTT 428

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        429 CATTACCGTAATCAAGGCTGGCGCTCTGTTGAGACCACGGGTGTGGCTGAGGAGGAGGCT 488

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        489 ACTTCCGGTCTGGTAATGCTTTGCATTCATGGCTCTCCTGTTAATTCCTACACTAATACA 548

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCACTAGAGCTTGAATTTAGGAATTTG 608

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        609 ACACCCGGGAACACCAACACCCGTGTTTCCCGGTATACCAGCACAGCCCGCCACCGGCTG 668

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CGCCGTGGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCCACACGTTTCATGAAG 728

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||  |||       |||||||||||||||||   ||||||||||||||||||||||
Db        729 GACCTGCACTTCGCTGGCACGAATGGCGTTGGTGAGGTGGGTCGTGGTATCGCCCTGACA 788

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        789 CTGTTCAATCTCGCTGATACGCTTCTCGGCGGTTTACCGACAGAATTGATTTCGTCGGCT 848

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 GGGGGCCAACTGTTTTACTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAG 908

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        909 TTATATACATCTGTTGAGAATGCGCAGCAAGACAAGGGCATCACCATTCCACATGATATA 968

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        969 GACCTGGGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCAYGAA 1019
```

RESULT 23
AAT27112
ID AAT27112 standard; DNA; 984 BP.
XX
AC AAT27112;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Mexico strain) SG3 antigen DNA.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; ds.
XX
OS Hepatitis E virus; Mexico strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
DR P-PSDB; AAR96094.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Disclosure; Page 75-76; 125pp; English.
XX
CC A DNA sequence (AAT27112) codes for SG3 antigen (AAR96094) comprising the
CC C-terminal 327 amino acids of hepatitis E virus (HEV) Mexico strain
CC capsid protein (AAR96090). It is obtd. by PCR amplification using a pBET1
CC clone plasmid contg. the HEV ORF-2 (AAT27108) and ORF-3 (AAT27116). The
CC amplified fragment is inserted into pBluescript and the cloned insert is
CC ligated into vector pGEX for prodn. of SG3 in E. coli cells. SG3 shows
CC low antigenicity when compared with 62K antigen (see also AAR96091-92 and
CC AAR96101-04) from HEV Burma and Mexico strain capsid proteins, produced
CC using a baculovirus expression system. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 984 BP; 192 A; 282 C; 264 G; 246 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.36	Length:	984
Score:	305.00	Matches:	305
Percent Similarity:	93.27%	Conservative:	0
Best Local Similarity:	93.27%	Mismatches:	22
Query Match:	55.56%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AAT27112 (1-984)

```
Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAAGATCTC 60

Qy        243 TyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPhe 262
                ||||||     ||||||||||||||||   ||||||||||||||||||||||
Db         61 CACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACATTACTT 120

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCTGGCGGG 180

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTAT 240

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        241 ACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATCGATCTT 300

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGGCCCACC 360

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTTTGGCTG 420

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTAT 480

Qy        383 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCCCGATCG 540

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422
              |||||||||   ||||||||||||||||||||||||||   |||       |||||||||
Db        541 CTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAATATTCC 600

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGCACAACA 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATTGAAAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        721 GCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGTCCGGTC 780

Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThr 502
              |||||||||   ||||||||||||||   |||||||||||||||||||||||||||||
Db        781 GCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAGGATACT 840

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||   |||
Db        841 TTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGCGCTTTA 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        901 GGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||
Db        961 GTGGGTAAAACTCGGGAGTTG 981
```

RESULT 24
AAT96966
ID AAT96966 standard; DNA; 984 BP.
XX

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AC   AAT96966;
XX
DT   17-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   26-FEB-1998  (first entry)
XX
DE   Hepatitis E virus Mexico strain peptide antigen SG3 encoding DNA.
XX
KW   Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
KW   diagnosis; HEV; ds.
XX
OS   Hepatitis E virus; - Mexico strain.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag=  a
FT                   /product= "Peptide_antigen_SG3"
XX
PN   US5686239-A.
XX
PD   11-NOV-1997.
XX
PF   09-MAY-1994;   94US-00240049.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   17-JAN-1992;   92US-00822335.
PR   20-APR-1992;   92US-00870985.
PR   01-MAY-1992;   92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Tam AW,  Reyes GR,  Yarbough PO;
XX
DR   WPI; 1997-558132/51.
DR   P-PSDB; AAW35821.
XX
PT   Diagnosis of hepatitis E virus Burma and Mexico strain infection - by
PT   immunoassay with hepatitis E virus peptide antigens.
XX
PS   Disclosure; Col 31-32; 36pp; English.
XX
CC   A method has been developed for detecting hepatitis E virus (HEV)
CC   antibodies (Ab). The method comprises: (a) reacting a serum sample with a
CC   HEV peptide antigen; and (b) examining the peptide for the presence of
CC   bound Ab, where the presence of bound Ab indicates the presence of HEV
CC   Ab. The present sequence encodes a specifically claimed HEV peptide
CC   antigen. The method can be used to diagnose infection with the
CC   enterically transmitted non-A/non-B viral hepatitis agent HEV,
CC   specifically the HEV Burma and Mexico strains. (Updated on 25-MAR-2003 to
CC   correct PF field.) (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ   Sequence 984 BP; 192 A; 282 C; 264 G; 246 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.36          Length:         984
Score:                  305.00        Matches:        305
Percent Similarity:     93.27%        Conservative:   0
Best Local Similarity:  93.27%        Mismatches:     22
Query Match:            55.56%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AAT96966 (1-984)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAAGATCTC 60

Qy        243 TyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPhe 262
              ||||||      ||||||||||||||||   ||||||||||||||||||||||||
Db         61 CACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACATTACTT 120

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCTGGCGGG 180

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTAT 240

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        241 ACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATCGATCTT 300

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGGCCCACC 360

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTTTGGCTG 420

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTAT 480

Qy        383 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCCCGATCG 540

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422
              |||||||||   ||||||||||||||||||||||||||||   |||       |||||||||
Db        541 CTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAATATTCC 600

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGCACAACA 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATTGAAAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        721 GCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGTCCGGTC 780

Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThr 502
              |||||||||   ||||||||||||||   |||||||||||||||||||||||||||||||
Db        781 GCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAGGATACT 840

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522
              |||||||||   ||||||||||||||||||||||||||||||||||||||||   |||||||
Db        841 TTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGCGCTTTA 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        901 GGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||
Db        961 GTGGGTAAAACTCGGGAGTTG 981

RESULT 25
AAZ00279
ID   AAZ00279 standard; DNA; 1026 BP.
XX
AC   AAZ00279;
XX
DT   12-OCT-1999  (first entry)
XX
DE   HEV US and CMP-KDO synthetase (CKS) fusion protein cksorf2m-2 DNA.
XX
```

```
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
DR   P-PSDB; AAY31400.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 10; Page 233-234; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a DNA encoding a HEV US and CKS fusion
CC   protein
XX
SQ   Sequence 1026 BP; 215 A; 285 C; 248 G; 278 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.62          Length:          1026
Score:                    305.00        Matches:         305
Percent Similarity:       93.56%        Conservative:    0
Best Local Similarity:    93.56%        Mismatches:      21
Query Match:              55.56%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x AAZ00279 (1-1026)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCCACACGTTTCATGAAGGACCTG 69

Qy        243 TyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPhe 262
                  |||     ||||||||||||||||||    ||||||||||||||||||||||||||
Db         70 CACTTCGCTGGCACGAATGGCGTTGGTGAGGTGGGTCGTGGTATCGCCCTGACACTGTTC 129

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 AATCTCGCTGATACGCTTCTCGGCGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGC 189

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CAACTGTTTTACTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATAT 249

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||    ||||||||||||||||||||||
Db        250 ACATCTGTTGAGAATGCGCAGCAAGACAAGGGCATCACCATTCCACATGATATAGACCTG 309

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCATGAGCAAGACCGACCTACT 369

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CCGTCACCTGCCCCCTCTCGCCCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTT 429

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||    ||||||||||||||||||    |||   |||
Db        430 TCCCTCACTGCCGCTGAGTATGACCAGACTACGTATGGGTCGTCCACCAACCCTATGTAT 489

Qy        383 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GTCTCTGACACAGTTACGCTTGTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCC 549

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 CTTGATTGGTCTAAAGTTACTCTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCT 609

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 AAGACATTTTATGTTCTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACT 669

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAGGCCGGCTACCCTTACAATTATAATACTACCGCTAGTGACCAAATTTTGATTGAGAAT 729

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 GCGGCCGGCCACCGTGTCGCTATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACC 789

Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThr 502
              ||||||||||||||    ||||||||||||||||||||||||||||||||||||||||||
Db        790 TCGATCTCTGCGGTCGGCGTACTGGCTCCACACTCTGCCCTTGCCGTTCTTGAGGATACT 849

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 ATTGATTACCCCGCCCGTGCCCATACTTTTGATGATTTTTGCCCGGAGTGCCGTACCCTA 909

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLys 542
              ||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        910 GGTTTGCAGGGTTGTGCATTCCAGTCTACTATTGCTGAGCTCCAGCGTTTAAAAATGAAG 969

Qy        543 ValGlyLysThrArgGlu 548
              ||||||||||||||||||
Db        970 GTAGGTAAAACCCGGGAG 987

RESULT 26
AAZ00282
ID   AAZ00282 standard; DNA; 960 BP.
XX
AC   AAZ00282;
XX
DT   12-OCT-1999  (first entry)
XX
DE   HEV US recombinant protein plorf2-2.6 DNA.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
DR   P-PSDB; AAY31401, AAY31403.
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XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 10; Page 235-236; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a DNA encoding a recombinant HEV protein
XX
SQ   Sequence 960 BP; 188 A; 274 C; 230 G; 268 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.96          Length:          960
Score:                    296.00        Matches:         296
Percent Similarity:       93.38%        Conservative:    0
Best Local Similarity:    93.38%        Mismatches:      21
Query Match:              53.92%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x AAZ00282 (1-960)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCCACACGTTTCATGAAGGACCTG 69

Qy        243 TyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPhe 262
                 |||      ||||||||||||||||||  ||||||||||||||||||||||||||||
Db         70 CACTTCGCTGGCACGAATGGCGTTGGTGAGGTGGGTCGTGGTATCGCCCTGACACTGTTC 129

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 AATCTCGCTGATACGCTTCTCGGCGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGC 189

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CAACTGTTTTACTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATAT 249

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        250 ACATCTGTTGAGAATGCGCAGCAAGACAAGGGCATCACCATTCCACATGATATAGACCTG 309

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCATGAGCAAGACCGACCTACT 369

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CCGTCACCTGCCCCCTCTCGCCCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTT 429

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||  ||||||||||||||||  |||  |||||||||||||
Db        430 TCCCTCACTGCCGCTGAGTATGACCAGACTACGTATGGGTCGTCCACCAACCCTATGTAT 489

Qy        383 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GTCTCTGACACAGTTACGCTTGTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCC 549

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422
              |||||||||  ||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        550 CTTGATTGGTCTAAAGTTACTCTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCT 609

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 AAGACATTTTATGTTCTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACT 669

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||  |||  ||||||
Db        670 AAGGCCGGCTACCCTTACAATTATAATACTACCGCTAGTGACCAAATTTTGATTGAGAAT 729

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 GCGGCCGGCCACCGTGTCGCTATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACC 789

Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThr 502
              ||||||||||||||  ||||||||||||||||||||||||||||  ||||||||||||
Db        790 TCGATCTCTGCGGTCGGCGTACTGGCTCCACACTCTGCCCTTGCCGTTCTTGAGGATACT 849

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        850 ATTGATTACCCCGCCCGTGCCCATACTTTTGATGATTTTTGCCCGGAGTGCCGTACCCTA 909

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeu 539
              ||||||||||||||||||||||||||||  ||||||||||||||||||
Db        910 GGTTTGCAGGGTTGTGCATTCCAGTCTACTATTGCTGAGCTCCAGCGTTTA 960

RESULT 27
AAZ00129
ID   AAZ00129 standard; DNA; 899 BP.
XX
AC   AAZ00129;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Nucleic acid sequence of HEV clone df-orf2/3.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 3; Page 144-145; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a HEV US subtype specific sequence obtained
CC   by PCR amplification
XX
SQ   Sequence 899 BP; 176 A; 253 C; 207 G; 263 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                7.59          Length:          899
Score:                    284.00        Matches:         284
Percent Similarity:       95.62%        Conservative:    0
Best Local Similarity:    95.62%        Mismatches:      13
```

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Query Match:          51.73%      Indels:        0
DB:                   1           Gaps:          0

US-09-769-066-15 (1-549) x AAZ00129 (1-899)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              |||     ||||||  ||||||  ||||||||||||||||||||||||||||||||||||
Db          8 GCCATATCACCAGCCCCTGATACAGCTCCTGTACCTGATGTTGACTCACGTGGTGCTATT 67

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db         68 TTGCGCCGGCAGTACAATTTGTCTACGTCCCCGCTTACATCATCTGTTGCTTCTGGTACT 127

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db        128 AATCTGGTTCTCTATGCTGCCCCGCTGAACCCTCTCTTGCCTCTTCAGGATGGCACCAAC 187

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||
Db        188 ACTCATATTATGGCTACTGAGGCATCTAATTACGCCCAGTATCGGGTTGTTCGGGCTACG 247

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 ATTCGTTATCGCCCGTTGGTGCCAAATGCTGTTGGTGGTTATGCTATCTCTATTTCTTTC 307

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 TGGCCTCAAACTACAACTACCCCTACTTCTGTTGACATGAATTCTATCACTTCTACTGAT 367

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 GTCAGGATCTTGGTCCAGCCCGGTATAGCCTCCGAGTTAGTCATCCCTAGTGAACGCCTT 427

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        428 CACTACCGCAACCAAGGCTGGCGCTCTGTTGAGACCACGGGTGTGGCCGAAGAGGAGGCT 487

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        488 ACCTCCGGTCTGGTAATGCTTTGTATTCATGGCTCCCCTGTTAACTCCTACACTAATACA 547

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 CCTTACACCGGTGCATTGGGGCTTCTTGATTTTGCATTAGAACTTGAATTTAGAAATTTG 607

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        608 ACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACTAGCACAGCCCGCCACCGGCTG 667

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CGCCGCGGTGCTGATGGGACCGCTGAGCTCACCACCACAGCAGCCACACGCTTCATGAAG 727

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||  ||||||  ||||||||||||||||||  ||||||||||||||||||||||||
Db        728 GATTTGCATTTTACTGGTACGAACGGCGTTGGTGAGGTGGGTCGTGGTATTGCCCTGACT 787

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CTGTTTAATCTTGCTGATACGCTTCTTGGTGGTTTACCGACAGAATTGATTTCGTCGGCT 847

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 GGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCAGCCAATGGCGAGCCA 898

RESULT 28
AAS01434
ID   AAS01434 standard; cDNA; 810 BP.
XX
AC   AAS01434;
XX
DT   18-JUL-2001  (first entry)
XX
DE   Hepatitis E virus (HEV) E2 cDNA fragment derived from ORF2.
XX
KW   Hepatitis E virus; HEV; E2; pE2; ORF2; immunoreactive viral peptide;
KW   antigenic activity; viral infection; mutant; ss.
XX
OS   Hepatitis E virus; Chinese strain D11092.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .810
FT                   /*tag=  b
FT                   /note= "Corresponds to residues 1180-1990 of ORF2"
FT   CDS             1. .642
FT                   /*tag=  a
FT                   /partial
FT                   /product= "pE2 peptide"
FT                   /note= "Specifically claimed. This sequence lacks a start
FT                   codon"
FT   mutation        replace(631. .632, CAC)
FT                   /*tag=  c
XX
PN   WO200122916-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-IB001393.
XX
PR   30-SEP-1999;   99CA-02283538.
XX
PA   (UYHK-) UNIV HONG KONG.
XX
PI   Ng MH,  Im S,  Zhang J;
XX
DR   WPI; 2001-266109/27.
DR   P-PSDB; AAU00496.
XX
PT   New immunoreactive peptide pE2, cloned from the genome of a Chinese
PT   strain of hepatitis E virus (HEV), for detecting and diagnosing HEV
PT   infection and for use as a vaccine for prevention of the viral infection
PT   in humans.
XX
PS   Claim 5; Fig 2B-2D; 101pp; English.
XX
CC   The present sequence for hepatitis E virus (HEV) E2 cDNA fragment encodes
CC   for a novel peptide, pE2 which is cloned from ORF2 (AAS01448) of the HEV
CC   Chinese strain D11092 genome. During the cloning of the E2 fragment a
CC   single base deletion (presumed to be a PCR amplification error) at
CC   position 1811 of ORF2 resulted in a frame shift causing the premature
CC   termination at a new stop codon at position 1820-1822, and giving rise to
CC   a smaller peptide, pE2. Peptide pE2 is a highly immunoreactive viral
CC   peptide which can be used in the development of diagnostic methods for
CC   the detection of HEV. Peptide pE2 which has antigenic activity is also
CC   useful as a vaccine for immunising an individual against infection from
CC   HEV and for determining the presence of HEV antibodies in a biological
CC   test sample such as human blood serum or plasma for detection and
CC   diagnosis of HEV infection. An antibody against pE2 is useful for
CC   detecting an HEV particle, in a biological test sample. The use of
CC   recombinant peptides such as pE2 peptide have advantage over the prior
CC   art of using live intact virus particles by avoiding the potential risk
CC   of infectivity. The ORF3 (AAS01449) of HEV Chinese strain D11092 is used
CC   to clone a cDNA fragment E3 (AAS001450) which encodes pE3 peptide
XX
SQ   Sequence 810 BP; 150 A; 249 C; 192 G; 219 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              10.2          Length:        810
Score:                  252.00        Matches:       265
Percent Similarity:     99.25%        Conservative:  0
Best Local Similarity:  99.25%        Mismatches:    2
Query Match:            45.90%        Indels:        1
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AAS01434 (1-810)
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```
Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAGCTTTAT 60

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATCGACCTC 120

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGACCGACA 180

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTTTGGCTT 240

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCAGTCTAT 300

Qy        383 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCA 360

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAGTATTCA 420

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGTACTACT 480

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTTGAGAAT 540

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTC 600

Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThr 502
              |||||||||||||||||||||||||||||||    |||||||||||||||||||||||||||||
Db        601 TCTATTTCCGCGGTTGCTGTTTTAGCCCCCCC-TCCGCGCTAGCATTGCTTGAGGATACC 659

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 ATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGCCCCCTT 719

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 GGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAG 779

Qy        543 ValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||
Db        780 GTGGGTAAAACTCGGGAGTTA 800
```

RESULT 29
AAZ00193
ID AAZ00193 standard; DNA; 960 BP.
XX
AC AAZ00193;
XX
DT 12-OCT-1999 (first entry)
XX
DE Nucleic acid sequence of HEV clone 3p RACE.
XX
KW Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW vaccine; passive immunisation; ss.
XX
OS Hepatitis E virus.
XX
PN WO9919732-A1.
XX
PD 22-APR-1999.
XX
PF 15-OCT-1998; 98WO-US021941.
XX
PR 15-OCT-1997; 97US-0061199P.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Schlauder GG, Erker JC, Desai SM, Dawson GJ, Mushahwar IK;
XX
DR WPI; 1999-288017/24.
XX
PT Detection of United States isolates of hepatitis E virus.
XX
PS Example 3; Page 160; 260pp; English.
XX
CC The invention provides a method for detecting a US (sub)type hepatitis E
CC virus (US-HEV), or its naturally occurring variants in a sample by
CC treatment with a binding partner specific for a marker of the virus, and
CC then detecting any complex formed. The method is used to diagnose
CC infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC are useful in vaccines or for passive immunisation. The polypeptides are
CC also used to raise specific antibodies (useful as immunoassay reagents).
CC Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC usual hybridisation and amplification assays for detecting infection. The
CC present sequence represents a HEV US subtype specific sequence obtained
CC by PCR amplification
XX
SQ Sequence 960 BP; 198 A; 262 C; 213 G; 283 T; 0 U; 4 Other;

Alignment Scores:

Pred. No.:	10.6	Length:	960
Score:	262.00	Matches:	262
Percent Similarity:	93.24%	Conservative:	0
Best Local Similarity:	93.24%	Mismatches:	19
Query Match:	47.72%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AAZ00193 (1-960)

```
Qy        268 LeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSer 287
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CTTCTTGGTGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCC 62

Qy        288 ArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsn 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGCCCTGTTGTCTCGGCCAATGGCGAGCCAACAGTAAAGTTATACACATCTGTTGAGAAT 122

Qy        308 AlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSerArgVal 327
              |||||||||||||||||||    |||||||||||||||||||||||    |||||||||
Db        123 GCGCAGCAAGACAAGGGCATCACCATTCCACACGACATAGATTTAGGTGACTCCCGTGTG 182

Qy        328 ValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaPro 347
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GTTATCCAGGATTATGATAACCAGCACGAACAAGATCGACCTACCCCGTCACCTGCCCCC 242

Qy        348 SerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAla 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 TCCCGCCCTTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTCTCTCTCACTGCCGCT 302

Qy        368 GluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerVal 387
              ||||||   |||   |||||||||||||||||   |||   ||||||||||   |||
Db        303 GAGTACGRCCAGACCACGTATGGGTCGTCCACCAACCCTATGTATGTCTCTGATACAGTC 362

Qy        388 ThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLys 407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        363 ACGCTTGTTAATGTAGCCACTGGTGCTCAGGCTGTTGCCCGCTCTCTTGACTGGTCTAAA 422

Qy        408 ValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheVal 427
              |||||||||||||||||||||||    ||||||||||||||||||||    |||   |||
Db        423 GTTACTCTGGATGGTCGCCCTCTTACTACCATTCAGCAGTATTCTAAGAAATTTTATGTT 482
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Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 CTCCCGCTTCGSGGGAAGCTGTCCTTTTGGGAGGCTGGTACGACCAAGGCCGGCTACCCG 542

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||||||   |||   ||||||||||||||||||||||
Db        543 TATAATTATAATACCACTGCTAGTGACCAAATTTTGATTGAGAACGCGGCCGGTCACCGT 602

Qy        468 ValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaVal 487
              ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        603 GTCGCCATTTCTACTTATACCACTAGTTTGGGTGCCGGCCCTACCTCGATYTCTGCGGTC 662

Qy        488 AlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAla 507
              ||||||||||||||||||||||||||||   ||||||||||   ||||||||||||||||
Db        663 GGTGTACTAGCTCCACATTCGGCCCTTGCTGTTCTCGAGGATACTGTTGATTATCCTGCT 722

Qy        508 ArgAlaHisThrPheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGlyCys 527
              ||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        723 CGTGCCCATACTTTTGATGATTTCTGCCCGGAGTGTCGCACCCTTGGTCTGCAGGGTTGT 782

Qy        528 AlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArg 547
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        783 GCATTCCAATCTACTATTGCTGAACTTCAGCGTCTTAAAATGAAGGTAGGTAAAACCCGG 842

Qy        548 Glu 548
              |||
Db        843 GAG 845
```

RESULT 30
AAZ00277
ID AAZ00277 standard; DNA; 920 BP.
XX
AC AAZ00277;
XX
DT 12-OCT-1999 (first entry)
XX
DE Nucleic acid sequence of HEV clone z12-3p.con.
XX
KW Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW vaccine; passive immunisation; ss.
XX
OS Hepatitis E virus.
XX
PN WO9919732-A1.
XX
PD 22-APR-1999.
XX
PF 15-OCT-1998; 98WO-US021941.
XX
PR 15-OCT-1997; 97US-0061199P.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Schlauder GG, Erker JC, Desai SM, Dawson GJ, Mushahwar IK;
XX
DR WPI; 1999-288017/24.
XX
PT Detection of United States isolates of hepatitis E virus.
XX
PS Example 13; Page 230; 260pp; English.
XX
CC The invention provides a method for detecting a US (sub)type hepatitis E
CC virus (US-HEV), or its naturally occurring variants in a sample by
CC treatment with a binding partner specific for a marker of the virus, and
CC then detecting any complex formed. The method is used to diagnose
CC infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC are useful in vaccines or for passive immunisation. The polypeptides are
CC also used to raise specific antibodies (useful as immunoassay reagents).
CC Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC usual hybridisation and amplification assays for detecting infection. The
CC present sequence represents a HEV US subtype specific sequence obtained
CC by PCR amplification
XX
SQ Sequence 920 BP; 198 A; 254 C; 207 G; 261 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	11.1	Length:	920
Score:	255.00	Matches:	255
Percent Similarity:	92.73%	Conservative:	0
Best Local Similarity:	92.73%	Mismatches:	20
Query Match:	46.45%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AAZ00277 (1-920)

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Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTAATTTCGTCGGCTGGGGGTCAACTGTTCTACTCCCGCCCTGTCGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTCAAGTTATACACATCTGTTGAGAATGCACAGCAGGATAAGGGG 121

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
              ||||||||||||||||||||||||||||||||   |||||   ||||||||||||||||||
Db        122 ATAGCTATTCCACATGACATAGATTTGGGCGACTCTCGTTTGGTAATCCAGGATTACGAT 181

Qy        334 AsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgProPheSerVal 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AATCAGCACGAGCAGGACCGGCCCACCCCTTCGCCCGCCCCGTCTCGTCCTTTCTCGGTC 241

Qy        354 LeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThr 373
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||   |||
Db        242 CTCCGCGCTAATGATGCTTTGTGGCTTTCTCTTACCGCTGCTGAGTATGACCAGACTACA 301

Qy        374 TyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeuValAsnValAla 393
              ||||||||||||||   |||   ||||||||||   ||||||   ||||||||||||
Db        302 TATGGGTCGTCCACCAACCCGATGTATGTCTCAGACACTGTTACATTTGTCAATGTGGCC 361

Qy        394 ThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArg 413
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        362 ACAGGGGCTCAGGCTGTCGCCCGTTCTCTTGATTGGTCTAAAGTTACCCTGGACGGCCGC 421

Qy        414 ProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLys 433
              ||||||   ||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        422 CCTCTTACTACCATCCAGCAGTACTCTAAGACATTTTATGTTCTCCCACTTCGCGGGAAG 481

Qy        434 LeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThr 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 TTATCTTTTTGGGAGGCTGGCACAACTAAAGCCGGTTACCCTTATAATTATAACACAACT 541

Qy        454 AlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyr 473
              ||||||||||||   |||   ||||||||||||||||||||||||||||||||||||||
Db        542 GCTAGTGACCAGATTCTGATTGAAAACGCGGCTGGCCATCGTGTCGCTATATCTACTTAT 601

Qy        474 ThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAlaProHis 493
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||||||
Db        602 ACTACTAGCCTGGGCGCCGGCCCTGTGTCAGTTTCTGCGGTTGGTGTGTTAGCCCCACAC 661

Qy        494 SerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAsp 513
              |||   ||||||   ||||||||||||   ||||||||||||||||||||||||||||||
Db        662 TCGAGCCTTGCTATTCTTGAAGACACTGTTGACTATCCGGCCCGTGCTCACACTTTTGAT 721

Qy        514 AspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrVal 533
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        722 GACTTCTGTCCGGAATGCCGTGCCCTGGGTCTGCAGGGGTGTGCTTTTCAATCTACTATC 781

Qy        534 AlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArgGlu 548
              |||||||||||||||||||||||||||||||||||||||||||||
Db        782 GCTGAGCTCCAGCGTCTTAAAATGAAGGTAGGCAAAACCCGGGAG 826
```

RESULT 31
AAZ00255
ID AAZ00255 standard; DNA; 901 BP.

```
XX
AC   AAZ00255;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Nucleic acid sequence of HEV clone us2-3p.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 5; Page 198-199; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a HEV US subtype specific sequence obtained
CC   by PCR amplification
XX
SQ   Sequence 901 BP; 198 A; 250 C; 195 G; 257 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:              12.8          Length:         901
Score:                  242.00        Matches:        242
Percent Similarity:     93.44%        Conservative:   0
Best Local Similarity:  93.44%        Mismatches:     17
Query Match:            44.08%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AAZ00255 (1-901)

Qy        290 ValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGln 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATATACATCTGTTGAGAATGCGCAG 60

Qy        310 GlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIle 329
              ||||||||||||||||  ||||||||||||||||||||||||  ||||||||||||||||
Db         61 CAAGACAAGGGCATCACCATTCCACATGATATAGACCTGGGTGACTCCCGTGTGGTTATC 120

Qy        330 GlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArg 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGGATTATGATAACCAGCAYGAGCAAGACCGACCTACTCCGTCACCTGCCCCCTCTCGC 180

Qy        350 ProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyr 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTTTCCCTCACTGCCGCTGAGTAT 240

Qy        370 AspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeu 389
              ||||||   ||||||||||||||||||   |||   ||||||||||||   |||||||||

Db        241 GACCAGACTACGTATGGGTCGTCCACCAACCCTATGTATGTCTCTGACACAGTTACGCTT 300

Qy        390 ValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThr 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCCCTTGATTGGTCTAAAGTTACT 360

Qy        410 LeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuPro 429
              ||||||||||||||||||  ||||||||||||||||||||||||||||||  |||||||||
Db        361 CTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCTAAGACATTTTATGTTCTCCCG 420

Qy        430 LeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsn 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACTAAGGCCGGCTACCCTTACAAT 480

Qy        450 TyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAla 469
              ||||||||||||||||||||||||  |||  ||||||||||||||||||||||||||||||
Db        481 TATAATACTACCGCTAGTGACCAAATTTTGATTGAGAATGCGGCCGGCCACCGTGTCGCT 540

Qy        470 IleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaVal 489
              ||||||||||||||||||||||||||||||||  ||||||||||||||  |||
Db        541 ATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACCTCGATCTCTGCGGTCGGCGTA 600

Qy        490 LeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAla 509
              ||||||||||||||||||||||||  ||||||||||||  ||||||||||||||||||||
Db        601 CTGGCTCCACACTCTGCCCTTGCCGTTCTTGAGGATACTATTGATTACCCCGCCCGTGCC 660

Qy        510 HisThrPheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPhe 529
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        661 CATACTTTTGATGATTTTTGCCCGGAGTGCCGTACCCTAGGTTTGCAGGGTTGTGCATTC 720

Qy        530 GlnSerThrValAlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArgGlu 548
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGTCTACTATTGCTGAGCTCCAGCGTTTAAAAATGAAGGTAGGTAAAACCCGGGAG 777

RESULT 32
AAZ00276
ID   AAZ00276 standard; DNA; 890 BP.
XX
AC   AAZ00276;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Nucleic acid sequence of HEV clone z12-3p.race.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 13; Page 229-230; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
```

```
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a HEV US subtype specific sequence obtained
CC   by PCR amplification
XX
SQ   Sequence 890 BP; 190 A; 246 C; 203 G; 251 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              13.1          Length:         890
Score:                  239.00        Matches:        239
Percent Similarity:     92.28%        Conservative:   0
Best Local Similarity:  92.28%        Mismatches:     20
Query Match:            43.53%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AAZ00276 (1-890)

Qy        290 ValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGln 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCGTCTCGGCCAATGGCGAGCCGACTGTCAAGTTATACACATCTGTTGAGAATGCACAG 60

Qy        310 GlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIle 329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGATAAGGGGATAGCTATTCCACATGACATAGATTTGGGCGACTCTCGTTTGGTAATC 120

Qy        330 GlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArg 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGGATTACGATAATCAGCACGAGCAGGACCGGCCCACCCCTTCGCCCGCCCCGTCTCGT 180

Qy        350 ProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyr 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTTTCTCGGTCCTCCGCGCTAATGATGCTTTGTGGCTTTCTCTTACCGCTGCTGAGTAT 240

Qy        370 AspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeu 389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACCAGACTACATATGGGTCGTCCACCAACCCGATGTATGTCTCAGACACTGTTACATTT 300

Qy        390 ValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThr 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTCAATGTGGCCACAGGGGCTCAGGCTGTCGCCCGTTCTCTTGATTGGTCTAAAGTTACC 360

Qy        410 LeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuPro 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGGACGGCCGCCCTCTTACTACCATCCAGCAGTACTCTAAGACATTTTATGTTCTCCCA 420

Qy        430 LeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsn 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTTCGCGGGAAGTTATCTTTTTGGGAGGCTGGCACAACTAAAGCCGGTTACCCTTATAAT 480

Qy        450 TyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAla 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TATAACACAACTGCTAGTGACCAGATTCTGATTGAAAACGCGGCTGGCCATCGTGTCGCT 540

Qy        470 IleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaVal 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATATCTACTTATACTACTAGCCTGGGCGCCGGCCCTGTGTCAGTTTCTGCGGTTGGTGTG 600

Qy        490 LeuAlaProHisSerAlaLeuAlaLeuGluAspThrLeuAspTyrProAlaArgAla 509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTAGCCCCACACTCGAGCCTTGCTATTCTTGAAGACACTGTTGACTATCCGGCCCGTGCT 660

Qy        510 HisThrPheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPhe 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACACTTTTGATGACTTCTGTCCGGAATGCCGTGCCCTGGGTCTGCAGGGGTGTGCTTTT 720

Qy        530 GlnSerThrValAlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArgGlu 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAATCTACTATCGCTGAGCTCCAGCGTCTTAAAATGAAGGTAGGCAAAACCCGGGAG 777

RESULT 33
AAZ00212
ID   AAZ00212 standard; DNA; 678 BP.
XX
AC   AAZ00212;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Nucleic acid sequence of HEV clone us2-667.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 5; Page 187; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a HEV US subtype specific sequence obtained
CC   by PCR amplification
XX
SQ   Sequence 678 BP; 138 A; 197 C; 155 G; 187 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:              14.1          Length:         678
Score:                  212.00        Matches:        212
Percent Similarity:     94.22%        Conservative:   0
Best Local Similarity:  94.22%        Mismatches:     13
Query Match:            38.62%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AAZ00212 (1-678)

Qy        268 LeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSer 287
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CTTCTTGGTGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGCCAACTGTTTTACTCC 62

Qy        288 ArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsn 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATATACATCTGTTGAGAAT 122

Qy        308 AlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSerArgVal 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GCGCAGCAAGACAAGGGCATCACCATTCCACATGATATAGACCTGGGTGACTCCCGTGTG 182

Qy        328 ValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaPro 347
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GTTATCCAGGATTATGATAACCAGCAYGAGCAAGACCGACCTACTCCGTCACCTGCCCCC 242

Qy        348 SerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAla 367
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 TCTCGCCCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTTTCCCTCACTGCCGCT 302

Qy        368 GluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerVal 387
              ||||||||||||   ||||||||||||||||||   |||   ||||||||||||   |||
Db        303 GAGTATGACCAGACTACGTATGGGTCGTCCACCAACCCTATGTATGTCTCTGACACAGTT 362

Qy        388 ThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLys 407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        363 ACGCTTGTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCCCTTGATTGGTCTAAA 422

Qy        408 ValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheVal 427
              ||||||||||||||||||||||   ||||||||||||||||||||||||||   |||
Db        423 GTTACTCTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCTAAGACATTTTATGTT 482

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 CTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACTAAGGCCGGCTACCCT 542

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||||||   |||   ||||||||||||||||||||
Db        543 TACAATTATAATACTACCGCTAGTGACCAAATTTTGATTGAGAATGCGGCCGGCCACCGT 602

Qy        468 ValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaVal 487
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        603 GTCGCTATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACCTCGATCTCTGCGGTC 662

Qy        488 AlaValLeuAlaPro 492
              ||||||||||||
Db        663 GGTGTACTAGCTCCA 677

RESULT 34
AAZ00309
ID   AAZ00309 standard; DNA; 250 BP.
XX
AC   AAZ00309;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Conserved Nucleic acid sequence derived from HEV.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 11; Page 9B; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection.
CC   Sequences AAZ00300-312 represent conserved nucleic acid sequences from
CC   various strains of HEV
XX
SQ   Sequence 250 BP; 57 A; 65 C; 62 G; 66 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                25.7          Length:          250
Score:                    83.00         Matches:         83
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              15.12%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x AAZ00309 (1-250)

Qy        258 AlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCG 181

Qy        318 HisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CATGACATTGACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAA 241

Qy        338 GlnAspArg 340
              ||||||||
Db        242 CAAGATCGG 250

RESULT 35
AAZ00307
ID   AAZ00307 standard; DNA; 250 BP.
XX
AC   AAZ00307;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Conserved Nucleic acid sequence derived from HEV.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 11; Page 9B; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
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CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection.
CC   Sequences AAZ00300-312 represent conserved nucleic acid sequences from
CC   various strains of HEV
XX
SQ   Sequence 250 BP; 56 A; 68 C; 64 G; 62 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              25.7          Length:          250
Score:                  83.00         Matches:         83
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            15.12%        Indels:          0
DB:                     1             Gaps:            0

US-09-769-066-15 (1-549) x AAZ00307 (1-250)

Qy        258 AlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGCTTACCCTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGTGGCCAGCTGTTCTACTCTCGCCCCGTCGTCTCAGCCAATGGCGAGCCG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACTGTTAAGCTGTATACATCTGTGGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCG 181

Qy        318 HisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CATGACATCGACCTCGGGGAATCCCGTGTAGTTATTCAGGATTATGACAACCAACATGAG 241

Qy        338 GlnAspArg 340
              |||||||||
Db        242 CAGGACCGA 250

RESULT 36
AAZ00308
ID   AAZ00308 standard; DNA; 250 BP.
XX
AC   AAZ00308;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Conserved Nucleic acid sequence derived from HEV.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 11; Page 9B; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection.
CC   Sequences AAZ00300-312 represent conserved nucleic acid sequences from
CC   various strains of HEV
XX
SQ   Sequence 250 BP; 56 A; 67 C; 64 G; 63 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              25.7          Length:          250
Score:                  83.00         Matches:         83
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            15.12%        Indels:          0
DB:                     1             Gaps:            0

US-09-769-066-15 (1-549) x AAZ00308 (1-250)

Qy        258 AlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGCTTACCCTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGTGGCCAGCTGTTCTACTCTCGCCCCGTCGTCTCAGCCAATGGCGAGCCG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACTGTTAAGCTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCG 181

Qy        318 HisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CATGACATCGACCTCGGGGAATCTCGAGTTGTTATTCAGGATTATGACAACCAACATGAG 241

Qy        338 GlnAspArg 340
              |||||||||
Db        242 CAGGACCGG 250

RESULT 37
AAI66164
ID   AAI66164 standard; cDNA; 182 BP.
XX
AC   AAI66164;
XX
DT   14-JAN-2002  (first entry)
XX
DE   Hepatitis E virus peptide HE70 related polynucleotide.
XX
KW   Hepatitis E virus; HE40; HE60; HE70; medicine; molecular biology;
KW   genetic engineering; ss.
XX
OS   Hepatitis E virus.
XX
PN   RU2172346-C2.
XX
PD   20-AUG-2001.
XX
PF   26-OCT-1998;   98RU-00119633.
XX
PR   26-OCT-1998;   98RU-00119633.
XX
PA   (BIOS=) BIOSERVIS BIOTECHNOLOGY STOCK CO.
XX
PI   Alatortseva GI,  Goltsov VA,  Grinev AA,  Zverev VV,  Sukhanova LL;
PI   Titaev AV;
```

```
XX
DR   WPI; 2001-569715/64.
XX
PT   Method of synthesis of polypeptide eliciting antigenic activity of
PT   hepatitis e virus and set for assay of antibody raised to hepatitis e
PT   pathogen.
XX
PS   Example 7; Col 23-24; 14pp; Russian.
XX
CC   The invention relate to a method for preparing recombinant polypeptides
CC   for use in set for assaying antibodies raised to hepatitis E virus. Set
CC   has a series of recombinant antigens synthesised in Escherichia coli
CC   cells transformed with recombinant DNAs. Recombinant DNAs involve
CC   fragment of the second and the third open reading frames of hepatitis E
CC   virus genome. Sets can contain E. coli beta-galactosidase as a control
CC   antigen. The antibodies are useful in medicine, molecular biology and
CC   genetic engineering of proteins. The present sequence is that of a
CC   hepatitis E virus peptide HE70 related polynucleotide, useful to the
CC   invention
XX
SQ   Sequence 182 BP; 55 A; 38 C; 38 G; 51 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              25.9          Length:         182
Score:                  58.00         Matches:        58
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            10.56%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AAI66164 (1-182)

Qy        292 SerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAsp 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 TCCGCTAATGGAGAACCTACTGTTAAACTTTATACTAGTGTTGAAAATGCTCAGCAGGAT 62

Qy        312 LysGlyIleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAsp 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 AAAGGAATCGCTATCCCTCATGATATCGATCTTGGAGAAAGTCGAGTTGTTATCCAGGAT 122

Qy        332 TyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArg 349
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TATGATAATCAGCATGAACAGGATCGACCTACTCCTAGTCCTGCTCCTAGTAGA 176

RESULT 38
AAZ00290
ID   AAZ00290 standard; DNA; 197 BP.
XX
AC   AAZ00290;
XX
DT   12-OCT-1999  (first entry)
XX
DE   HEV isolate 1440o2.seq ORF1 DNA sequence.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
DR   P-PSDB; AAY31407.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 14; Page 246; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a HEV US subtype specific sequence obtained
CC   by PCR amplification
XX
SQ   Sequence 197 BP; 54 A; 44 C; 47 G; 48 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.:              25.9          Length:         197
Score:                  64.00         Matches:        64
Percent Similarity:     98.46%        Conservative:   0
Best Local Similarity:  98.46%        Mismatches:     1
Query Match:            11.66%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AAZ00290 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTRATTTCGTCGGCTGGAGGTCAACTGTTCTACTCCCGCCCGGTTGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTTAAGTTATACACCTCTGTCGAGAATGCACAGCAGGATAAGGGC 121

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
              |||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        122 ATTGCTATACCACATGATATAGACTTAGGGGATTCCCGTGTGGTTATACAAGATTATGAY 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCARCAYGAACAA 196

RESULT 39
AAZ00292
ID   AAZ00292 standard; DNA; 197 BP.
XX
AC   AAZ00292;
XX
DT   12-OCT-1999  (first entry)
XX
DE   HEV isolate 2015o2.seq ORF1 DNA sequence.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
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```
DR   WPI; 1999-288017/24.
DR   P-PSDB; AAY31409.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 14; Page 248; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a HEV US subtype specific sequence obtained
CC   by PCR amplification
XX
SQ   Sequence 197 BP; 53 A; 50 C; 47 G; 43 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.:                25.9          Length:          197
Score:                    64.00         Matches:         64
Percent Similarity:       98.46%        Conservative:    0
Best Local Similarity:    98.46%        Mismatches:      1
Query Match:              11.66%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x AAZ00292 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTRATTTCGTCGGCTGGAGGCCAGCTCTTCTACTCCCGCCCAGTCGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTTAAATTGTATACATCCGTCGAGAATGCGCAGCAGGACAAGGGC 121

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
              |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        122 ATTGCCATACCACATGATATAGATCTAGGAGATTCCCGCGTGGTTATCCAGGATTATGAY 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCARCAYGAACAA 196

RESULT 40
AAZ00272
ID   AAZ00272 standard; DNA; 197 BP.
XX
AC   AAZ00272;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Nucleic acid sequence of HEV isolate z12-orf2.con.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 13; Page 228-229; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a HEV US subtype specific sequence obtained
CC   by PCR amplification
XX
SQ   Sequence 197 BP; 54 A; 46 C; 48 G; 49 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                26.2          Length:          197
Score:                    63.00         Matches:         63
Percent Similarity:       96.92%        Conservative:    0
Best Local Similarity:    96.92%        Mismatches:      2
Query Match:              11.48%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x AAZ00272 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTAATTTCGTCGGCTGGGGGTCAACTGTTCTACTCCCGCCCTGTCGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTCAAGTTATACACATCTGTTGAGAATGCACAGCAGGATAAGGGG 121

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
              |||||||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||
Db        122 ATAGCTATTCCACATGACATAGATTTGGGCGACTCTCGTTTGGTAATCCAGGATTATGAT 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCAACACGAACAA 196

RESULT 41
AAZ00253
ID   AAZ00253 standard; DNA; 197 BP.
XX
AC   AAZ00253;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Nucleic acid sequence of HEV clone us2-orf2.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
```

```
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 5; Page 198; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a HEV US subtype specific sequence obtained
CC   by PCR amplification
XX
SQ   Sequence 197 BP; 53 A; 47 C; 50 G; 46 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:                26.2          Length:         197
Score:                    63.00         Matches:        63
Percent Similarity:       96.92%        Conservative:   0
Best Local Similarity:    96.92%        Mismatches:     2
Query Match:              11.48%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x AAZ00253 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTGATTTCGTCGGCTGGGGGCCAACTGTTTTACTCCCGCCCGGTTGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCAACAGTAAAGTTATATACATCTGTTGAGAATGCGCAGCAAGACAAGGGC 121

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
              |||   ||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        122 ATCACCATTCCACATGATATAGACCTGGGTGACTCCCGTGTGGTTATCCAGGATTATGAT 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCAGCAYGAGCAA 196

RESULT 42
AAZ00310
ID   AAZ00310 standard; DNA; 250 BP.
XX
AC   AAZ00310;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Conserved Nucleic acid sequence derived from HEV.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 11; Page 9B; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection.
CC   Sequences AAZ00300-312 represent conserved nucleic acid sequences from
CC   various strains of HEV
XX
SQ   Sequence 250 BP; 56 A; 66 C; 65 G; 63 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                26.6          Length:         250
Score:                    80.00         Matches:        80
Percent Similarity:       96.39%        Conservative:   0
Best Local Similarity:    96.39%        Mismatches:     3
Query Match:              14.57%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x AAZ00310 (1-250)

Qy        258 AlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTCTAACATTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCA 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        122 ACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCC 181

Qy        318 HisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        182 CACGATATCGATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAG 241

Qy        338 GlnAspArg 340
              ||||||||
Db        242 CAGGATCGG 250

RESULT 43
AAZ00311
ID   AAZ00311 standard; DNA; 250 BP.
XX
AC   AAZ00311;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Conserved Nucleic acid sequence derived from HEV.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
```

XX
PF 15-OCT-1998; 98WO-US021941.
XX
PR 15-OCT-1997; 97US-0061199P.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Schlauder GG, Erker JC, Desai SM, Dawson GJ, Mushahwar IK;
XX
DR WPI; 1999-288017/24.
XX
PT Detection of United States isolates of hepatitis E virus.
XX
PS Example 11; Page 9B; 260pp; English.
XX
CC The invention provides a method for detecting a US (sub)type hepatitis E
CC virus (US-HEV), or its naturally occurring variants in a sample by
CC treatment with a binding partner specific for a marker of the virus, and
CC then detecting any complex formed. The method is used to diagnose
CC infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC are useful in vaccines or for passive immunisation. The polypeptides are
CC also used to raise specific antibodies (useful as immunoassay reagents).
CC Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC usual hybridisation and amplification assays for detecting infection.
CC Sequences AAZ00300-312 represent conserved nucleic acid sequences from
CC various strains of HEV
XX
SQ Sequence 250 BP; 53 A; 63 C; 60 G; 74 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	30.8	Length:	250
Score:	66.00	Matches:	66
Percent Similarity:	79.52%	Conservative:	0
Best Local Similarity:	79.52%	Mismatches:	17
Query Match:	12.02%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AAZ00311 (1-250)

```
Qy        258 AlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCCTGACTCTGTTTAATCTTGCTGATACGCTTCTTGGTGGTTTACCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCTGTTCAGAATTGATTTCGTCGGCTG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIlePro 317
                 |||         |||           ||||||||||||||||||    ||||||
Db        122 GGGGTCAACTGTTTTACTCCCGCCCTGTTTGCGCAGCAAGACAAGGGCATCACCATTCCA 181

Qy        318 HisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        182 CACGACATAGATTTAGGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCACGAA 241

Qy        338 GlnAspArg 340
              ||||||||
Db        242 CAAGATCGA 250
```

Search completed: July 26, 2005, 08:58:39
Job time : 70 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2005, 08:57:28 ; Search time 24 Seconds
(without alignments)
2.381 Million cell updates/sec

Title: US-09-769-066-15
Perfect score: 549
Sequence: 1 AVAPAHDTPPVPDVDSRGAI.....QSTVAELQRLKMKVGKTREL 549

Scoring table: UNITARY_AA
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 43 seqs, 52040 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 43 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=soft -Q=Pending_Patents_AA_Main:US-09-769-066-15
-DB=rng15.seq -SUFFIX=pto -OUT=foley066-15.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=unitary_AA -TRANS=human40.cdi
-LIST=43 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=43
-MODE=LOCAL -OUTFMT=pto -NORM=stat -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-NCPU=6 -NEG_SCORES=0 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : rng15.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	549	100.0	1647	1	AAT27109	Hepatitis E virus
2	548	99.8	1647	1	AAV61686	Hepatitis E virus
3	549	100.0	1983	1	AAT96959	Hepatitis E virus
4	548	99.8	1983	1	AAV61688	Hepatitis E virus
5	547	99.6	1984	1	AAQ86592	Hepatitis E virus
6	547	99.6	1990	1	ABL60053	Hepatitis E virus
7	547	99.6	1990	1	ADB97808	HEV ORF2 DNA #SEQ
8	549	100.0	2049	1	AAT27107	Hepatitis E virus
9	549	100.0	2094	1	AAQ47129	HEV third and seco
10	549	100.0	2094	1	AAQ46813	Burma strain HEV O
11	547	99.6	2054	1	AAS01448	Hepatitis E virus
12	520	94.7	1647	1	AAT27110	Hepatitis E virus
13	533	97.1	1989	1	ABL60054	Hepatitis E virus
14	533	97.1	1989	1	ADB97809	HEV related DNA #S
15	519	94.5	1980	1	ABZ23919	Swine HEV open rea
16	520	94.7	2058	1	AAT27108	Hepatitis E virus
17	510	92.9	2019	1	AAI71516	Hepatitis E virus
18	506.5	92.3	1980	1	AAT96960	Hepatitis E virus
19	482.5	87.9	1643	1	AAQ27436	DNA encoding epide
20	327	59.6	984	1	AAT27111	Hepatitis E virus
21	327	59.6	984	1	AAT96965	Hepatitis E virus
22	322	58.7	1020	1	AAZ00231	Nucleic acid seque
23	305	55.6	984	1	AAT27112	Hepatitis E virus
24	305	55.6	984	1	AAT96966	Hepatitis E virus
25	305	55.6	1026	1	AAZ00279	HEV US and CMP-KDO
26	296	53.9	960	1	AAZ00282	HEV US recombinant
27	284	51.7	899	1	AAZ00129	Nucleic acid seque
28	252	45.9	810	1	AAS01434	Hepatitis E virus
29	262	47.7	960	1	AAZ00193	Nucleic acid seque
30	255	46.4	920	1	AAZ00277	Nucleic acid seque
31	242	44.1	901	1	AAZ00255	Nucleic acid seque
32	239	43.5	890	1	AAZ00276	Nucleic acid seque
33	212	38.6	678	1	AAZ00212	Nucleic acid seque
34	83	15.1	250	1	AAZ00309	Conserved Nucleic
35	83	15.1	250	1	AAZ00307	Conserved Nucleic
36	83	15.1	250	1	AAZ00308	Conserved Nucleic
37	58	10.6	182	1	AAI66164	Hepatitis E virus
38	64	11.7	197	1	AAZ00290	HEV isolate 1440o2
39	64	11.7	197	1	AAZ00292	HEV isolate 2015o2
40	63	11.5	197	1	AAZ00272	Nucleic acid seque
41	63	11.5	197	1	AAZ00253	Nucleic acid seque
42	80	14.6	250	1	AAZ00310	Conserved Nucleic
43	66	12.0	250	1	AAZ00311	Conserved Nucleic

ALIGNMENTS

RESULT 1
AAT27109
ID AAT27109 standard; DNA; 1647 BP.
XX
AC AAT27109;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Burma strain) 62K antigen DNA.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid; ds.
XX
OS Hepatitis E virus; Burma strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
DR P-PSDB; AAR96090.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Disclosure; Page 72-73; 125pp; English.
XX
CC A DNA sequence (AAT27109) codes for 62K antigen (AAR96091) comprising the
CC C-terminal 549 amino acids of hepatitis E virus (HEV) Burma strain capsid
CC protein (AAR96089). It is obtd. by PCR amplification of HEV Burma ORF-2
CC (AAT27107) from pBET1 plasmid. The amplified fragment is inserted into
CC vector pGEX for prodn. 62K in E. coli cells. Expression of full-length
CC ORF-2 in Sf9 insect cells using a baculovirus system also results in
CC prodn. of 62K antigen (see also AAR96101 and AAR96103). 62K represents an
CC improved antigen, in comparison to bacterial expressed proteins, for use
CC in HEV diagnostic assays, and also has excellent immunogenic properties.
CC (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 1647 BP; 302 A; 533 C; 391 G; 421 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.454	Length:	1647
Score:	549.00	Matches:	549
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AAT27109 (1-1647)

```
Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 60

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 120

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
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Db        121 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 180

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 240

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 300

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        301 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 360

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 420

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 480

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 540

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 600

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 660

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Db        661 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 720

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
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Db        721 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 780

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 840

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Db        841 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 900

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
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Db        901 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 960

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Db        961 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1020

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Db       1021 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1080

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Db       1081 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1140

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       1141 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1200

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
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Db       1201 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1260

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Db       1261 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1320

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1380

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1440

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1500

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1560

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1620

Qy        541 MetLysValGlyLysThrArgGluLeu 549
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Db       1621 ATGAAGGTGGGTAAAACTCGGGAGTTG 1647
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```
RESULT 2
AAV61686
ID   AAV61686 standard; DNA; 1647 BP.
XX
AC   AAV61686;
XX
DT   03-DEC-1998  (first entry)
XX
DE   Hepatitis E virus hollow particle protein ORF2 DNA.
XX
KW   Hollow particle protein; virus; antibody; detection; immunoassay;
KW   infection; ss.
XX
OS   Hepatitis virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1647
FT                   /*tag= a
FT                   /product= "hollow particle protein"
FT                   /note= "No start codon given for ORF2"
XX
PN   JP10234383-A.
XX
PD   08-SEP-1998.
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XX
PF 28-FEB-1997; 97JP-00062445.
XX
PR 28-FEB-1997; 97JP-00062445.
XX
PA (DENK-) DENKA SEIKEN KK.
PA (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR WPI; 1998-535037/46.
DR P-PSDB; AAW76367.
XX
PT Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids
PT encoding it - useful for more accurate detection of HEV in samples, using
PT immuno-assays and nucleic acid hybridisation.
XX
PS Claim 1; Page 15-17; 29pp; Japanese.
XX
CC This sequence encodes a Hepatitis E viral hollow particle protein
CC described as ORF2. This polypeptide can be used to raise antibodies to
CC detect HEV infection in samples, e.g. by immuno-assay based techniques,
CC and the nucleic acid can be used for the same in nucleic acid
CC hybridisation assays. The polypeptide and nucleic acid allow more
CC accurate detection of HEV than previously possible
XX
SQ Sequence 1647 BP; 303 A; 535 C; 390 G; 419 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.46	Length:	1647
Score:	548.00	Matches:	548
Percent Similarity:	99.82%	Conservative:	0
Best Local Similarity:	99.82%	Mismatches:	1
Query Match:	99.82%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AAV61686 (1-1647)

```
Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
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Db          1 GCGGTCGCTCCAGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCTCGCGGCGCCATC 60

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGCGCCGGCAGTATAATCTATCAACATCTCCCCTCACCTCTTCCGTGGCCACCGGCACT 120

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAAT 180

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 240

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTC 300

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 360

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 420

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 480

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
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Db        481 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAACACA 540

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Db        541 CCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 600

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Db        601 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 660

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAG 720

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 780

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGTTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 840

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Db        841 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCGGCCAATGGCGAGCCGACTGTTAAG 900

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
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Db        901 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 960

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Db        961 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGG 1020

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Db       1021 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1080

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Db       1081 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1140

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       1141 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1200

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
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Db       1201 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1260

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Db       1261 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1320

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
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Db       1321 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1380

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
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Db       1381 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1440

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuGluGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCCGTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1500

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
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Db       1501 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1560

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
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Db       1561 CCTCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1620

Qy        541 MetLysValGlyLysThrArgGluLeu 549
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Db       1621 ATGAAGGTGGGTAAAACTCGGGAGTTA 1647

RESULT 3
AAT96959
ID   AAT96959 standard; DNA; 1983 BP.
XX
AC   AAT96959;
XX
DT   17-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   26-FEB-1998  (first entry)
XX
DE   Hepatitis E virus Burma strain ORF2.
XX
KW   Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
KW   diagnosis; HEV; ds.
XX
OS   Hepatitis E virus; - Burma strain.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1983
FT                   /*tag=  a
FT                   /product= "ORF2_protein"
XX
PN   US5686239-A.
XX
PD   11-NOV-1997.
XX
PF   09-MAY-1994;   94US-00240049.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   17-JAN-1992;   92US-00822335.
PR   20-APR-1992;   92US-00870985.
PR   01-MAY-1992;   92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Tam AW,  Reyes GR,  Yarbough PO;
XX
DR   WPI; 1997-558132/51.
DR   P-PSDB; AAW35826.
XX
PT   Diagnosis of hepatitis E virus Burma and Mexico strain infection - by
PT   immunoassay with hepatitis E virus peptide antigens.
XX
PS   Disclosure; Col 23-24; 36pp; English.
XX
CC   A method has been developed for detecting hepatitis E virus (HEV)
CC   antibodies (Ab). The method comprises: (a) reacting a serum sample with a
CC   HEV peptide antigen; and (b) examining the peptide for the presence of
CC   bound Ab, where the presence of bound Ab indicates the presence of HEV
CC   Ab. The present sequence encodes the protein from the open reading frame,
CC   ORF2, from HEV Burma strain. The method can be used to diagnose infection
CC   with the enterically transmitted non-A/non-B viral hepatitis agent HEV,
CC   specifically the HEV Burma and Mexico strains. (Updated on 25-MAR-2003 to
CC   correct PF field.) (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ   Sequence 1983 BP; 340 A; 665 C; 486 G; 492 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                0.547          Length:          1983
Score:                    549.00         Matches:         549
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-15 (1-549) x AAT96959 (1-1983)
```

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Qy         1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
Db       334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 393

Qy        21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
Db       394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy        41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
Db       454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 513

Qy        61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
Db       514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy        81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
Db       574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy       101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
Db       634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy       121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
Db       694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy       141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
Db       754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy       161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
Db       814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873

Qy       181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
Db       874 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy       201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
Db       934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy       221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
Db       994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1053

Qy       241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
Db      1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy       261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
Db      1114 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy       281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
Db      1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy       301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
Db      1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy       321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
Db      1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1353

Qy       341 ProThrProSerProAlaProSerArgProProheSerValLeuArgAlaAsnAspValLeu 360
Db      1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413
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```
Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
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Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
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Db       1774 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
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Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTG 1980
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RESULT 4
AAV61688
ID AAV61688 standard; DNA; 1983 BP.
XX
AC AAV61688;
XX
DT 03-DEC-1998 (first entry)
XX
DE Hepatitis E virus hollow particle protein DNA #2.
XX
KW Hollow particle protein; virus; antibody; detection; immunoassay;
KW infection; ss.
XX
OS Hepatitis virus.
XX
PN JP10234383-A.
XX
PD 08-SEP-1998.
XX
PF 28-FEB-1997; 97JP-00062445.
XX
PR 28-FEB-1997; 97JP-00062445.
XX
PA (DENK-) DENKA SEIKEN KK.
PA (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR WPI; 1998-535037/46.
DR P-PSDB; AAW76369.
XX
PT Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids
PT encoding it - useful for more accurate detection of HEV in samples, using
PT immuno-assays and nucleic acid hybridisation.
XX
PS Claim 13; Page 24-26; 29pp; Japanese.
XX
CC This sequence encodes a Hepatitis E viral hollow particle protein. This
CC polypeptide can be used to raise antibodies to detect HEV infection in
CC samples, e.g. by immuno-assay based techniques, and the nucleic acid can
CC be used for the same in nucleic acid hybridisation assays. The
CC polypeptides and nucleic acids allow more accurate detection of HEV than
CC previously possible
XX
SQ Sequence 1983 BP; 342 A; 665 C; 485 G; 491 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.554	Length:	1983
Score:	548.00	Matches:	548
Percent Similarity:	99.82%	Conservative:	0
Best Local Similarity:	99.82%	Mismatches:	1
Query Match:	99.82%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AAV61688 (1-1983)

```
Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GCGGTCGCTCCAGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCTCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 TTGCGCCGGCAGTATAATCTATCAACATCTCCCCTCACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
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Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAACACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Db        934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAG 1053

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113
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Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CTGTTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCGGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1774 CCCGTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 CCTCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTA 1980

RESULT 5
AAQ86592
ID   AAQ86592 standard; DNA; 1984 BP.
XX
AC   AAQ86592;
XX
DT   25-MAR-2003  (revised)
DT   28-SEP-1995  (first entry)
XX
DE   Hepatitis E virus ORF2.
XX
KW   HEV; ORF2; antigen; vaccine; immunogen; ss.
XX
OS   Hepatitis E virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1983
FT                   /*tag= a
XX
PN   WO9508632-A1.
XX
PD   30-MAR-1995.
XX
PF   23-SEP-1994;   94WO-AU000572.
XX
PR   24-SEP-1993;   93AU-00001423.
PR   15-DEC-1993;   93AU-00002964.
XX
PA   (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX
PI   Anderson DA,  Locarnini SA,  Torresi J,  Li F,  Hui Z;
XX
DR   WPI; 1995-139601/18.
DR   P-PSDB; AAR70323.
XX
PT   Antigens of hepatitis E virus (HEV) - selectively immuno:reactive to
PT   convalescent and/or acute phase circulating antibodies to HEV.
XX
PS   Disclosure; Page 39-41; 78pp; English.
XX
CC   RNA from an HEV strain isolated in the Xinjiang region of China was
CC   subjected to RT-PCR to obtain fragments corresp. to ORF2 (given in
CC   AAQ86592) and ORF3 (AAQ86593) that encoded antigenic proteins (AAR70323-
CC   24, respectively). DNA fragments were manipulated into pGEX vectors for
CC   production of GST fusion proteins in E. coli. Applications include HEV
CC   infection diagnosis, therapy and vaccine development. (Updated on 25-MAR-
CC   2003 to correct PN field.)
XX
SQ   Sequence 1984 BP; 347 A; 666 C; 481 G; 490 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                0.562          Length:          1984
Score:                    547.00         Matches:         547
Percent Similarity:       99.64%         Conservative:    0
Best Local Similarity:    99.64%         Mismatches:      2
Query Match:              99.64%         Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-15 (1-549) x AAQ86592 (1-1984)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGTCGCGGTGCAGATGGGACTGCCGAGCTTACCACCACGGCTGCTACCCGCTTCATGAAG 1053

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 1113

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGTGGCCAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 1293

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1774 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCCGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1893

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTA 1980

RESULT 6
ABL60053
ID   ABL60053 standard; DNA; 1990 BP.
XX
AC   ABL60053;
XX
DT   16-AUG-2002  (first entry)
XX
DE   Hepatitis E virus ORF-2 DNA #1.
XX
KW   Hepatitis E virus; ORF-2; HEV; virucide; immunisation; gene; ds.
XX
OS   Hepatitis E virus.
XX
PN   WO200240681-A1.
XX
PD   23-MAY-2002.
XX
PF   30-SEP-2001; 2001WO-CN001469.
XX
PR   30-SEP-2000; 2000CN-00130634.
XX
PA   (YANG-) YANG SHENG TANG CO LTD.
XX
PI   Xia N,  Zhang J,  Li S,  Ge S,  Gu Y,  He Z;
XX
DR   WPI; 2002-427096/45.
XX
PT   Polypeptide fragments of hepatitis E virus (HEV) for vaccine compositions
PT   and diagnosis in preventing and treating HEV infection.
XX
PS   Example 1; Page 82-83; 91pp; Chinese.
XX
CC   The sequence encodes hepatitis E virus (HEV) ORF-2 polypeptide. The
CC   invention relates to novel n-mer polypeptides comprising amino acids of
CC   ORF-2 of HEV where n = 2-180. The polypeptides of the invention have
CC   virucide activity. The polypeptide of HEV, its fragments, and chimeric
CC   proteins, are useful for vaccine compositions and diagnosis in preventing
CC   and treating HEV infection by immunisation, which may also be applied in
CC   the diagnosis of HEV infection
XX
SQ   Sequence 1990 BP; 348 A; 666 C; 481 G; 495 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                0.563          Length:          1990
Score:                    547.00         Matches:         547
Percent Similarity:       99.64%         Conservative:    0
Best Local Similarity:    99.64%         Mismatches:      2
Query Match:              99.64%         Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-15 (1-549) x ABL60053 (1-1990)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 453
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Qy        41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
Db       454 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 513

Qy        61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
Db       514 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 573

Qy        81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
Db       574 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 633

Qy       101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
Db       634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 693

Qy       121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
Db       694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 753

Qy       141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
Db       754 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 813

Qy       161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
Db       814 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 873

Qy       181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
Db       874 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 933

Qy       201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
Db       934 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 993

Qy       221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
Db       994 CGTCGCGGTGCAGATGGGACTGCCGAGCTTACCACCACGGCTGCTACCCGCTTCATGAAG 1053

Qy       241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
Db      1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 1113

Qy       261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
Db      1114 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 1173

Qy       281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
Db      1174 GGTGGCCAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy       301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
Db      1234 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 1293

Qy       321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
Db      1294 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1353

Qy       341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
Db      1354 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1413

Qy       361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
Db      1414 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1473

Qy       381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
Db      1474 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy       401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
Db      1534 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1593

Qy       421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
Db      1594 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1653

Qy       441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
Db      1654 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1713

Qy       461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
Db      1714 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy       481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
Db      1774 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCCGCGCTAGCATTGCTTGAG 1833

Qy       501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
Db      1834 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1893

Qy       521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
Db      1894 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy       541 MetLysValGlyLysThrArgGluLeu 549
Db      1954 ATGAAGGTGGGTAAAACTCGGGAGTTA 1980
```

RESULT 7
ADB97808
ID ADB97808 standard; DNA; 1990 BP.
XX
AC ADB97808;
XX
DT 04-DEC-2003 (first entry)
XX
DE HEV ORF2 DNA #SEQ ID 2.
XX
KW Hepatitis E virus; HEV; virucide; vaccine; monoclonal antibody; NE2;
KW infection; ds.
XX
OS Hepatitis E virus.
XX
PN WO2003040187-A1.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-CN000797.
XX
PR 08-NOV-2001; 2001CN-00134643.
XX
PA (YANG-) YANG SHENG TANG CO LTD.
XX
PI Xia N, Zhang J, Gu Y, Li S, Ge S, He Z;
XX
DR WPI; 2003-441530/41.
XX
PT Hepatitis E virus monoclonal antibodies and their active fragments, for
PT use in diagnosis and developing remedies e.g. vaccines for preventing or
PT treating hepatitis E virus infection.
XX
PS Example 1; Page 131-133; 165pp; Chinese.
XX
CC The invention relates to a monoclonal antibody that binds specifically to
CC hepatitis E virus open-reading frame (ORF) 2. Also disclosed are
CC nucleotide sequences encoding the heavy-chain and/or light-chain variable
CC region of their degeneration sequences. The monoclonal antibody is
CC selected from anti-HEV monoclonal antibody 8C11 secreted by hybridoma
CC CCTCC-C200116, anti-HEV monoclonal antibody 13D8 secreted by hybridoma

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CC   CCTCC-C200114, anti-HEV monoclonal antibody 8H3 secreted by hybridoma
CC   CCTCC-C200117, and anti-HEV monoclonal antibody 16D7 secreted by
CC   hybridoma CCTCC-C200114. The monoclonal antibodies and their active
CC   fragments are useful in diagnosis and developing remedies e.g. vaccines
CC   for preventing or treating hepatitis E virus infection. From the whole
CC   HEV gene obtained in patients, the HEV ORF fragment was prepared by using
CC   the method of Aye et al. The polypeptide NE2 was then expressed and
CC   isolated after biotechnological manipulations, which was characterised.
CC   Its analogs were also produced for immunising mice and construction of
CC   hybridomas. Tests were carried out to confirm usefulness of such
CC   polypeptides and monoclonal antibodies. The current sequence represents
CC   the HEV ORF2 encoding DNA.
XX
SQ   Sequence 1990 BP; 348 A; 666 C; 481 G; 495 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                0.563          Length:          1990
Score:                    547.00         Matches:         547
Percent Similarity:       99.64%         Conservative:    0
Best Local Similarity:    99.64%         Mismatches:      2
Query Match:              99.64%         Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-15 (1-549) x ADB97808 (1-1990)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db        814 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGTCGCGGTGCAGATGGGACTGCCGAGCTTACCACCACGGCTGCTACCCGCTTCATGAAG 1053

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 1113

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGTGGCCAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 1293

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuGluGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1774 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCCGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1893

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTA 1980

RESULT 8
AAT27107
ID   AAT27107 standard; DNA; 2049 BP.
XX
AC   AAT27107;
XX
DT   16-OCT-2003  (revised)
DT   06-AUG-1996  (first entry)
XX
```

DE Hepatitis E virus (Burma strain) ORF-2.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid; ds.
XX
OS Hepatitis E virus; Burma strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
DR P-PSDB; AAR96089.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Disclosure; Page 69-70; 125pp; English.
XX
CC The hepatitis E virus (HEV) Burma strain ORF-2 (AAT27107) codes for the
CC putative capsid protein (AAR96089). PCR amplification of ORF-2 allows
CC prodn. of capsid protein or of C-terminal regions of the capsid protein
CC (see also AAR96091, AAR96093 and AAR96095) and expression in Spodoptera
CC frugiperda Sf9 insect cells using a baculovirus vector provides
CC recombinant C-terminal regions (see also AAR96101 and AAR96103) useful as
CC diagnostic reagents and in vaccines. The HEV Mexico strain ORF-2
CC (AAT27108) may similarly be used. (Updated on 16-OCT-2003 to standardise
CC OS field)
XX
SQ Sequence 2049 BP; 344 A; 686 C; 496 G; 523 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.565	Length:	2049
Score:	549.00	Matches:	549
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AAT27107 (1-2049)

```
Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
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Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1053

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db       1114 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
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Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
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Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
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Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773
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Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
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Db       1774 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
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Db       1894 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTG 1980
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RESULT 9
AAQ47129
ID AAQ47129 standard; DNA; 2094 BP.
XX
AC AAQ47129;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 11-JAN-1994 (first entry)
XX
DE HEV third and second ORFs.
XX
KW Enterically transmitted non-A non-B hepatitis; ET-NANB; vaccine; ss.
XX
OS Hepatitis E virus; Burma strain.
XX
FH Key Location/Qualifiers
FT CDS 5. .376
FT /*tag= a
FT /label= ORF3
FT CDS 46. .2094
FT /*tag= b
FT /label= ORF2
FT misc_RNA 275. .376
FT /*tag= c
FT /label= 406.4-2
FT misc_RNA 718. .2029
FT /*tag= d
FT /label= C2
FT misc_RNA 1045. .2029
FT /*tag= e
FT /label= SG3
FT misc_RNA 1882. .2029
FT /*tag= f
FT /label= 406.3-2
XX
PN WO9314116-A1.
XX
PD 22-JUL-1993.
XX
PF 15-JAN-1993; 93WO-US000459.
XX
PR 17-JAN-1992; 92US-00822335.
PR 01-MAY-1992; 92US-00876941.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
PA (USSH) US SEC DEPT HEALTH.
XX
PI Reyes GR, Bradley DW, Tam AW, Carl M;
XX
DR WPI; 1993-243144/30.
DR P-PSDB; AAR38784, AAR38785.
XX
PT New immunogenic hepatitis E virus (HEV) peptide(s) - are from the ORF1,
PT ORF2 and ORF3 regions of HEV, useful as a vaccine against HEV infection.
XX
PS Disclosure; Fig 7; 48pp; English.
XX
CC Immunogenic hepatitis E virus (HEV) peptides are selected from the ORF1,
CC ORF2 and ORF3 regions of HEV. The peptides can be used in vaccines to
CC prevent infection by HEV. The antibodies can neutralise and block HEV
CC infection and can be used to prevent or treat HEV infection. The peptides
CC and antibodies can also be used as diagnostic reagents. (Updated on 25-
CC MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 2094 BP; 353 A; 697 C; 508 G; 536 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.578	Length:	2094
Score:	549.00	Matches:	549
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AAQ47129 (1-2094)

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Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
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Db        379 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 438

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 498

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 558

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 618

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db        619 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 678

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 738

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 798

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 858

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 918

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 978

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 1038

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1098

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1158
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Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db       1159 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1218

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Db       1219 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1278

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
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Db       1279 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1338

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Db       1339 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1398

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1458

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Db       1459 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1518

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1578

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1579 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1638

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1639 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1698

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1699 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1758

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1759 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1818

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1819 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1878

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
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Db       1879 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1938

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
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Db       1939 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1998

Qy        541 MetLysValGlyLysThrArgGluLeu 549
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RESULT 10
AAQ46813
ID AAQ46813 standard; DNA; 2094 BP.
XX
AC AAQ46813;
XX
DT 25-MAR-2003 (revised)
DT 14-FEB-1994 (first entry)
XX
DE Burma strain HEV ORF2 and ORF3.
XX
KW Hepatitis E virus; vaccine; neutralising antibodies; infection; block;
KW open reading frame; antibodies; ss.
XX
OS Hepatitis E virus.
XX
FH Key   Location/Qualifiers
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FT   /note= "ORF2"
FT CDS   46. .2094
FT   /*tag= b
FT   /note= "ORF3"
XX
PN WO9314208-A2.
XX
PD 22-JUL-1993.
XX
PF 19-JAN-1993; 93WO-US000475.
XX
PR 17-JAN-1992; 92US-00822335.
PR 20-APR-1992; 92US-00870985.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Reyes GR, Bradley DW, Twu J, Purdy MA, Tam AW, Krawczynski KZ;
XX
DR WPI; 1993-243223/30.
DR P-PSDB; AAR39305, AAR39306.
XX
PT Antigen and antibody vaccines against hepatitis E virus infection -
PT contain peptide(s) derived from capsid protein C-terminal or antibodies
PT against protein.
XX
PS Disclosure; Fig 7; 43pp; English.
XX
CC The sequence is that encoding Burma strain hepatitis E virus (HEV) open
CC reading frames ORF2 and ORF3. ORF2 encodes the putative capsid protein of
CC the virus, this protein or peptide fragments of it may be used in a
CC vaccine composition for immunising an individual against HEV. Antibodies
CC raised against these peptides can also be used in such vaccines. (Updated
CC on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 2094 BP; 353 A; 697 C; 508 G; 536 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.578	Length:	2094
Score:	549.00	Matches:	549
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AAQ46813 (1-2094)

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Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 438

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 498

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 558

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 618

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 678
```

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Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 738

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 798

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 858

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 918

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 978

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 1038

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1098

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1158

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1218

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1278

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1338

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1398

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1458

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1518

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1578

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1579 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1638

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1639 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1698

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1699 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1758

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1759 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1818

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1819 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1878

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1879 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1938

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1939 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1998

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1999 ATGAAGGTGGGTAAAACTCGGGAGTTG 2025
```

RESULT 11
AAS01448
ID AAS01448 standard; cDNA; 2054 BP.
XX
AC AAS01448;
XX
DT 11-SEP-2003 (revised)
DT 18-JUL-2001 (first entry)
XX
DE Hepatitis E virus (HEV) ORF2 cDNA.
XX
KW Hepatitis E virus; HEV; E2; pE2; ORF2; immunoreactive viral peptide;
KW antigenic activity; viral infection; ss.
XX
OS Hepatitis E virus; Chinese strain D11092.
XX
FH Key   Location/Qualifiers
FT CDS   1. .1983
FT   /*tag= a
FT   /product= "Major HEV structural protein"
FT misc_feature   1180. .1990
FT   /*tag= b
FT   /note= "Corresponds to residues 1-810 of E2"
FT mutation   replace(1810. .1812, CC)
FT   /*tag= c
FT   /note= "Single base deletion present in E2"
XX
PN WO200122916-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-IB001393.
XX
PR 30-SEP-1999; 99CA-02283538.
XX
PA (UYHK-) UNIV HONG KONG.
XX
PI Ng MH, Im S, Zhang J;
XX
DR WPI; 2001-266109/27.
XX
PT New immunoreactive peptide pE2, cloned from the genome of a Chinese
PT strain of hepatitis E virus (HEV), for detecting and diagnosing HEV
PT infection and for use as a vaccine for prevention of the viral infection
PT in humans.
XX
PS Disclosure; Fig 2A-2D; 101pp; English.
XX
CC The present sequence for hepatitis E virus (HEV) ORF2 cDNA is used to
CC clone a cDNA fragment E2 (AAS01434) which encodes for a novel peptide,
CC pE2. During the cloning of the E2 fragment a single base deletion
CC (presumed to be a PCR amplification error) at position 1811 of ORF2
CC resulted in a frame shift causing the premature termination at a new stop

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CC   codon at position 1820-1822, and giving rise to a smaller peptide, pE2.
CC   Peptide pE2 is a highly immunoreactive viral peptide which can be used in
CC   the development of diagnostic methods for the detection of HEV. Peptide
CC   pE2 which has antigenic activity is also useful as a vaccine for
CC   immunising an individual against infection from HEV and for determining
CC   the presence of HEV antibodies in a biological test sample such as human
CC   blood serum or plasma for detection and diagnosis of HEV infection. An
CC   antibody against pE2 is useful for detecting an HEV particle, in a
CC   biological test sample. The use of recombinant peptides such as pE2
CC   peptide have advantage over the prior art of using live intact virus
CC   particles by avoiding the potential risk of infectivity. The ORF3
CC   (AAS01449) of HEV Chinese strain D11092 is used to clone a cDNA fragment
CC   E3 (AAS001450) which encodes pE3 peptide. (Updated on 11-SEP-2003 to
CC   standardise OS field)
XX
SQ   Sequence 2054 BP; 355 A; 687 C; 491 G; 521 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                0.582          Length:          2054
Score:                    547.00         Matches:         547
Percent Similarity:       99.64%         Conservative:    0
Best Local Similarity:    99.64%         Mismatches:      2
Query Match:              99.64%         Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-15 (1-549) x AAS01448 (1-2054)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        814 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGTCGCGGTGCAGATGGGACTGCCGAGCTTACCACCACGGCTGCTACCCGCTTCATGAAG 1053

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 1113

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGTGGCCAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 1293

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1774 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCCGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1893

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTA 1980

RESULT 12
AAT27110
ID   AAT27110 standard; DNA; 1647 BP.
XX
AC   AAT27110;
XX
DT   16-OCT-2003  (revised)
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DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Mexico strain) 62K antigen DNA.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid; ds.
XX
OS Hepatitis E virus; Mexico strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
DR P-PSDB; AAR96092.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Disclosure; Page 73-74; 125pp; English.
XX
CC A DNA sequence (AAT27110) codes for 62K antigen (AAR96092) comprising the
CC C-terminal 549 amino acids of hepatitis E virus (HEV) Mexico strain
CC capsid protein (AAR96090). It is obtd. by PCR amplification of HEV Mexico
CC ORF-2 (AAT27108). The amplified fragment is inserted into vector pGEX for
CC prodn. 62K in E. coli cells. Expression of full-length ORF-2 in Sf9
CC insect cells using a baculovirus system also results in prodn. of 62K
CC antigen (see also AAR96101 and AAR96103). 62K represents an improved
CC antigen, in comparison to bacterial expressed proteins, for use in HEV
CC diagnostic assays, and also has excellent immunogenic properties.
CC (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 1647 BP; 327 A; 497 C; 400 G; 423 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.663	Length:	1647
Score:	520.00	Matches:	520
Percent Similarity:	94.72%	Conservative:	0
Best Local Similarity:	94.72%	Mismatches:	29
Query Match:	94.72%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AAT27110 (1-1647)

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Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db          1 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 60

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 120

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||  |||  ||||||||||||||||||||||||||||
Db        121 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 180

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 240

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 300

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 360

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 420

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 480

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        481 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 540

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 600

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACGGCCCGTCACCGGCTC 660

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 720

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||  ||||||  ||||||||||||||  ||||||||||||||||||||||||||||
Db        721 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 780

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 840

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 900

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        901 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 960

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1020

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1080

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1140

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1200

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||  ||||||||||||||||||||||||  |||  |||
Db       1201 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1260

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1320

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db       1321 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1380
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Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db       1381 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1440

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
              ||||||  |||||||||  ||||||||||||||  ||||||||||||||||||||||||||
Db       1441 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1500

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||  |||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1560

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1620

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1621 GTTAAGGTGGGTAAAACTCGGGAGTTG 1647
```

RESULT 13
ABL60054
ID ABL60054 standard; DNA; 1989 BP.
XX
AC ABL60054;
XX
DT 16-AUG-2002 (first entry)
XX
DE Hepatitis E virus ORF-2 DNA #2.
XX
KW Hepatitis E virus; ORF-2; HEV; virucide; immunisation; gene; ds.
XX
OS Hepatitis E virus.
XX
PN WO200240681-A1.
XX
PD 23-MAY-2002.
XX
PF 30-SEP-2001; 2001WO-CN001469.
XX
PR 30-SEP-2000; 2000CN-00130634.
XX
PA (YANG-) YANG SHENG TANG CO LTD.
XX
PI Xia N, Zhang J, Li S, Ge S, Gu Y, He Z;
XX
DR WPI; 2002-427096/45.
XX
PT Polypeptide fragments of hepatitis E virus (HEV) for vaccine compositions
PT and diagnosis in preventing and treating HEV infection.
XX
PS Example 1; Page 83-84; 91pp; Chinese.
XX
CC The sequence encodes hepatitis E virus (HEV) ORF-2 polypeptide. The
CC invention relates to novel n-mer polypeptides comprising amino acids of
CC ORF-2 of HEV where n = 2-180. The polypeptides of the invention have
CC virucide activity. The polypeptide of HEV, its fragments, and chimeric
CC proteins, are useful for vaccine compositions and diagnosis in preventing
CC and treating HEV infection by immunisation, which may also be applied in
CC the diagnosis of HEV infection
XX
SQ Sequence 1989 BP; 347 A; 666 C; 481 G; 495 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.676	Length:	1989
Score:	533.00	Matches:	546
Percent Similarity:	99.45%	Conservative:	0
Best Local Similarity:	99.45%	Mismatches:	3
Query Match:	97.09%	Indels:	1
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x ABL60054 (1-1989)

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Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        814 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGTCGCGGTGCAGATGGGACTGCCGAGCTTACCACCACGGCTGCTACCCGCTTCATGAAG 1053

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 1113

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGTGGCCAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 1293

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Db       1414 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1474 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420

Db       1534 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1594 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460

Db       1654 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480

Db       1714 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500

Db       1774 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCC-TCCGCGCTAGCATTGCTTGAG 1832

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1833 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1892

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1893 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1952

Qy        541 MetLysValGlyLysThrArgGluLeu 549

Db       1953 ATGAAGGTGGGTAAAACTCGGGAGTTA 1979
```

RESULT 14
ADB97809
ID ADB97809 standard; DNA; 1989 BP.
XX
AC ADB97809;
XX
DT 04-DEC-2003 (first entry)
XX
DE HEV related DNA #SEQ ID 3.
XX
KW Hepatitis E virus; HEV; virucide; vaccine; monoclonal antibody; NE2;
KW infection; ds.
XX
OS Unidentified.
XX
PN WO2003040187-A1.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-CN000797.
XX
PR 08-NOV-2001; 2001CN-00134643.
XX
PA (YANG-) YANG SHENG TANG CO LTD.
XX
PI Xia N, Zhang J, Gu Y, Li S, Ge S, He Z;
XX
DR WPI; 2003-441530/41.
XX
PT Hepatitis E virus monoclonal antibodies and their active fragments, for
PT use in diagnosis and developing remedies e.g. vaccines for preventing or
PT treating hepatitis E virus infection.
XX
PS Example 1; Page 133-135; 165pp; Chinese.
XX
CC The invention relates to a monoclonal antibody that binds specifically to
CC hepatitis E virus open-reading frame (ORF) 2. Also disclosed are
CC nucleotide sequences encoding the heavy-chain and/or light-chain variable
CC region of their degeneration sequences. The monoclonal antibody is
CC selected from anti-HEV monoclonal antibody 8C11 secreted by hybridoma
CC CCTCC-C200116, anti-HEV monoclonal antibody 13D8 secreted by hybridoma
CC CCTCC-C200114, anti-HEV monoclonal antibody 8H3 secreted by hybridoma
CC CCTCC-C200117, and anti-HEV monoclonal antibody 16D7 secreted by
CC hybridoma CCTCC-C200114. The monoclonal antibodies and their active
CC fragments are useful in diagnosis and developing remedies e.g. vaccines
CC for preventing or treating hepatitis E virus infection. From the whole
CC HEV gene obtained in patients, the HEV ORF fragment was prepared by using
CC the method of Aye et al. The polypeptide NE2 was then expressed and
CC isolated after biotechnological manipulations, which was characterised.
CC Its analogs were also produced for immunising mice and construction of
CC hybridomas. Tests were carried out to confirm usefulness of such
CC polypeptides and monoclonal antibodies. The current sequence represents a
CC HEV related DNA.
XX
SQ Sequence 1989 BP; 347 A; 666 C; 481 G; 495 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.676	Length:	1989
Score:	533.00	Matches:	546
Percent Similarity:	99.45%	Conservative:	0
Best Local Similarity:	99.45%	Mismatches:	3
Query Match:	97.09%	Indels:	1
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x ADB97809 (1-1989)

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Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20

Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40

Db        394 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60

Db        454 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

Db        514 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        574 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db        754 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180

Db        814 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        874 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGTCGCGGTGCAGATGGGACTGCCGAGCTTACCACCACGGCTGCTACCCGCTTCATGAAG 1053

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 1113

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGTGGCCAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 1293

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
                ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db       1774 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCC-TCCGCGCTAGCATTGCTTGAG 1832

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1833 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1892

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1893 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1952

Qy        541 MetLysValGlyLysThrArgGluLeu 549
                |||||||||||||||||||||||||||
Db       1953 ATGAAGGTGGGTAAAACTCGGGAGTTA 1979

RESULT 15
ABZ23919
```

```
ID   ABZ23919 standard; DNA; 1980 BP.
XX
AC   ABZ23919;
XX
DT   18-MAR-2003  (first entry)
XX
DE   Swine HEV open reading frame (ORF) 2 protein encoding DNA.
XX
KW   Swine; hepatitis E virus; HEV; open reading frame; ORF 2; virucide;
KW   immunostimulant; vaccine; anti-viral; gene; ds.
XX
OS   Swine hepatitis E virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1980
FT                   /*tag=  a
FT                   /product= "ORF2 protein"
FT                   /partial
FT                   /note= "the stop codon is not indicated"
XX
PN   WO200289733-A2.
XX
PD   14-NOV-2002.
XX
PF   02-MAY-2002; 2002WO-US014100.
XX
PR   07-MAY-2001; 2001US-0289220P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Meng X,  Purcell RH,  Emerson SU;
XX
DR   WPI; 2003-129157/12.
DR   P-PSDB; ABB82786.
XX
PT   New swine hepatitis E virus open-reading frame-2 protein and DNA encoding
PT   the protein, useful for immunizing a mammal, producing antibodies and
PT   detecting antibodies to hepatitis E virus in a biological sample.
XX
PS   Disclosure; Fig 1B; 70pp; English.
XX
CC   This DNA encodes a swine hepatitis E virus (HEV) open reading frame (ORF)
CC   2 protein. The protein can be expressed by standard recombinant
CC   methodology. The ORF2 protein is useful for detecting antibodies to HEV
CC   in a biological sample and for producing antibodies. The antibodies are
CC   useful for detecting HEV in a biological sample, which is useful in
CC   diagnosis of infection and disease caused by swine HEV, and for
CC   monitoring the progression of such disease. The method is also useful for
CC   monitoring the efficacy of therapeutic agents during the course of
CC   treatment of HEV infection and disease in a mammal. The ORF2 protein can
CC   be useful as diagnostic agent and as vaccine. The antibodies are useful
CC   as anti-viral agent, and as a means for enhancing the immune response.
CC   The ORF2 protein is sufficiently closely related to human HEV, and allows
CC   evaluation as a potential source of infection in humans
XX
SQ   Sequence 1980 BP; 356 A; 620 C; 484 G; 520 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0.809          Length:          1980
Score:                  519.00         Matches:         519
Percent Similarity:     94.71%         Conservative:    0
Best Local Similarity:  94.71%         Mismatches:      29
Query Match:            94.54%         Indels:          0
DB:                     1              Gaps:            0

US-09-769-066-15 (1-549) x ABZ23919 (1-1980)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
                ||||||   ||||||   ||||||   ||||||||||||||||||||||||||||||||
Db        334 GCTGTATCACCGGCCCCCGACACAGCTCCTGTACCTGATGTTGACTCACGTGGTGCTATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
```

```
Db        394 CTGCGCCGGCAGTACAATCTGTCTACGTCCCCGCTCACGTCATCTGTCGCTGCTGGTACC 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60

Db        454 AACCTGGTTCTCTATGCCGCCCCGCTGAATCCTCTCTTGCCCCTCCAGGATGGCACCAAC 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

Db        514 ACTCATATTATGGCTACTGAGGCGTCCAATTATGCTCAGTATCGGGTTGTTCGAGCTACG 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        574 ATCCGTTATCGCCCGCTGGTGCCAAATGCTGTTGGTGGCTATGCTATCTCTATTTCTTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        634 TGGCCTCAAACTACAACCACCCCTACTTCAGTTGACATGAACTCTATTACCTCCACTGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db        694 GTCAGGATTTTGGTTCAGCCCGGTATTGCCTCCGAGTTAGTCATCCCTAGTGAGCGCCTT 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db        754 CATTACCGCAATCAAGGCTGGCGCTCTGTAGAGACCACGGGCGTGGCCGAGGAGGAAGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180

Db        814 ACCTCCGGTCTGGTAATGCTTTGCATTCACGGTTCTCCTGTTAACTCCTATACTAACACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        874 CCTTACACTGGTGCATTGGGGCTCCTTGATTTTGCATTAGAGCTTGAATTCAGAAATTTG 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db        934 ACACCCGGGAACACTAACACCCGTGTTTCCCGGTACACCAGCACAGCCCGCCATCGGCTG 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db        994 CGCCGCGGTGCTGATGGGACCGCAGAGCTTACCACCACAGCAGCCACACGTTTCATGAAG 1053

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260

Db       1054 GACTTGCATTTCACCGGCACGAACGGCGTTGGTGAGGTGGGTCGCGGTATAGCTCTAACA 1113

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db       1114 CTGTTTAACCTTGCTGATACGCTTCTTGGTGGTTTACCGACAGAATTGATTTCGTCGGCC 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db       1174 GGGGGCCAACTGTTTTACTCCCGCCCTGTCGTCTCGGCCAATGGCGAGCCGACGGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320

Db       1234 TTATATACATCTGTTGAGAATGCGCAGCAGGACAAGGGCATTACCATCCCACACGATATA 1293

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db       1294 GATCTGGGTGATTCCCGTGTGGTTATTCAGGATTATGATAACCAGCACGAGCAAGACCGA 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1354 CCTACTCCGTCACCAGCCCCCTCTCGCCCTTTCTCAGTTCTTCGCGCCAATGATGTTCTG 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1414 TGGCTCTCCCTCACCGCCGCTGAGTACGATCAGACTACATATGGGTCGTCCACCAACCCT 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1474 ATGTATGTCTCCGATACGGTCACGCTAGTTAATGTGGCCACTGGTGCTCAGGCTGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420

Db       1534 CGCTCTCTTGATTGGTCTAAAGTCACTCTGGATGGCCGCCCCCTCACTACCATTCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1594 TATTCAAAGACATTCTATGTTCTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGT 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460

Db       1654 ACCACTAAGGCCGGCTACCCGTATAATTATAATACCACTGCTAGTGATCAAATTTTGATT 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480

Db       1714 GAGAACGCGGCTGGCCACCGTGTTGCTATCTCTACCTATACCACTAGCTTGGGTGCCGGC 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500

Db       1774 CCTACCTCGATTTCCGCCGTTGGTGTGCTAGCCCCACACTCGGCTCTCGCCGTCCTTGAG 1833

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1834 GATACTGTTGATTACCCTGCTCGTGCTCATACTTTTGATGATTTCTGCCCGGAGTGCCGC 1893

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1894 ACCCTTGGTTTGCAGGGTTGTGCATTCCAGTCTACTATTGCTGAGCTTCAGCGTCTTAAA 1953

Qy        541 MetLysValGlyLysThrArgGlu 548

Db       1954 ATGAAGGTAGGTAAAACCCGGGAG 1977
```

RESULT 16
AAT27108
ID AAT27108 standard; DNA; 2058 BP.
XX
AC AAT27108;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Mexico strain) ORF-2.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid; ds.
XX
OS Hepatitis E virus; Mexico strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
DR P-PSDB; AAR96090.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Disclosure; Page 71-72; 125pp; English.
XX
CC The hepatitis E virus (HEV) Mexico strain ORF-2 (AAT27108) codes for the
CC putative capsid protein (AAR96090). PCR amplification of ORF-2 allows

```
CC   prodn. of capsid protein or of C-terminal regions of the capsid protein
CC   (see also AAR96092, AAR96094 and AAR96096) and expression in Spodoptera
CC   frugiperda Sf9 insect cells using a baculovirus vector provides
CC   recombinant C-terminal regions (see also AAR96102 and AAR96104) useful as
CC   diagnostic reagents and in vaccines. The HEV Burma strain ORF-2
CC   (AAT27107) may similarly be used. (Updated on 16-OCT-2003 to standardise
CC   OS field)
XX
SQ   Sequence 2058 BP; 372 A; 649 C; 507 G; 530 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0.83          Length:          2058
Score:                  520.00        Matches:         520
Percent Similarity:     94.72%        Conservative:    0
Best Local Similarity:  94.72%        Mismatches:      29
Query Match:            94.72%        Indels:          0
DB:                     1             Gaps:            0

US-09-769-066-15 (1-549) x AAT27108 (1-2058)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              |||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        334 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              |||||||||||||||||||||||||||||   |||   |||||||||||||||||||||||
Db        454 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              |||||||||||||||||||||||||||||||   |||||||||||||||||||||||||||
Db        814 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACGGCCCGTCACCGGCTC 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1053

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||  ||||||      ||||||||||||||   ||||||||||||||||||||||
Db       1054 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1113

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db       1234 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1293

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              .  ||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||   ||||||||||||||||||||||||   |||   |||||||||||
Db       1534 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||||
Db       1654 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
              ||||||  |||||||||  ||||||||||||||||  ||||||||||||||||||||||||
Db       1774 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1833

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||  |||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db       1834 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1893

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1953

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||
Db       1954 GTTAAGGTGGGTAAAACTCGGGAGTTG 1980

RESULT 17
AAI71516
ID   AAI71516 standard; DNA; 2019 BP.
XX
AC   AAI71516;
XX
DT   10-JAN-2002  (first entry)
XX
DE   Hepatitis E virus HEV-T1 sequence related DNA #3.
XX
KW   Hepatitis E virus; HEV-T1; hepatitis infection; ds.
XX
OS   Unidentified.
XX
```

PN CN1300771-A.
XX
PD 27-JUN-2001.
XX
PF 23-DEC-1999; 99CN-00125741.
XX
PR 23-DEC-1999; 99CN-00125741.
XX
PA (CHME-) CHINESE MEDICINE & BIOLOGIC PROD APPRAIS.
XX
PI Wang Y, Zhang H, Li H;
XX
DR WPI; 2001-550442/62.
XX
PT Hepatitis E virus gene sequence and its application.
XX
PS Claim 4; Page 29-30(Disclosure); 34pp; Chinese.
XX
CC The present invention relates to a novel nucleotide sequence and protein
CC of a new hepatitis E virus HEV-T1 and the application of the nucleotide
CC sequence and protein in diagnosing, preventing and treating hepatitis.
CC The present sequence is a DNA described in the exemplification of the
CC invention
XX
SQ Sequence 2019 BP; 368 A; 603 C; 480 G; 568 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.923	Length:	2019
Score:	510.00	Matches:	510
Percent Similarity:	93.07%	Conservative:	0
Best Local Similarity:	93.07%	Mismatches:	38
Query Match:	92.90%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AAI71516 (1-2019)

```
Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||  ||||||  ||||||||||||  ||||||||||||||||||||
Db        370 GCTGTGGCTCCGGCTCCTGACACTGCACCTGTCCCCGATGCTGATTCCCGTGGCGCTATT 429

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db        430 CTACGCCGCCAGTACAATTTGTCCACATCCCCGCTCACGTCCACTATTGCAACTGGCACC 489

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 AATTTTGTGCTATATGCTGCCCCACTTAGTCCCCTGCTACCGCTTCAGGATGGCACCAAT 549

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||
Db        550 ACCCACATCATGGCTACTGAAGCATCTAATTATGCCCAGTATCGTGTTGTTCGTGCTACC 609

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 ATCCGATATCGCCCCTTGGTGCCGAATGCCGTTGGCGGGTATGCCATATCTATCTCCTTT 669

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 TGGCCTCAGACAACGACCACCCCAACGTCTGTTGATATGAATTCAATTACCTCCACTGAT 729

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        730 GTCCGCATTCTTGTCCAGCCTGGTATAGCTTCTGAGTTGGTAACTCCCAGTGAGCGCCTG 789

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CATTATCGAAATCAAGGATGGCGTTCGGTTGAGACCTCTGGTGTCGCTGAGGAAGAAGCG 849

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        850 ACCTCTGGCCTTGTTATGCTTTGCATTCATGGGTCACCTGTGAATTCCTATACTAATACA 909

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 CCTTATACCGGTGCCCTCGGCTTACTTGACTTTGCACTCGAGCTCGAGTTTCGCAATTTG 969

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||  |||||||||  |||||
Db        970 ACACCTGGTAACACCAATACGCGCGTTTCTCGTTATTCGAGTAGCGCGCGTCACAAACTG 1029

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 CGCCGAGGGCCTGATGGTACTGCTGAGTTGACTACTACTGCCGCCACACGTTTTATGAAA 1089

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||  ||||||  ||||||||||||||||||  ||||||||||||||||||||||||
Db       1090 GACCTCCATTTTACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACT 1149

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1150 TTGTTTAATCTTGCTGATACGCTTCTCGGTGGGCTTCCGACAGAATTGATTTCGTCGGCA 1209

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db       1210 GGGGGTCAGTTATTCTACTCCCGCCCCGTTGTCTCAGCCAATGGCGAGCTGACAGTGAAA 1269

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db       1270 CTTTACACTTCAGTCGAGAACGCTCAGCAGGACAAGGGTGTAGCTATTCCACATGATATT 1329

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 GACCTTGGTGAGTCCCGTGTGGTTATTCAGGATTATGACAACCAACATGAGCAAGATCGT 1389

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 CCCACTCCCTCCCCTGCTCCCTCTCGTCCATTTTCTGTTCTTCGTGCTAATGATGTGCTT 1449

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||  |||||||
Db       1450 TGGCTTTCACTTACTGCTGCTGAGTATGATCAAACGACTTATGGCTCCTCTACCAACCCT 1509

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||  ||||||  ||||||||||||||||||||||||||||  |||||||||
Db       1510 ATGTATGTTTCTGACACTGTTACATTTGTTAACGTAGCGACTGGTGCCCAGGGGGTTTCG 1569

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||  ||||||||||||||||||||||||||||  ||||||||||||||
Db       1570 CGCTCTCTGGATTGGTCTAAGGTCACTCTCGATGGCCGTCCACTCACCACCATCCAGCAG 1629

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db       1630 TATTCTAAGACTTTCTATGTCTTGCCCCTTCGTGGTAAGCTTTCCTTTTGGGAGGCCGGC 1689

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||
Db       1690 ACCACTAAAGCCGGCTACCCTTATAATTATAACACTACTGCTAGTGACCAGATCCTGATT 1749

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||  ||||||||||||||||||  ||||||  |||||||||||
Db       1750 GAGAATGCAGCGGGCCACCGAGTTTGCATCTCTACCTACACTACTAACCTGGGCTCCGGG 1809

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuGluLeu 500
              |||||||||  ||||||||  ||||||||||||||||||||||||||||||  ||||||||
Db       1810 CCTGTGTCTGTATCTGCTGTTGGTGTCCTCGCCCCTCACTCTGCGCTGGCTGCTTTGGAG 1869

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1870 GATACCGCTGACTACCCTGCTCGCGCCCATACTTTTGATGATTTCTGCCCTGAATGCCGT 1929

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db       1930 GCACTCGGCCTTCAGGGTTGTGCCTTCCAATCTACTGTTGGTGAGTTACAGCGTCTTAAA 1989

Qy        541 MetLysValGlyLysThrArgGlu 548
              ||||||||||||||||||||||||
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```
Db       1990 ATGAAGGTGGGTAAAACCCGGGAG 2013

RESULT 18
AAT96960
ID   AAT96960 standard; DNA; 1980 BP.
XX
AC   AAT96960;
XX
DT   17-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   26-FEB-1998  (first entry)
XX
DE   Hepatitis E virus Mexico strain ORF2.
XX
KW   Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
KW   diagnosis; HEV; ds.
XX
OS   Hepatitis E virus; - Mexico strain.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1980
FT                   /*tag= a
FT                   /product= "ORF2_protein"
XX
PN   US5686239-A.
XX
PD   11-NOV-1997.
XX
PF   09-MAY-1994;   94US-00240049.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   17-JAN-1992;   92US-00822335.
PR   20-APR-1992;   92US-00870985.
PR   01-MAY-1992;   92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Tam AW,  Reyes GR,  Yarbough PO;
XX
DR   WPI; 1997-558132/51.
DR   P-PSDB; AAW35827.
XX
PT   Diagnosis of hepatitis E virus Burma and Mexico strain infection - by
PT   immunoassay with hepatitis E virus peptide antigens.
XX
PS   Disclosure; Col 25-28; 36pp; English.
XX
CC   A method has been developed for detecting hepatitis E virus (HEV)
CC   antibodies (Ab). The method comprises: (a) reacting a serum sample with a
CC   HEV peptide antigen; and (b) examining the peptide for the presence of
CC   bound Ab, where the presence of bound Ab indicates the presence of HEV
CC   Ab. The present sequence encodes the protein from the open reading frame,
CC   ORF2, from HEV Mexico strain. The method can be used to diagnose
CC   infection with the enterically transmitted non-A/non-B viral hepatitis
CC   agent HEV, specifically the HEV Burma and Mexico strains. (Updated on 25-
CC   MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to standardise OS
CC   field)
XX
SQ   Sequence 1980 BP; 364 A; 624 C; 493 G; 499 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                0.948          Length:          1980
Score:                    506.50         Matches:         517
Percent Similarity:       94.17%         Conservative:    0
Best Local Similarity:    94.17%         Mismatches:      31
Query Match:              92.26%         Indels:          1
DB:                       1              Gaps:            1
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```
US-09-769-066-15 (1-549) x AAT96960 (1-1980)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              |||||||||||||||||||||||    |||||||||||||||||||||||||||||||||
Db        334 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        394 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              |||||||||||||||||||||||||||    |||   ||||||||||||||||||||||||
Db        454 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              |||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        814 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||       |||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCAC---TCC 990

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1050

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||  ||||||      ||||||||||||||   ||||||||||||||||||||||
Db       1051 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1110

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1170

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1230

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db       1231 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1290

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1291 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1350

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1410
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 14, 2005, 02:26:53 ; Search time 9.08019 Seconds
(without alignments)
5563.078 Million cell updates/sec

Title: US-09-769-066-15_COPY_1_525
Perfect score: 2694
Sequence: 1 AVAPAHDTPPVPDVDSRGAI.....PARAHTFDDFCPECRPLGLQ 525

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2694	100.0	660	1	VHWWH2	structural protein
2	2542.5	94.4	659	1	B44212	structural protein
3	135.5	5.0	1041	2	S55862	probable membrane
4	129.5	4.8	2130	2	AB0821	probable exported
5	127	4.7	583	2	S67571	hypothetical prote
6	125.5	4.7	1306	2	S25370	MSB2 protein - yea
7	125.5	4.7	1879	2	S74915	extracellular nucl
8	125	4.6	3282	2	E82750	hemagglutinin-like
9	125	4.6	3442	2	E82589	hemagglutinin-like
10	125	4.6	3455	2	B82519	hemagglutinin-like
11	124.5	4.6	3570	2	T45025	mucin MUC5B, trach
12	122	4.5	1180	2	E86719	hypothetical prote
13	122	4.5	5188	2	B85547	probable RTX famil
14	122	4.5	5291	2	F90696	hypothetical prote
15	121.5	4.5	766	1	A47001	transcription fact
16	120.5	4.5	687	2	T09994	arginine-tRNA liga
17	120.5	4.5	1483	2	C97012	probably celluloso
18	120	4.5	636	2	S63131	probable membrane
19	120	4.5	1131	2	T41144	hypothetical serin
20	119.5	4.4	948	2	T11678	hypothetical prote
21	118	4.4	725	2	A41258	a-agglutinin core
22	117	4.3	1802	2	S69703	HKR1 protein precu
23	117	4.3	3972	2	S75251	hypothetical prote
24	116.5	4.3	796	2	T21460	hypothetical prote
25	116.5	4.3	918	2	T02759	hypothetical prote
26	116.5	4.3	1161	2	S57180	probable membrane
27	116	4.3	1367	1	S48478	glucan 1,4-alpha-g
28	115.5	4.3	1077	2	H96007	probable acriflavi
29	115.5	4.3	3507	2	T34513	hypothetical prote
30	115	4.3	1213	2	T51032	hypothetical prote
31	115	4.3	3083	2	AH2493	hypothetical prote
32	114.5	4.3	739	2	I56187	transcription fact
33	114	4.2	1350	2	AF2005	RNA polymerase bet
34	114	4.2	2054	2	T46612	multi PDZ domain p
35	113.5	4.2	1419	2	T30531	agglutinin-like ad
36	113.5	4.2	4199	2	S76412	hypothetical prote
37	113	4.2	2383	2	D64962	probable membrane
38	112.5	4.2	547	2	T41213	probable zinc fing
39	112.5	4.2	1014	1	NMCLSS	exo-alpha-sialidas
40	112.5	4.2	1324	2	S52863	DNA-binding protei
41	112.5	4.2	3013	2	AB0480	probable invasin Y
42	112	4.2	4753	1	A47437	LDL-receptor-relat
43	111.5	4.1	1104	2	S59310	probable membrane
44	110.5	4.1	448	2	AB3043	oxidoreductase Atu
45	110.5	4.1	468	2	B98243	hypothetical prote

ALIGNMENTS

RESULT 1
VHWWH2
structural protein 2 precursor - hepatitis E virus (strain Burma)
C;Species: hepatitis E virus
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: C40778
R;Tam, A.W.; Smith, M.M.; Guerra, M.E.; Huang, C.C.; Bradley, D.W.; Fry, K.E.; Reyes, G.P
Virology 185, 120-131, 1991
A;Title: Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length vi
A;Reference number: A40778; MUID:92024067; PMID:1926770
A;Accession: C40778
A;Molecule type: genomic RNA
A;Residues: 1-660 <TAM>
A;Cross-references: UNIPROT:P29326; GB:M73218; NID:g330023; PIDN:AAA45736.1; PID:g330026
A;Note: the authors translated the codon CGC for residue 2 as Ala
C;Superfamily: hepatitis E virus structural protein 2
C;Keywords: structural protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-660/Product: structural protein 2 #status predicted <SP2>

Query Match 100.0%; Score 2694; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 6.7e-180;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531
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Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 2
B44212
structural protein 2 precursor - hepatitis E virus (strain Mexico)
C;Species: hepatitis E virus
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: B44212
R;Huang, C.C.; Nguyen, D.; Fernandez, J.; Yun, K.Y.; Fry, K.E.; Bradley, D.W.; Tam, A.W.
Virology 191, 550-558, 1992
A;Title: Molecular cloning and sequencing of the Mexico isolate of hepatitis E virus (HE
A;Reference number: A44212; MUID:93079857; PMID:1448913
A;Accession: B44212
A;Molecule type: genomic RNA
A;Residues: 1-659 <HUA>
A;Cross-references: UNIPROT:Q03500; GB:M74506; NID:g330017; PIDN:AAA45732.1; PID:g330020
C;Superfamily: hepatitis E virus structural protein 2
C;Keywords: structural protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-659/Product: structural protein 2 #status predicted <SP2>

  Query Match             94.4%;  Score 2542.5;  DB 1;  Length 659;
  Best Local Similarity   94.1%;  Pred. No. 2.4e-169;
  Matches  494;  Conservative   13;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              |||||||| ||||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||  ||||||||||||||   ||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:|||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||:|||||||||||||||||||:|||||||| |::|||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||:|:|||||||||||||||| ||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              ||:||| ||||| ||||||||| ||| ||||||||||||| ||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 635


RESULT 3
S55862
probable membrane protein YNL327w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N0320
C;Species: Saccharomyces cerevisiae
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55862; S63308; S51288
R;Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin, C.
Yeast 11, 567-572, 1995
A;Title: Sequencing analysis of a 15.4 kb fragment of yeast chromosome XIV identifies the
A;Reference number: S55859; MUID:95373280; PMID:7645347
A;Accession: S55862
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1041 <MAF>
A;Cross-references: UNIPROT:P42835; EMBL:Z46259; NID:g633655; PIDN:CAA86371.1; PID:g63365
R;Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin, C.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63287
A;Accession: S63308
A;Molecule type: DNA
A;Residues: 1-1041 <MAW>
A;Cross-references: EMBL:Z71603; NID:g1302444; PID:e239572; PID:g1302445; MIPS:YNL327w
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:EGT2
A;Cross-references: SGD:S0005271; MIPS:YNL327w
A;Map position: 14L
C;Keywords: transmembrane protein
F;4-20/Domain: transmembrane #status predicted <TM1>
F;1025-1041/Domain: transmembrane #status predicted <TM2>

  Query Match              5.0%;  Score 135.5;  DB 2;  Length 1041;
  Best Local Similarity   20.6%;  Pred. No. 0.28;
  Matches  125;  Conservative   82;  Mismatches  211;  Indels  189;  Gaps   27;

Qy         29 TSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEASNYAQYRVAR---ATIRYRP 85
              |:| :|  || |  :: :| :|          :|     |::::       |    :|: |
Db        405 TTPSSSLSATETYSIISSASISVTQASYIDNSTTTAVTQSTSTIAVSSAEKLSSTLSY-- 462

Qy         86 LVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQ 145
                  ||:|    | ||||: |  || | :   :|
Db        463 -----TSNVTISVSSATQHTTTPSYVS-NSTTLSSSSVL---------------------- 495

Qy        146 GWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPY---------TGALGLLDFALELE 196
              || :|        ||        |  :  || ||      |     :  ||: :
Db        496 --ESVISSPYLANTTVSG-------ASSASQSTNPPYVSNSTTSSATQLATIAPFAINIT 546

Qy        197 FRNLTPGNTNTRVSRYSSTARHRLRRG--------ADGTAELTTTAATRFMKDL------ 242
               :::   |||  |  |||    |  |        | |:  ||||  :  : ::
Db        547 GTSISSSITNT--SSVSSTT-SSLSSGPFVSNTAVASGSYILTTTTESAQLTEIGSLIPI 603

Qy        243 ----YFTSTNGVGEIGRG-------IALTLFNLADTLLGGLPTELISSA----------- 280
                  |:|:|  :  |          || :: | :   :  : |   ::|
Db        604 STITTSTTTSGTDKTGSNKVASSTEIAQSIVNNSSLSVSTINTNAATAAANARNATFTHA 663

Qy        281 --GGQL---FYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQ 335
                | |   ::|  ::|:  :   |: |:  :  :|   ::      | :| |   |
Db        664 THSGSLQPSYHSSSLLSSTID--TKVTTATTSTSRDGSSSLAFTTGLNQSVVTGTD---- 717

Qy        336 HEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQ----STY------GSSTGPVYVSD 385
                    |  :||: : :   |   |||    ||       |:|    :
Db        718 ----------KSDTYSVISSTE----SAQVTEYDSLLPISTLKPTVVTGTSRNSTFSMV 762

Qy        386 SVTLVNVATG-----AQAVARSLDWTKVTLDGR--PLSTIQ------------------ 419
              | | :  ||      | :|  |    :||  |   |:||::
Db        763 SSTKLTEATATDKGDAYSVISSTQSAQVTEYGSMLPISTLETPTVIMSTDESGYFTLTTC 822

Qy        420 -------QYSKTFFVLPLRGKLSFWEAG--------TTKAGYPYNYNTTASDQLLVENAA 464
                    :|      :  | | : :   |         ||      | :|:    : |
Db        823 TESGQATEYGSLIPISTLDGSVIYTFTGESVVVGYSTTVGAAQYAQHTSL---VPVSTIK 879

Qy        465 GHRVAIST-------YTTSLGAG---------PVSI---SAVAVLAPHSALALLEDTLDY 505
              | : ::||       |:|::||           |||    |  ::    | :|     |:|
Db        880 GSKTSLSTEESVVAGYSTTVGAAQYAQHTSLVPVSTIKGSKTSLSTEESVVAGYSTTVDS 939

Qy        506 PARA-HT 511
```

```
Db        940 AQYAEHT 946


RESULT 4
AB0821
probable exported protein STY2760 [imported] - Salmonella enterica subsp. enterica serov
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB0821
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0821
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2130 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02718.1; PID:g16503731; GSPDB:GN00176
C;Genetics:
A;Gene: STY2760

  Query Match             4.8%;  Score 129.5;  DB 2;  Length 2130;
  Best Local Similarity   21.4%;  Pred. No. 2.1;
  Matches  108;  Conservative   59;  Mismatches  217;  Indels  121;  Gaps   21;

Qy         28 STSPLTSSVATGTNLVLYAAPLSPLLPLQ--DGTNTHIMATEASNYAQYRVARATIRYRP 85
              :||  || :|:  | | |  : |: | |  ||:  | :  :  :  | :|       :|
Db        985 NTSVYTSCLAS-DNPVPAAITIEPVDPSQWYDGSGVHALKVKKGDTLQLKVTVKDASGKP 1043

Qy         86 LVPNAV------GGYAISISFWP-------QTTTTPTSVDMNSITSTDVRILVQPGIASE 132
               || |       ||     :         |   || :|  |:  |  ::  | |
Db       1044 -VPEAPFVLTRGDGYDRKGEKYTAQDGSDLQNIVTPVVIDGESLAWTTTKMGSQTGPDGT 1102

Qy        133 LVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFA 192
              :|    |       | |:  |: : |  | |  :        : :   :|        | :
Db       1103 RIISVTRPD--THGTRTAITATLYENVAVSASI------DTIFTVVTSP--------DVS 1146

Qy        193 LELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAE--------------LTTTAATR 237
              :   : ::||  |    : |    :        | ||              | | :
Db       1147 VARMWGHMTPSLTAADSAVYKRPLLYDELASKTGAAEYPEDNERWVVFYGPNTTKTVSPE 1206

Qy        238 FMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEP 297
                || |   :                |:|    |   |                :| | |
Db       1207 ACSKGYFPSVEQL--------------DSLYSKYPNGAIK------------TAQGWP 1238

Qy        298 TVKLYTSVENAQQDKGIAIPHD---IDLGES--RVV--IQDYDNQHEQDRPTPSPAPSRP 350
               :: | |  ||       | |:|   :|| :   | |  | | | |::    || |   |
Db       1239 IIRSYWSGTNAGTITPGAPPYDYYTVDLNDDAHRKVPNISDSDRQYQICAATPQPLAGR- 1297

Qy        351 FSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTL 410
                    :   | | : |       :       |||: | | |   |    : :|  :|
Db       1298 --------ITLTSTLATDSDIQAVKAKN-----SDSIPL--VITTTDAAGNPVPYTPFSL 1342

Qy        411 DGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYN------TTASDQLLVENAA 464
               |   | :  | ||      |  :   |  | :   : ||          | :|
Db       1343 I-RDAGTARNTSYTF-----TGSTNMMLAPPTGSAQQFYYNGYTIYGATGAD-------- 1388

Qy        465 GHRVAISTYTTSLGAGPVSISAVAV 489
                |: | | : | |  ::   |:
Db       1389 --GTAVLTLTQAAGPGVKNVITAAL 1411


RESULT 5
S67571
hypothetical protein YDL038c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein D2726
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C;Accession: S67571
R;Paulin, L.; Saren, A.M.; Laamanen, P.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67560
A;Accession: S67571
A;Molecule type: DNA
A;Residues: 1-583 <PAU>
A;Cross-references: UNIPROT:Q99175; EMBL:Z74087; NID:g1431021; PID:e252991; PID:g1431023;
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YDL038c
A;Cross-references: SGD:S0002196
A;Map position: 4L
C;Superfamily: pig submaxillary mucin

  Query Match             4.7%;  Score 127;  DB 2;  Length 583;
  Best Local Similarity   20.6%;  Pred. No. 0.47;
  Matches  106;  Conservative   82;  Mismatches  241;  Indels   86;  Gaps   17;

Qy         28 STSPLTSS-VATGTNLVLYAAPLSPLLPLQD---GTNTHIMATEASNYAQYRVARATIRY 83
              | | :|| | | |        | : |:    |    |: :|    :::     :  :|
Db         79 SIDPTSSSDVITSTVQTTSIEPTTSLVSSNDITTSTSLNISVVISTSTDSTSLIESTTTV 138

Qy         84 RPLVPNAVGG-YAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIAS---ELVIPSER 139
                |   ::| | |    |    |:| |||        |:||     |  :|    || |:
Db        139 GPHASSSVAGMYRTRSSDEVTTSTDPTS-------SSDVATSADPTSSSAVTTLVDPTTS 191

Qy        140 LHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFALELEFRN 199
              :         | :: | :  ::      :    |:::| :  | | |           :
Db        192 V---------VISTSVDQTSSSDVATSVDPTTSVISSTSADPTTSA------------DS 230

Qy        200 LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIAL 259
              |     | |   ||           |    ||::  |          ::||   :
Db        231 TTSTVQTTSVDPTSSVVSSAPVDPASSVVSLTSSYPTSSSTVTISANSNGSATLA----- 285

Qy        260 TLFNLADTLLGGLPTELISSAGGQLFYSRP--------VVSANGEPTVKLYTSVE-NAQQ 310
                | |       : ::||:|      |           | | : |||  : :|    : :
Db        286 -----AQTTSIDPVSSIVSSSGATTIISSASIDPASSVVSSTSSEPTSFIVSSTSVYSTR 340

Qy        311 DKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYD 370
              |     |:      :::        ||  | | : :   |   : |:   |:  :: |
Db        341 PSGPTTSTDLATFSDTIILRVSTTSTSQDTQTVSSSLTDMVSSTGSADLSVSSIQRSQVD 400

Qy        371 QSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTK-----------VTLDGRPLSTI 418
              ||:  |  ||| : |    : :||    : ||  ::             |||     ::
Db        401 PSTFAVSNSPVYPTASTG--STSTGIPIASESLSLSRQQGISATSSSSIVTLTPVDSASS 458

Qy        419 QQYSKTFFVLP----------LRGKLSFWEA-GTTKAGYP----YNYNTTASDQLLV-EN 462
              : | |  : |           :  :|  :|  :||: ||     :  | ||:  ||  :
Db        459 SRSSATSIIKPNMPVSSNDSKTQSSVSVVDAFQSTKSSYPSITSADPTTLASENGLVGSS 518

Qy        463 AAGHRVAIS-TYTTSLGAGPVSISAVAVLAPHSAL 496
              :: | : :  || ::  :    :| |      |: |
Db        519 SSAHPITLDRTYASAHASVTDIVSRVTDSTRHTTL 553


RESULT 6
S25370
MSB2 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein G4017; protein YGR014w
C;Species: Saccharomyces cerevisiae
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S25370; S64305
R;Bender, A.; Pringle, J.R.
Yeast 8, 315-323, 1992
A;Title: A Ser/Thr-rich multicopy suppressor of a cdc24 bud emergence defect.
A;Reference number: S25370; MUID:92383951; PMID:1514328
A;Accession: S25370
A;Molecule type: DNA
A;Residues: 1-1306 <BEN>
A;Cross-references: UNIPROT:P32334; GB:M77354; NID:g171993; PIDN:AAA34798.1; PID:g171994
R;Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996
```

A;Reference number: S64071
A;Accession: S64305
A;Molecule type: DNA
A;Residues: 1-1306 <RIE>
A;Cross-references: EMBL:Z72799; NID:g1322977; PID:g1322978; MIPS:YGR014w
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:MSB2
A;Cross-references: SGD:S0003246; MIPS:YGR014w
A;Map position: 7R
C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase
C;Keywords: transmembrane protein
F;3-19/Domain: transmembrane #status predicted <TM1>
F;1189-1205/Domain: transmembrane #status predicted <TM2>

Query Match 4.7%; Score 125.5; DB 2; Length 1306;
Best Local Similarity 19.9%; Pred. No. 1.9;
Matches 110; Conservative 91; Mismatches 212; Indels 141; Gaps 24;

```
Qy         27 LSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEASNYAQYRVARATIRYRP- 85
Db        441 LDSSSLASSSASSSDLTDYGVSSTASIPLLSASE------QASTSSSFSVVSPSVSFVPS 494

Qy         86 ---------LVPNAV-----------GG-----------YAISISFWPQTTTTPTSVDM 113
Db        495 QSSSDVASTSAPSVVSSSFSYTSLQAGGSSMTNPSSSTIVYSSSTGSSEESAASTASATL 554

Qy        114 NSITSTDV--RILVQPGIASELVIPSERLH---------------YRNQGW--------- 147
Db        555 SGSSSTYMAGNLQSQPPSTSSLLSESQATSTSAVLASSSVSTTSPYTTAGGASTEASSLI 614

Qy        148 --RSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTG-----ALGLLDFALELEFRNL 200
Db        615 SSTSAETSQVSYSQSTTALQTSSFASSSTTEGSETSSQGFSTSSVLVQMPSSISSEF--- 671

Qy        201 TPGNTNTRVSRYSSTARHR------LRRGADGTAELTTTAAT-RFMKDL---YFTSTNGV 250
Db        672 SPSQTTTQMNSASSSSQYTISSTGILSQVSDTSVSYTTSSSSVSQVSDTPVSYTTSSSSV 731

Qy        251 GEIG-RGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQ 309
Db        732 SQVSDTPVSYTTSSSSVSQVSDTPVSYTTSSSS--------VSQVSDTPVSYTTSSSSVS 783

Qy        310 QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAE- 368
Db        784 QVSDTSVPST----SSRSSV-------SQVSDTPVPSTSSRSSVSQTSSSLQPTTTSSQR 832

Qy        369 YDQSTYGSSTGPVYVSDSVTLVNVATGAQAVA-RSLDWTKVTLDGRPLSTIQQYSKTFFV 427
Db        833 FTISTHGALSESSSVSQQASEITSSINATASEYHSIQTTAAT----------QSTT--- 878

Qy        428 LPLRGKLSFWEAGTTKAGYPYNYNTT-------ASDQLLVENAAG-HRVAIST-YTTSLG 478
Db        879 ------LSFTDANSSSASAPLEVATSTPTPSSKASSLLLTPSTSSLSQVATNTNVQTSL- 931

Qy        479 AGPVSISAVAVLAP 492
Db        932 ----TTESTTVLEP 941
```

RESULT 7
S74915
extracellular nuclease - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein sll0656
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74915
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis s.

A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74915
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1879 <KAN>
A;Cross-references: UNIPROT:P72938; EMBL:D90902; GB:AB001339; NID:g1652027; PIDN:BAA1695
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: nucH
A;Start codon: GTG

Query Match 4.7%; Score 125.5; DB 2; Length 1879;
Best Local Similarity 20.6%; Pred. No. 3.3;
Matches 118; Conservative 72; Mismatches 196; Indels 187; Gaps 26;

```
Qy         28 STSPLTSSVATGTNLVLYAAPLSPLLPLQD--------GTNT-HIMATEASNYAQYRVAR 78
Db        466 NAAPVTVSVANGVNNLLENANTTSAIKLGNIIIGDDSLGTNTLSLSGADASNF------- 518

Qy         79 ATIRYRPLVPNAV------------GGYAISISFWPQTT-TTPTSVDMNSITSTDVRIL 124
Db        519 ------EIVGNGLFLKAGTVLDFSTQSSYEVTIAVDDATLGNTP-----DAITTFTLDIT 567

Qy        125 VQPGIASELVIPSERLHYRNQGWRSVETSGVAE--EEATSGLVMLCIHGSLVN----SYT 178
Db        568 NTAGI-SDLIISEV------APWSSGNSSVGADWFEVTNTGANAIDITGWKVDDDSASFA 620

Qy        179 NTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRF 238
Db        621 NASALAGV-----------TNIAPGQSVVFV--------------DGDAN-TITA---- 649

Qy        239 MKDLYFTSTNGVG-EIGR---------GIALTLFNLADTLLGGLPTELISSAGGQLFYSR 288
Db        650 FIDLWFGGTAPAGLAIGTYGGPGLGTGGDAINLFDATGSLITG---------------- 692

Qy        289 PVVSANGEPTVKLYTSVENAQQDKGIAIPHD---------IDLGE--------------- 324
Db        693 --VTFGSSPSTSPFSTFDNALGNPSVANLSTVGSNGAFSVIDAGEGVILNGSPGAIAGSV 750

Qy        325 ---SRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYG-SSTGP 380
Db        751 SSNTTVGIAATGATGSENGPTPG-----EFTILRTGD----TSTALDVTYSISGDAANGT 801

Qy        381 VYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAG 440
Db        802 DYAAIDPTTVTIPAGQSQVKISIN---------PIDDVIIESTESIVITLTDTANYDVAT 852

Qy        441 TTKAG--------YPYNYNTTASDQLLVENAAGHRVAISTYTTS-------------LGA 479
Db        853 SASSATVNIEDNDTPITVSRLQITEFMYSGADGEFIEFTNIDTSSVDMTGWSFSDSGRVA 912

Qy        480 GPVSISAVAVLAPHSALALLEDTLDYPARAHTF 512
Db        913 GSVDLSAFGVVQPGESVILTE------ADAETF 939
```

RESULT 8
E82750
hemagglutinin-like secreted protein XF0889 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82750
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82750
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3282 <SIM>
A;Cross-references: UNIPROT:Q9PEY9; GB:AE003928; GB:AE003849; NID:g9105798; PIDN:AAF8369
A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0889

Query Match 4.6%; Score 125; DB 2; Length 3282;
Best Local Similarity 21.6%; Pred. No. 8;
Matches 130; Conservative 63; Mismatches 212; Indels 196; Gaps 26;

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Qy          1 AVAPAHDTP------PVP-----------------DVDSRGAILRRQYNLSTSPLTSSV 36
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Db        439 SVPPATDTPPSTGTMPIPSHPQTAPVLAAGRLTLENDIDNRGGHITAGGAIDAILTTLDN 498

Qy         37 ATGTNLVLYAAPLSPL-LPLQDGTNTH---IMATEA-------SNYAQYRVARATIRYRP 85
                ||      | |: | |  |   | |    :||||       :| |       |:
Db        499 RDGT------AALNRLTLQGQRLDNQHGILTLATEATIHTHTLNNAAGQLHVNGTLDLTA 552

Qy         86 LVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQ 145
                |   |: ::    ||: |  |  |:   ||  :         |  | : :  |
Db        553 QHLNNASGHLLTTG--PQSATL-TIADLLDNTSGTL------ASAGSLTLTAATL----- 598

Qy        146 GWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFALELEFRNLTPGNT 205
                          : | | |        ::: | | : | |   |           ||   |
Db        599 ------------DTTDGTVQSGQGPLHMDAATLTAHRGTLTSQD--------TLTLTGT 637

Qy        206 NTRVSRYSSTAR--------------------HRLRRGA------------DGTAELT 231
              :| :|  ::||:                    | |:  |            :|| :|
Db        638 HTDLSHATTTAQQITLHTGDLTTAGGHLTAYGTHTLQLEARTRLDNTGGTIATNGTLDLH 697

Qy        232 TTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELI----SSAGGQLFYS 287
              | |        |: |:|   |      | || | |  ||   || |      :: || |  :
Db        698 TAALDNTGGTLHSTAT---GPNRLDITDTLTNTAGHLLLNGPTTLTTGTWTNTGGHLQIT 754

Qy        288 RPVV-------------SANGEPTVKLYTSVENAQQDKGIAIPHD-IDLGESRVVIQDY 332
              |               :| |   :::  :: |  || |:    | : |  : ::
Db        755 GPATLHATTLDNRGGILHTATGPLDLRITGTLNN--QDNGLLTTTDALTLTAASLL---- 808

Qy        333 DNQH-EQDRPTPSPAP-----SRPFSVLRANDVLWL----------SLTAAEYDQSTYGS 376
               |||   |   |:          :|:    |||           :|||::    | |
Db        809 -NQHGTLDAAGPAHLTLTGLLDNTAGLLQTAHTLWLTSAGLTNRSGTLTASQLTLDTQGH 867

Qy        377 S-----------------TGPV-------------YVSDSVTLVNVATGAQAVARSLD 404
              :                 :||:                 : : || |   ||   | :||
Db        868 TLDNTRGRLGTTTGNLTLHSGPLDNTAGLLQTAAALTIDTGAATLTNRDGGALLAATALD 927

Qy        405 WTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAA 464
               |  ||| |   ||  : |          |       | ||:  :  |   |   : |
Db        928 LTTATLDNRG-GTIDSQTAT--------HLHTTTLDNTTAGHISSSGTLQIDGTTLTNTG 978

Qy        465 G 465
              |
Db        979 G 979
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RESULT 9
E82589
hemagglutinin-like secreted protein XF2196 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82589
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82589
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3442 <SIM>
A;Cross-references: UNIPROT:Q9PBE8; GB:AE004032; GB:AE003849; NID:g9107324; PIDN:AAF8499
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2196

Query Match 4.6%; Score 125; DB 2; Length 3442;
Best Local Similarity 21.6%; Pred. No. 8.5;
Matches 130; Conservative 63; Mismatches 212; Indels 196; Gaps 26;

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Qy          1 AVAPAHDTP------PVP-----------------DVDSRGAILRRQYNLSTSPLTSSV 36
              :| || |||      |:|                   |:|:||  :     :     |
Db        439 SVPPATDTPPSTGTMPIPSHPQTAPVLAAGRLTLENDIDNRGGHITAGGAIDAILTTLDN 498

Qy         37 ATGTNLVLYAAPLSPL-LPLQDGTNTH---IMATEA-------SNYAQYRVARATIRYRP 85
                ||      | |: | |  |   | |    :||||       :| |       |:
Db        499 RDGT------AALNRLTLQGQRLDNQHGILTLATEATIHTHTLNNAAGQLHVNGTLDLTA 552

Qy         86 LVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQ 145
                |   |: ::    ||: |  |  |:   ||  :         |  | : :  |
Db        553 QHLNNASGHLLTTG--PQSATL-TIADLLDNTSGTL------ASAGSLTLTAATL----- 598

Qy        146 GWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFALELEFRNLTPGNT 205
                          : | | |        ::: | | : | |   |           ||   |
Db        599 ------------DTTDGTVQSGQGPLHMDAATLTAHRGTLTSQD--------TLTLTGT 637

Qy        206 NTRVSRYSSTAR--------------------HRLRRGA------------DGTAELT 231
              :| :|  ::||:                    | |:  |            :|| :|
Db        638 HTDLSHATTTAQQITLHTGDLTTAGGHLTAYGTHTLQLEARTRLDNTGGTIATNGTLDLH 697

Qy        232 TTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELI----SSAGGQLFYS 287
              | |        |: |:|   |      | || | |  ||   || |      :: || |  :
Db        698 TAALDNTGGTLHSTAT---GPNRLDITDTLTNTAGHLLLNGPTTLTTGTWTNTGGHLQIT 754

Qy        288 RPVV-------------SANGEPTVKLYTSVENAQQDKGIAIPHD-IDLGESRVVIQDY 332
              |               :| |   :::  :: |  || |:    | : |  : ::
Db        755 GPATLHATTLDNRGGILHTATGPLDLRITGTLNN--QDNGLLTTTDALTLTAASLL---- 808

Qy        333 DNQH-EQDRPTPSPAP-----SRPFSVLRANDVLWL----------SLTAAEYDQSTYGS 376
               |||   |   |:          :|:    |||           :|||::    | |
Db        809 -NQHGTLDAAGPAHLTLTGLLDNTAGLLQTAHTLWLTSAGLTNRSGTLTASQLTLDTQGH 867

Qy        377 S-----------------TGPV-------------YVSDSVTLVNVATGAQAVARSLD 404
              :                 :||:                 : : || |   ||   | :||
Db        868 TLDNTRGRLGTTTGNLTLHSGPLDNTAGLLQTAAALTIDTGAATLTNRDGGALLAATALD 927

Qy        405 WTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAA 464
               |  ||| |   ||  : |          |       | ||:  :  |   |   : |
Db        928 LTTATLDNRG-GTIDSQTAT--------HLHTTTLDNTTAGHISSSGTLQIDGTTLTNTG 978

Qy        465 G 465
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Db        979 G 979


RESULT 10
B82519
hemagglutinin-like secreted protein XF2775 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82519
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: B82519
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3455 <SIM>
A;Cross-references: UNIPROT:Q9P9U6; GB:AE004082; GB:AE003849; NID:g9108003; PIDN:AAF8556
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2775

  Query Match             4.6%;  Score 125;  DB 2;  Length 3455;
  Best Local Similarity   21.6%;  Pred. No. 8.6;
  Matches  130;  Conservative   63;  Mismatches  212;  Indels  196;  Gaps   26;

Qy          1 AVAPAHDTP------PVP-----------------DVDSRGAILRRQYNLSTSPLTSSV 36
              :| || |||      |:|                 |:|:|| :     :      |
Db        439 SVPPATDTPPSTGTMPIPSHPQTAPVLAAGRLTLENDIDNRGGHITAGGAIDAILTTLDN 498

Qy         37 ATGTNLVLYAAPLSPL-LPLQDGTNTH---IMATEA-------SNYAQYRVARATIRYRP 85
                ||       | |: | | |   | |    :|||        :| |       |:
Db        499 RDGT------AALNRLTLQGQRLDNQHGILTLATEATIHTHTLNNAAGQLHVNGTLDLTA 552

Qy         86 LVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQ 145
              |   |: ::    ||: | | |  |:   || :       | | : :  |
Db        553 QHLNNASGHLLTTG--PQSATL-TIADLLDNTSGTL------ASAGSLTLTAATL----- 598

Qy        146 GWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFALELEFRNLTPGNT 205
                  : | | |          ::: | | : | |   |          ||   |
Db        599 ------------DTTDGTVQSGQGPLHMDAATLTAHRGTLTSQD--------TLTLTGT 637

Qy        206 NTRVSRYSSTAR--------------------HRLRRGA------------DGTAELT 231
              :| :|  ::||:                  | |:  |              :|| :|
Db        638 HTDLSHATTTAQQITLHTGDLTTAGGHLTAYGTHTLQLEARTRLDNTGGTIATNGTLDLH 697

Qy        232 TTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELI----SSAGGQLFYS 287
              | |       |: |:|     |      | || | |  ||   || |      :: || |  :
Db        698 TAALDNTGGTLHSTAT---GPNRLDITDTLTNTAGHLLLNGPTTLTTGTWTNTGGHLQIT 754

Qy        288 RPVV--------------SANGEPTVKLYTSVENAQQDKGIAIPHD-IDLGESRVVIQDY 332
              |                :| |   :::  :: |  || |:     | : |  : ::
Db        755 GPATLHATTLDNRGGILHTATGPLDLRITGTLNN--QDNGLLTTTDALTLTAASLL---- 808

Qy        333 DNQH-EQDRPTPSPAP-----SRPFSVLRANDVLWL----------SLTAAEYDQSTYGS 376
              |||    |   |:              :|:    |||          :|||::    | |
Db        809 -NQHGTLDAAGPAHLTLTGLLDNTAGLLQTAHTLWLTSAGLTNRSGTLTASQLTLDTQGH 867
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Qy        377 S------------------TGPV-------------YVSDSVTLVNVATGAQAVARSLD 404
              :                 :||:                 : : || |   ||   | :||
Db        868 TLDNTRGRLGTTTGNLTLHSGPLDNTAGLLQTAAALTIDTGAATLTNRDGGALLAATALD 927

Qy        405 WTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAA 464
              |  ||| |   ||   : |          |       | ||:  :  |   |    : |
Db        928 LTTATLDNRG-GTIDSQTAT--------HLHTTTLDNTTAGHISSSGTLQIDGTTLTNTG 978

Qy        465 G 465
              |
Db        979 G 979


RESULT 11
T45025
mucin MUC5B, tracheobronchial [imported] - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45025
R;Desseyn, J.L.; Guyonnet-Duperat, V.; Porchet, N.; Aubert, J.P.; Laine, A.
J. Biol. Chem. 272, 3168-3178, 1997
A;Title: Human mucin gene MUC5B, the 10.7 kb large central exon encodes various alternate
A;Reference number: Z22899; MUID:97166151; PMID:9013550
A;Accession: T45025
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3570 <DES>
A;Cross-references: EMBL:Z72496; NID:g1834502; PIDN:CAA96577.1; PID:g1834503
A;Experimental source: placenta
C;Genetics:
A;Gene: MUC5B

  Query Match             4.6%;  Score 124.5;  DB 2;  Length 3570;
  Best Local Similarity   19.8%;  Pred. No. 9.8;
  Matches  112;  Conservative   56;  Mismatches  252;  Indels  147;  Gaps   19;

Qy          8 TPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAP-LSPLLPLQDGTNTHIMAT 66
              | | | |                 ||| |:  || :      ::|  :  ||:   | |   ||
Db       2892 TAPPPKV------------LTSPATTPTATSSKATSSSSPRTATTLPVLTSTATKSTAT 2938

Qy         67 EASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSI---------- 116
                :                |:  : :|   :    |: |||| :  |::|
Db       2939 SVT--------------PIPSSTLG----TTGTLPEQTTTPVAT-MSTIHPSSTPETTH 2978

Qy        117 TSTDVRILVQPGIASELVIPSERLHYRNQGWRSVE----------TSGVAEEEATSGLVM 166
              ||| :       |    ||        |   |                |   |   :| |
Db       2979 TSTVLTTKATTRATSSTSTPSST---PGTTWILTELTTAATTTAGTGPTATPSSTPGTTW 3035

Qy        167 LCIHGSLVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADG 226
              :      |  : | |  ||:   |          :    |  | |  :   |||      :  |
Db       3036 ILT--ELTTTATTTASTGSTATLSSTPGTTWILTEPSTTATVTAPPGSTATASSTQATAG 3093

Qy        227 TAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFY 286
              |  ::||| |  :     ||:        | |  |  | |       |   :        |
Db       3094 TPHVSTTATTPTV-----TSSKATPSSSPGTATALPALRSTATTPTATSFTAIPSSSLGT 3148

Qy        287 SRPVVSANGEPTVKLYTSVENAQQDK-----------------GIAIPHDIDLGESRVV 328
              :   :|     ||  : |:  ::  :                    :| |
Db       3149 TWTRLSQTTTPTATMSTATPSSTPETVHTSTVLTTTATTTGATGSVATPSSTP------- 3201

Qy        329 IQDYDNQHEQDRP---------TPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTG 379
                  |        |        ||| :|    :      :|:| |       |  ::|
Db       3202 ----GTAHTTKVPTTTTTGFTATPSSSPGTALT-----PPVWISTT-------TTPTTTT 3245

Qy        380 PVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEA 439
              |     :||  ::  |    || | |  |:                       | ::   :
Db       3246 PTTSGSTVTPSSI-PGTTHTARVLTTTTTTV------------------ATGSMATPSS 3285

Qy        440 GTTKAGYPYNYNTTASDQLLVENAAGH---------RVAISTYTTSLGAGPVSISAVAVL 490
              |  :| | :  |||:         | |              |     ||:   | : |: |
Db       3286 STQTSGTPPSLTTTAT----TITATGSTTNPSSTPGTTPIPPVLTSMATTPAATSSKATS 3341

Qy        491 APHSALALLEDTLDYPARAHTFDDFCP 517
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Db       3342 SSSPRTATTLPVLTSTATKSTATSFTP 3368
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RESULT 12
E86719
hypothetical protein yhgD [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86719
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: E86719
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1180 <STO>
A;Cross-references: UNIPROT:Q9CHH4; GB:AE005176; PID:g12723674; PIDN:AAK04855.1; GSPDB:G
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: yhgD

Query Match 4.5%; Score 122; DB 2; Length 1180;
Best Local Similarity 19.8%; Pred. No. 2.9;
Matches 124; Conservative 76; Mismatches 205; Indels 220; Gaps 31;

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Qy         26 NLSTSPLT-----SSVATGTNLVLYAAPLSPLLP----LQDGTNTHIMATE---ASNYAQ 73
Db         49 NLAFQPKTEKAQAASVSSGT-----------LVPGNTSYDTGGHTY-SGTEFANSSNYAL 96

Qy         74 YRVARATIRYRPLVPNAVGGYAI-----SISFWPQTT--TTPTSVDMNSITS-TD----- 120
Db         97 YGKAVVASNWINLVSSTANSVGLGIFNGSVSAISATTGFTLKSTIKVDSGSSLTDFTKSG 156

Qy        121 --VRILVQPGIASELVIPSE---------------------RLHYRN------------ 144
Db        157 DAIGVILTGASKAQLAANAQSSQATNDGLGIRGLPNTVFLGRDLYSNLSNVSTGSLTGID 216

Qy        145 -----QGW----------RSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLL 189
Db        217 GSATVNGWTDGPGVVMAIRNTDSSGTLQAANYPSLGSAAPYSPVTNTQNGTAYT------ 270

Qy        190 DFALELEFR-----------------NLTPGNTNTRVSRYSSTARHRLRRGADGTAELTT 232
Db        271 -FATDTSYALGVASPITSSVQEPITVTWTPDATNTASTGYTS----------GTLTFNL 318

Qy        233 TAATRFMKDLYFTSTNGV--------GEIGRGIALTLFNLADTLLGGLPTELISSAGGQL 284
Db        319 IAQ---------TTSNGALIGASAVNGGTGGYTLTTHTNLQNSLTVG----FVGGTGGN- 364

Qy        285 FYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPS 344
Db        365 -YGNLSVSLNG-------ATITGSKGTEPVPI-------------NYLN-----KVTGQ 397

Qy        345 PAPSRPFSVLRA--NDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARS 402
Db        398 PIPSMAQSSITANVNDTIGAALTAP--------SSTSPDNNTYTYVVPAAPTGYQANSAT 449

Qy        403 LDWTKVTLDGRPLSTIQQYSKT---FFV------------LPLRGKLSF-W--EAGTTKA 444
Db        450 ---TTTVLAANPASTTNTSATTVSNPIVGTTNPNALNVSYTPSQQTVLFNWAKASGTTLA 506

Qy        445 GYP----YNYNTTASDQLLVENAAGHRVAISTYTTSL------------GAGPVSISAV 487
Db        507 NLPNQIAYGATGITDASVVTDNPFSNTTLLSSYATALSNAVPTGYNITQISNGTTTVSGA 566

Qy        488 AVLAPHSALALLEDTLDYPARAHTF 512
Db        567 TTAATLAAFTSQNPTVGATSTLNTY 591
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RESULT 13

B85547
probable RTX family exoprotein [imported] - Escherichia coli (strain O157:H7, substrain E
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85547
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85547
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5188 <STO>
A;Cross-references: UNIPROT:Q8X4H5; GB:AE005174; NID:g12513368; PIDN:AAG54838.1; GSPDB:GN
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z0615

Query Match 4.5%; Score 122; DB 2; Length 5188;
Best Local Similarity 21.8%; Pred. No. 25;
Matches 114; Conservative 68; Mismatches 208; Indels 134; Gaps 24;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
Db       2535 AVAISINTVASDDVINAA---EKGTNLTLSGSTSGIESGQTVT----------VTFGGK 2580

Qy         61 THIMATEASNYAQYRVARATIRYRP--------LVPNAVGGYAISISFWPQTTTTPTSVD 112
Db       2581 TYTASVAANGSWSVNVPAADLATLPEGAANVQASVSSASGNSASATHAYSVDASAPT-LT 2639

Qy        113 MNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGS 172
Db       2640 INTIASDDILNAAEAG--SPLTI----------------SGTSTAE-TGQTVTVTLNGA 2679

Qy        173 LVNSYTNTPY----------TGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRR 222
Db       2680 ---TYTGTVQADGSWSVSVPTSALGALNAS------NYTVSATVNDKAGNPGSASHNL-- 2728

Qy        223 GADGTA---ELTTTAATRFMKD------LYFTSTNGVGEIGRGIALTLFNLADTLLGGLP 273
Db       2729 AVDTTAPVLTINTVAGDDIINDAEHAQALVISGTSSGGEXGDVVSVVL------------ 2776

Qy        274 TELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIP-HDID-LGESRVVIQD 331
Db       2777 --------------------NG----KTYTTTLDASGNWSVGVPAADVTALGSGAQTI-- 2810

Qy        332 YDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAE---------YDQSTYGSSTGPVY 382
Db       2811 --TASVSDRAGNSDDASRTVTVSLSAPVISINTIAGDDVINATEKGSDLALSGTSDQPAG 2868

Qy        383 VSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ--YSKTFFVLPLRGKLSF---- 436
Db       2869 TAITVTL-NGQNYSATTDASGNWS-VTVPASAVSALGEATYSVTASVTNAQGNSSTASHN 2926

Qy        437 WEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
Db       2927 VQVNTALPG--ITINPVATDDIINASEAGSAQTISGQVTGAAAG 2968
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RESULT 14
F90696
hypothetical protein ECs0542 [imported] - Escherichia coli (strain O157:H7, substrain RI
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F90696
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genor
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90696
A;Status: preliminary

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A;Molecule type: DNA
A;Residues: 1-5291 <HAY>
A;Cross-references: UNIPROT:Q8X2T1; GB:BA000007; PIDN:BAB33965.1; PID:g13360000; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0542

  Query Match             4.5%;  Score 122;  DB 2;  Length 5291;
  Best Local Similarity   21.8%;  Pred. No. 26;
  Matches  114;  Conservative   68;  Mismatches  208;  Indels  134;  Gaps   24;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
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Db       2535 AVAISINTVASDDVINAA---EKGTNLTLSGSTSGIESGQTVT----------VTFGGK 2580

Qy         61 THIMATEASNYAQYRVARATIRYRP--------LVPNAVGGYAISISFWPQTTTTPTSVD 112
              |:  :  |:      |  | :   |         | :| |  | :   :    : || :
Db       2581 TYTASVAANGSWSVNVPAADLATLPEGAANVQASVSSASGNSASATHAYSVDASAPT-LT 2639

Qy        113 MNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGS 172
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Qy        173 LVNSYTNTPY----------TGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRR 222
                :|| |             | ||| |: :      | |   |    :   :| | |
Db       2680 ---TYTGTVQADGSWSVSVPTSALGALNAS------NYTVSATVNDKAGNPGSASHNL-- 2728

Qy        223 GADGTA---ELTTTAATRFMKD------LYFTSTNGVGEIGRGIALTLFNLADTLLGGLP 273
               | ||    : | |    : |      |  : |:  || |  ::: |
Db       2729 AVDTTAPVLTINTVAGDDIINDAEHAQALVISGTSSGGEAGDVVSVVL------------ 2776

Qy        274 TELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIP-HDID-LGESRVVIQD 331
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Db       2777 --------------------NG----KTYTTTLDASGNWSVGVPAADVTALGSGAQTI-- 2810

Qy        332 YDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAE---------YDQSTYGSSTGPVY 382
                        ||   |   ||  :|  :  |: ::  | :          |  :  |:|  |
Db       2811 --TASVSDRAGNSDDASRTVTVSLSAPVISINTIAGDDVINATEKGSDLALSGTSDQPAG 2868

Qy        383 VSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ--YSKTFFVLPLRGKLSF---- 436
               : :||| |    :     | :|: ||:    :| : :  || |  |   :|  |
Db       2869 TAITVTL-NGQNYSATTDASGNWS-VTVPASAVSALGEATYSVTASVTNAQGNSSTASHN 2926

Qy        437 WEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
               :  |   |      |  |:| ::  : ||    ||   |   ||
Db       2927 VQVNTALPG--ITINPVATDDIINASEAGSAQTISGQVTGAAAG 2968


RESULT 15
A47001
transcription factor Oct-1 - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Sep-1999
C;Accession: A47001; A31754
R;Sturm, R.A.; Cassady, J.L.; Das, G.; Romo, A.; Evans, G.A.
Genomics 16, 333-341, 1993
A;Title: Chromosomal structure and expression of the human OTF1 locus encoding the oct-1
A;Reference number: A47001; MUID:93300505; PMID:8314572
A;Accession: A47001
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-766 <STU>
A;Note: the sequence in GenBank entry HSOCT1, release 111.0, begins with Met-24
R;Sturm, R.A.; Das, G.; Herr, W.
Genes Dev. 2, 1582-1599, 1988
A;Title: The ubiquitous octamer-binding protein Oct-1 contains a POU domain with a homeo
A;Reference number: A31754; MUID:89107993; PMID:2905684
A;Accession: A31754
A;Molecule type: mRNA
A;Residues: 'P',8-400,'R',402-766 <ST2>
A;Cross-references: GB:X13403; NID:g35126; PIDN:CAA31767.1; PID:g35127
C;Genetics:
A;Gene: GDB:POU2F1; OTF1; OCT1
A;Cross-references: GDB:120254; OMIM:164175
A;Map position: 1q22-1q23
C;Superfamily: transcription factor Oct-1; homeobox homology; POU domain homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;310-377/Domain: POU domain homology <POU>
F;403-459/Domain: homeobox homology <HOX>

  Query Match             4.5%;  Score 121.5;  DB 1;  Length 766;
  Best Local Similarity   25.7%;  Pred. No. 1.7;
  Matches   78;  Conservative   40;  Mismatches  136;  Indels   49;  Gaps   13;

Qy         28 STSPL-------TSSVATGTNLVLYAA----PLSPLLPLQDGTNTHIMATEASNYAQYRV 76
              |:||:       || |||  :||  :|     :||:|||     |::  |  |:
Db        469 SSSPIKAIFPSPTSLVATTPSLVTSSAATTLTVSPVLPLTSAAVTNLSVTGTSDTTSNNT 528

Qy         77 ARATIRYRPLVPNAVGGYAISISFWPQ---TTTTPTSVDMNSITSTDVRILVQPGIASEL 133
              |   |    |   :||   ::| |  |    :|:  :|    | | |    |  |   |::
Db        529 A-TVISTAPPASSAVTSPSLSPS--PSASASTSEASSASETSTTQTTSTPLSSPLGTSQV 585

Qy        134 VIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFAL 193
              :: :  |    |   :    | |:  | : |  :     |  |        | | |
Db        586 MVTASGL----QTAAAAALQGAAQLPANASLAAMAAAAGLNPSLMAPSQFAAGGAL---- 637

Qy        194 ELEFRNLTPGNTNTRVS---RYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGV 250
                :| ||  :  :|     :||       : |:  :|:  ||    :| | :  |
Db        638 ----LSLNPGTLSGALSPALMSNSTLATIQALASGGSLPITSLDAT---GNLVFANAGGA 690

Qy        251 GEIGRGIALTLF----NLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVE 306
               |   :  ||    ||  :||   |  |:|:|      | || | :        || |
Db        691 PNI---VTAPLFLNPQNL--SLLTSNPVSLVSAAAASAGNSAPVASLHATS-----TSAE 740

Qy        307 NAQ 309
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Db        741 SIQ 743


Search completed: July 14, 2005, 15:51:34
Job time : 14.0802 secs
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 14, 2005, 15:53:09 ; Search time 4650 Seconds
(without alignments)
5720.842 Million cell updates/sec

Title: US-09-769-066-15
Perfect score: 2813
Sequence: 1 AVAPAHDTPPVPDVDSRGAI.....QSTVAELQRLKMKVGKTREL 549

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-USER=US09769066_@CGN_1_1_5136_@runat_13072005_133014_23057 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
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2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2813	100.0	1647	6	AR170406	AR170406 Sequence
2	2813	100.0	1983	6	I73139	I73139 Sequence 1
3	2813	100.0	2049	6	AR002160	AR002160 Sequence
4	2813	100.0	2049	6	AR170404	AR170404 Sequence
5	2813	100.0	2049	6	AR232465	AR232465 Sequence
6	2813	100.0	2094	6	AR002158	AR002158 Sequence
7	2813	100.0	2094	6	AR232463	AR232463 Sequence
8	2813	100.0	7195	6	AR150915	AR150915 Sequence
9	2813	100.0	7195	6	AR207633	AR207633 Sequence
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12	2806	99.8	1983	6	E17107	E17107 Hepatitis E
13	2806	99.8	7143	14	AF185822	AF185822 Hepatitis
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16	2804	99.7	1984	6	AR278906	AR278906 Sequence
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18	2802	99.6	1983	14	AF124407	AF124407 Hepatitis
19	2802	99.6	2173	14	AF065061	AF065061 Hepatitis
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21	2800	99.5	7138	14	HPEA	M80581 Hepatitis E
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23	2800	99.5	7168	6	AR167470	AR167470 Sequence
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26	2800	99.5	7168	6	AR487996	AR487996 Sequence
27	2800	99.5	7168	6	BD084498	BD084498 Recombina
28	2800	99.5	7193	14	HPEGENA	L25547 Hepatitis E
29	2800	99.5	7204	14	AF444002	AF444002 Hepatitis
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34	2795	99.4	7200	14	HPCEGENOM	M94177 Hepataitis
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40	2779	98.8	7199	14	AF051830	AF051830 Hepatitis
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42	2775	98.6	7099	6	AX211244	AX211244 Sequence
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45	2774	98.6	7206	14	AF459438	AF459438 Hepatitis

ALIGNMENTS

RESULT 1
AR170406
LOCUS AR170406 1647 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 3 from patent US 6291641.
ACCESSION AR170406
VERSION AR170406.1 GI:17908365
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1647)
AUTHORS Fuerst,T.R., McAtee,C.Patrick., Yarbough,P.O. and Zhang,Y.-F.
TITLE Hepatitis E virus antigens and uses therefor
JOURNAL Patent: US 6291641-A 3 18-SEP-2001;
FEATURES Location/Qualifiers
source 1. .1647
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:

Pred. No.:	1.6e-192	Length:	1647
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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-769-066-15 (1-549) x AR170406 (1-1647)

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Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
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Db          1 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 60

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
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Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 180

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Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        301 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 360

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Db        361 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 420

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
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Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
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Db        721 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 780

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Db        841 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 900

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
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Db        901 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 960

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Db        961 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1020

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
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Db       1201 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1260

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Db       1261 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1320

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1380

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1440

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1500

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1560

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1620

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1621 ATGAAGGTGGGTAAAACTCGGGAGTTG 1647
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RESULT 2
I73139

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LOCUS       I73139                 1983 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 1 from patent US 5686239.
ACCESSION   I73139
VERSION     I73139.1  GI:3009278
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1983)
  AUTHORS   Reyes,G.R., Tam,A.W. and Yarbough,P.O.
  TITLE     Hepatitis E virus peptides and methods
  JOURNAL   Patent: US 5686239-A 1 11-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .1983
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN
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Alignment Scores:

Pred. No.:	2.07e-192	Length:	1983
Score:	2813.00	Matches:	549
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-769-066-15 (1-549) x I73139 (1-1983)

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Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
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```

```
Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40

Db        394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60

Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db        754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180

Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        874 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db        934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db        994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1053

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260

Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db       1114 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320

Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420

Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460

Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480

Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500

Db       1774 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1894 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 MetLysValGlyLysThrArgGluLeu 549

Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTG 1980
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RESULT 3
AR002160

LOCUS	AR002160	2049 bp	DNA	linear	PAT 04-DEC-1998

DEFINITION Sequence 3 from patent US 5741490.
ACCESSION AR002160
VERSION AR002160.1 GI:3963714
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2049)
AUTHORS Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W., Krawczynski,K.Z. and Yarbough,P.D.
TITLE Hepatitis E virus vaccine and method
JOURNAL Patent: US 5741490-A 3 21-APR-1998;
FEATURES Location/Qualifiers
source 1. .2049
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:

Pred. No.:	2.16e-192	Length:	2049
Score:	2813.00	Matches:	549
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-769-066-15 (1-549) x AR002160 (1-2049)

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Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20

Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
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```
Db        394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60

Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db        754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180

Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        874 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db        934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db        994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1053

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260

Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db       1114 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320

Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420

Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460

Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480

Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500

Db       1774 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1894 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 MetLysValGlyLysThrArgGluLeu 549

Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTG 1980
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RESULT 4
AR170404

LOCUS	AR170404	2049 bp	DNA	linear	PAT 17-DEC-2001
DEFINITION	Sequence 1 from patent US 6291641.				
ACCESSION	AR170404				
VERSION	AR170404.1 GI:17908363				
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
	Unclassified.				
REFERENCE	1 (bases 1 to 2049)				
AUTHORS	Fuerst,T.R., McAtee,C.Patrick., Yarbough,P.O. and Zhang,Y.-F.				
TITLE	Hepatitis E virus antigens and uses therefor				
JOURNAL	Patent: US 6291641-A 1 18-SEP-2001;				

FEATURES Location/Qualifiers
source 1. .2049
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.:	2.16e-192	Length:	2049
Score:	2813.00	Matches:	549
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-769-066-15 (1-549) x AR170404 (1-2049)

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Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20

Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40

Db        394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
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Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr  80

Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db        754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180

Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        874 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db        934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db        994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1053

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260

Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db       1114 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320

Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420

Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460

Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480

Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500

Db       1774 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1894 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 MetLysValGlyLysThrArgGluLeu 549

Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTG 1980
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RESULT 5
AR232465
LOCUS AR232465 2049 bp mRNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6455492.
ACCESSION AR232465
VERSION AR232465.1 GI:27274534
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2049)
AUTHORS Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W., Krawczynski,K.Z. and Yarbough,P.O.
TITLE Hepatitis E virus vaccine and method
JOURNAL Patent: US 6455492-A 3 24-SEP-2002;
FEATURES Location/Qualifiers
source 1. .2049
/organism="unknown"
/mol_type="mRNA"
ORIGIN

Alignment Scores:

Pred. No.:	2.16e-192	Length:	2049
Score:	2813.00	Matches:	549
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-769-066-15 (1-549) x AR232465 (1-2049)

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Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20

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Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40

Db        394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60

Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 513
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Qy        61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy        81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy       101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy       121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy       141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy       161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873

Qy       181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       874 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy       201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy       221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1053

Qy       241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
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Db      1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy       261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db      1114 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy       281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy       301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy       321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1353

Qy       341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy       361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy       381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy       401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy       421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy       441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy       461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy       481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1774 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy       501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy       521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1894 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy       541 MetLysValGlyLysThrArgGluLeu 549
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Db      1954 ATGAAGGTGGGTAAAACTCGGGAGTTG 1980

RESULT 6
AR002158
LOCUS       AR002158               2094 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 1 from patent US 5741490.
ACCESSION   AR002158
VERSION     AR002158.1  GI:3963712
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2094)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.D.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 5741490-A 1 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .2094
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.23e-192       Length:         2094
Score:                  2813.00         Matches:        549
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-769-066-15 (1-549) x AR002158 (1-2094)

Qy         1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       379 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 438

Qy        21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       439 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 498

Qy        41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       499 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 558

Qy        61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       559 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 618
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Qy        81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       619 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 678

Qy       101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       679 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 738

Qy       121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       739 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 798

Qy       141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Db       799 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 858

Qy       161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
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Db       859 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 918

Qy       181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       919 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 978

Qy       201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       979 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 1038

Qy       221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Db      1039 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1098

Qy       241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
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Db      1099 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1158

Qy       261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db      1159 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1218

Qy       281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1219 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1278

Qy       301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1279 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1338

Qy       321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Db      1339 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1398

Qy       341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1399 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1458

Qy       361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Db      1459 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1518

Qy       381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1519 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1578

Qy       401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1579 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1638

Qy       421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1639 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1698

Qy       441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1699 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1758

Qy       461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1759 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1818

Qy       481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1819 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1878

Qy       501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1879 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1938

Qy       521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1939 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1998

Qy       541 MetLysValGlyLysThrArgGluLeu 549
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Db      1999 ATGAAGGTGGGTAAAACTCGGGAGTTG 2025
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RESULT 7
AR232463
LOCUS       AR232463               2094 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 1 from patent US 6455492.
ACCESSION   AR232463
VERSION     AR232463.1  GI:27274532
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2094)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.O.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 6455492-A 1 24-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .2094
                     /organism="unknown"
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ORIGIN

Alignment Scores:
Pred. No.:                2.23e-192      Length:          2094
Score:                    2813.00        Matches:         549
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-09-769-066-15 (1-549) x AR232463 (1-2094)

Qy         1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       379 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 438

Qy        21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       439 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 498

Qy        41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       499 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 558

Qy        61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
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Db       559 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 618

Qy        81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db        619 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 678

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 738

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 798

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 858

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 918

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 978

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 1038

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1098

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1158

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1218

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1278

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1338

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1398

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1458

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1518

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1578

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1579 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1638

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1639 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1698

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1699 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1758

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1759 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1818

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1819 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1878

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1879 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1938

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1939 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1998

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1999 ATGAAGGTGGGTAAAACTCGGGAGTTG 2025

RESULT 8
AR150915
LOCUS       AR150915                7195 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 6 from patent US 6229005.
ACCESSION   AR150915
VERSION     AR150915.1  GI:15115506
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 7195)
  AUTHORS   Reyes,G.R., Yarbough,P.O., Bradley,D.W., Krawczynski,K.Z., Tam,A.W.
            and Fry,K.E.
  TITLE     DNA sequences of enterically transmitted non-A/non-B hepatitis
            viral agent
  JOURNAL   Patent: US 6229005-A 6 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .7195
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:                1.21e-191      Length:          7195
Score:                    2813.00        Matches:         549
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-09-769-066-15 (1-549) x AR150915 (1-7195)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
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Db       5480 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 5539

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5540 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 5599

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5600 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 5659

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5660 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 5719

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5720 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 5779
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Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5780 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 5839

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5840 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 5899

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Db       5900 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 5959

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
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Db       5960 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 6019

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6020 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 6079

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6080 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 6139

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6140 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 6199

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6200 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 6259

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6260 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 6319

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6320 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 6379

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6380 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 6439

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6440 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 6499

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6500 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 6559

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6560 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 6619

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6620 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 6679

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6680 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 6739

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6740 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 6799

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6800 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 6859

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6860 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 6919

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuGluLeu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6920 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 6979

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6980 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 7039

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7040 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 7099

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       7100 ATGAAGGTGGGTAAAACTCGGGAGTTG 7126

RESULT 9
AR207633
LOCUS       AR207633                7195 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 6 from patent US 6379891.
ACCESSION   AR207633
VERSION     AR207633.1  GI:21507438
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 7195)
  AUTHORS   Reyes,G.R., Yarbough,P.O., Bradley,D.W., Krawczynski,K.Z., Tam,A.
            and Fry,K.E.
  TITLE     Method of detecting HEV infection
  JOURNAL   Patent: US 6379891-A 6 30-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .7195
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:                1.21e-191      Length:          7195
Score:                    2813.00        Matches:         549
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-09-769-066-15 (1-549) x AR207633 (1-7195)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5480 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 5539

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5540 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 5599

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
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Db       5600 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 5659

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5660 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 5719

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5720 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 5779

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5780 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 5839
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Qy       121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
Db      5840 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 5899

Qy       141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
Db      5900 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 5959

Qy       161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
Db      5960 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 6019

Qy       181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
Db      6020 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 6079

Qy       201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
Db      6080 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 6139

Qy       221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
Db      6140 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 6199

Qy       241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
Db      6200 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 6259

Qy       261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
Db      6260 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 6319

Qy       281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
Db      6320 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 6379

Qy       301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
Db      6380 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 6439

Qy       321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
Db      6440 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 6499

Qy       341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
Db      6500 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 6559

Qy       361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
Db      6560 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 6619

Qy       381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
Db      6620 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 6679

Qy       401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
Db      6680 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 6739

Qy       421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
Db      6740 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 6799

Qy       441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
Db      6800 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 6859

Qy       461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
Db      6860 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 6919

Qy       481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
Db      6920 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCCACTCTGCGCTAGCATTGCTTGAG 6979

Qy       501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
Db      6980 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 7039

Qy       521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
Db      7040 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 7099

Qy       541 MetLysValGlyLysThrArgGluLeu 549
Db      7100 ATGAAGGTGGGTAAAACTCGGGAGTTG 7126
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RESULT 10
HPESVP
LOCUS       HPESVP                  7207 bp ss-RNA     linear   VRL 19-DEC-2000
DEFINITION  Hepatitis E structural and nonstructural protein mRNA, complete
            cds'.
ACCESSION   M73218
VERSION     M73218.1  GI:330023
KEYWORDS    nonstructural protein; viral structural protein.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 7207)
  AUTHORS   Tam,A.W., Smith,M.M., Guerra,M.E., Huang,C.C., Bradley,D.W.,
            Fry,K.E. and Reyes,G.R.
  TITLE     Hepatitis E virus (HEV): molecular cloning and sequencing of the
            full-length viral genome
  JOURNAL   Virology 185 (1), 120-131 (1991)
  MEDLINE   92024067
   PUBMED   1926770
COMMENT     Original source text: Hepatitis E virus cDNA to genomic RNA.
FEATURES             Location/Qualifiers
     source          1. .7207
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
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                     VTYEGDTSAGYNHDVSNLRSWIRTTKVTGDHPLVIERVRAIGCHFVLLLTAAPEPSPM
                     PYVPYPRSTEVYVRSIFGPGGTPSLFPTSCSTKSTFHAVPAHIWDRLMLFGATLDDQA
                     FCCSRLMTYLRGISYKVTVGTLVANEGWNASEDALTAVITAAYLTICHQRYLRTQAIS
                     KGMRRLEREHAQKFITRLYSWLFEKSGRDYIPGRQLEFYAQCRRWLSAGFHLDPRVLV
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                     LGNKTFRTSFVDGAVLETNGPERHNLSFDASQSTMAAGPFSLTYAASAAGLEVRYVAA
                     GLDHRAVFAPGVSPRSAPGEVTAFCSALYRFNREAQRHSLIGNLWFHPEGLIGLFAPF
                     SPGHVWESANPFCGESTLYTRTWSEVDAVSSPARPDLGFMSEPSIPSRAATPTLAAPL
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                     DYRLEHNPKRLEAAYRETCSRLGTAAYPLLGTGIYQVPIGPSFDAWERNHRPGDELYL
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                     TAGVPGSGKSRSITQADVDVVVVPTRELRNAWRRRGFAAFTPHTAARVTQGRRVVIDE
                     APSLPPHLLLLHMQRAATVHLLGDPNQIPAIDFEHAGLVPAIRPDLGPTSWWHVTHRW
                     PADVCELIRGAYPMIQTTSRVLRSLFWGEPAVGQKLVFTQAAKPANPGSVTVHEAQGA
                     TYTETTIIATADARGLIQSSRAHAIVALTRHTEKCVIIDAPGLLREVGISDAIVNNFF
                     LAGGEIGHQRPSVIPRGNPDANVDTLAAFPPSCQISAFHQLAEELGHRPVPVAAVLPP
                     CPELEQGLLYLPQELTTCDSVVTFELTDIVHCRMAAPSQRKAVLSTLVGRYGGRTKLY
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                     LIRSAWILQAPKESLRGFWKKHSGEPGTLLWNTVWNMAVITHCYDFRDFQVAAFKGDD
                     SIVLCSEYRQSPGAAVLIAGCGLKLKVDFRPIGLYAGVVVAPGLGALPDVVRFAGRLT
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                     /product="structural viral protein"
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                     /db_xref="GI:330025"
                     /translation="MNNMSPAAPMGSRPCALGLFCCCSSCFCLCCPRHRPVSRLAAVV
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                     TRPSAPPLPHVVDLPQLGPRR"
     CDS             5147. .7129
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                     /product="structural viral protein"
                     /protein_id="AAA45736.1"
                     /db_xref="GI:330026"
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                     SPLLPLQDGTNTHIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTT
                     PTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLV
                     MLCIHGSLVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRG
                     ADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAG
                     GQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQD
                     RPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQ
                     AVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTAS
                     DQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLEDTLDYPARAHTFD
                     DFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTREL"
ORIGIN

Alignment Scores:
Pred. No.:                1.21e-191      Length:          7207
Score:                    2813.00        Matches:         549
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       14             Gaps:            0

US-09-769-066-15 (1-549) x HPESVP (1-7207)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5480 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 5539

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5540 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 5599

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5600 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 5659

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5660 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 5719

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5720 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 5779

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5780 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 5839

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5840 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 5899

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5900 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 5959

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
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Db       5960 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 6019

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6020 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 6079

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6080 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 6139

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6140 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 6199

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6200 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 6259

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db       6260 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 6319

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6320 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 6379

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6380 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 6439

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6440 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 6499

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6500 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 6559

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Db       6560 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 6619

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6620 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 6679

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6680 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 6739

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6740 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 6799

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6800 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 6859

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6860 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 6919

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6920 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 6979

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6980 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 7039
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Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7040 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 7099

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       7100 ATGAAGGTGGGTAAAACTCGGGAGTTG 7126

RESULT 11
E17105
LOCUS       E17105                  1647 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  DNA encoding HEV hollow particle.
ACCESSION   E17105
VERSION     E17105.1  GI:5711788
KEYWORDS    JP 1998234383-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1647)
  AUTHORS   Takeda,N., Ri,T. and Miyamura,T.
  TITLE     HEPATITIS E VIRUS HOLLOW PARTICLE, GENE ENCODING THE SAME AND
            PREPARATION OF RECOMBINATION VECTOR CONTAINING THE GENE AND
            UTILIZATION OF THE RECOMBINATION VECTOR
  JOURNAL   Patent: JP 1998234383-A 1 08-SEP-1998;
            DENKA SEIKEN CO LTD, KOKURITSU KANSENSHIYOU KENKYUSHO
COMMENT     OS   Hepatitis E virus
            PN   JP 1998234383-A/1
            PD   08-SEP-1998
            PF   28-FEB-1997 JP 1997062445
            PI   TAKEDA NAOKAZU, RI TENSEI, MIYAMURA TATSUO
            PC   C12N15/09,C07K14/08,C12N5/10,C12P21/02;
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .1647
            FT                   /organism='Hepatitis E virus' FT   mat_peptide
               1. .1647
            FT                   /product='hollow particle'.
FEATURES             Location/Qualifiers
     source          1. .1647
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                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              5.1e-192        Length:         1647
Score:                  2806.00         Matches:        548
Percent Similarity:     99.82%          Conservative:   0
Best Local Similarity:  99.82%          Mismatches:     1
Query Match:            99.75%          Indels:         0
DB:                     6               Gaps:           0

US-09-769-066-15 (1-549) x E17105 (1-1647)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGGTCGCTCCAGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCTCGCGGCGCCATC 60

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
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Db         61 TTGCGCCGGCAGTATAATCTATCAACATCTCCCCTCACCTCTTCCGTGGCCACCGGCACT 120

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAAT 180

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 240

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTC 300

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 360

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 420

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 480

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAACACA 540

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 600

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 660

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAG 720

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
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Db        721 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 780

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGTTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 840

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCGGCCAATGGCGAGCCGACTGTTAAG 900

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 960

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGG 1020

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1080

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1140

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1200

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1260

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1320

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
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Db       1321 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1380

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480

Db       1381 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1440

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500

Db       1441 CCCGTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1500

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1501 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1560

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1561 CCTCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1620

Qy        541 MetLysValGlyLysThrArgGluLeu 549

Db       1621 ATGAAGGTGGGTAAAACTCGGGAGTTA 1647

RESULT 12
E17107
LOCUS       E17107                  1983 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Hepatitis E virus ORF2.
ACCESSION   E17107
VERSION     E17107.1  GI:5711790
KEYWORDS    JP 1998234383-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1983)
  AUTHORS   Takeda,N., Ri,T. and Miyamura,T.
  TITLE     HEPATITIS E VIRUS HOLLOW PARTICLE, GENE ENCODING THE SAME AND
            PREPARATION OF RECOMBINATION VECTOR CONTAINING THE GENE AND
            UTILIZATION OF THE RECOMBINATION VECTOR
  JOURNAL   Patent: JP 1998234383-A 3 08-SEP-1998;
            DENKA SEIKEN CO LTD, KOKURITSU KANSENSHIYOU KENKYUSHO
COMMENT     OS   Hepatitis E virus
            PN   JP 1998234383-A/3
            PD   08-SEP-1998
            PF   28-FEB-1997 JP 1997062445
            PI   TAKEDA NAOKAZU, RI TENSEI, MIYAMURA TATSUO
            PC   C12N15/09,C07K14/08,C12N5/10,C12P21/02;
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .1983
            FT                   /organism='Hepatitis E virus' FT   CDS
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            FT                   /product='structural protein'.
FEATURES            Location/Qualifiers
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                    /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              6.58e-192      Length:          1983
Score:                  2806.00        Matches:         548
Percent Similarity:     99.82%         Conservative:    0
Best Local Similarity:  99.82%         Mismatches:      1
Query Match:            99.75%         Indels:          0
DB:                     6              Gaps:            0

US-09-769-066-15 (1-549) x E17107 (1-1983)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20

Db        334 GCGGTCGCTCCAGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCTCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40

Db        394 TTGCGCCGGCAGTATAATCTATCAACATCTCCCCTCACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60

Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

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Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        874 CCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

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Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260

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RESULT 13
AF185822
LOCUS AF185822 7143 bp RNA linear VRL 14-JUN-2001
DEFINITION Hepatitis E virus nonstructural polyprotein gene, partial cds; structural protein gene, complete cds; and unknown gene.
ACCESSION AF185822
VERSION AF185822.1 GI:10336832
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 7143)
AUTHORS van Cuyck-Gandre,H., Zhang,H.Y., Tsarev,S.A., Warren,R.L., Caudill,J.D., Snellings,N.J., Begot,L., Innis,B.L. and Longer,C.F.
TITLE Short report: phylogenetically distinct hepatitis E viruses in Pakistan
JOURNAL Am. J. Trop. Med. Hyg. 62 (2), 187-189 (2000)
MEDLINE 20271579
PUBMED 10813471
REFERENCE 2 (bases 1 to 7143)
AUTHORS van Cuyck-Gandre,H., Zhang,H.Y., Tsarev,S.A., Warren,R.L., Caudill,J.D., Snellings,N.J., Begot,L., Innis,B.L., Longer,C.F. and Ticehurst,J.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-1999) Agents Transmissibles, CRSSA, 24 Ave des Maquis du Gresivausan, BP 87, La Tronche 38702, France
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ORIGIN

Alignment Scores:

Pred. No.:	3.8e-191	Length:	7143
Score:	2806.00	Matches:	548
Percent Similarity:	99.82%	Conservative:	0
Best Local Similarity:	99.82%	Mismatches:	1
Query Match:	99.75%	Indels:	0
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US-09-769-066-15 (1-549) x AF185822 (1-7143)

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ACCESSION   E17109
VERSION     E17109.1  GI:5711792
KEYWORDS    JP 1998234383-A/5.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 7194)
  AUTHORS   Takeda,N., Ri,T. and Miyamura,T.
  TITLE     HEPATITIS E VIRUS HOLLOW PARTICLE, GENE ENCODING THE SAME AND
            PREPARATION OF RECOMBINATION VECTOR CONTAINING THE GENE AND
            UTILIZATION OF THE RECOMBINATION VECTOR
  JOURNAL   Patent: JP 1998234383-A 5 08-SEP-1998;
            DENKA SEIKEN CO LTD, KOKURITSU KANSENSHIYOU KENKYUSHO
COMMENT     OS   Hepatitis E virus
            PN   JP 1998234383-A/5
            PD   08-SEP-1998
            PF   28-FEB-1997 JP 1997062445
            PI   TAKEDA NAOKAZU, RI TENSEI, MIYAMURA TATSUO
            PC   C12N15/09,C07K14/08,C12N5/10,C12P21/02;
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ORIGIN
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Best Local Similarity:    99.82%          Mismatches:     1
Query Match:              99.75%          Indels:         0
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US-09-769-066-15 (1-549) x E17109 (1-7194)

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Db       6200 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 6259

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db       6260 CTGTTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 6319

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Db       6320 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCGGCCAATGGCGAGCCGACTGTTAAG 6379

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
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Db       6380 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 6439

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Db       6440 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGG 6499

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Db       6500 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 6559

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       6620 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 6679

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
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Db       6680 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 6739

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
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Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
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Db       6860 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 6919

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
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Db       6920 CCCGTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 6979

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
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Db       7040 CCTCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 7099

Qy        541 MetLysValGlyLysThrArgGluLeu 549
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Db       7100 ATGAAGGTGGGTAAAACTCGGGAGTTA 7126

RESULT 15
AR278920
LOCUS       AR278920               1686 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 19 from patent US 6514690.
ACCESSION   AR278920
VERSION     AR278920.1  GI:29713554
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1686)
  AUTHORS   Li,F., Hui,Z., Anderson,D.A., Logarnini,S.A. and Torresi,J.
  TITLE     Immunoreactive antigens of Hepatitis E Virus
  JOURNAL   Patent: US 6514690-A 19 04-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .1686
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:                7.33e-192       Length:         1686
Score:                    2804.00         Matches:        547
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Percent Similarity: 99.82% Conservative: 1
Best Local Similarity: 99.64% Mismatches: 1
Query Match: 99.68% Indels: 0
DB: 6 Gaps: 0

US-09-769-066-15 (1-549) x AR278920 (1-1686)

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Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 97

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
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Db         98 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 157

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
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Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
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Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db        278 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 337

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        338 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 397

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Db        398 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 457

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
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Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Db        578 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 637

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Db        638 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 697

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
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Db        758 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 817

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        818 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 877

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
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Db        938 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 997

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Db        998 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1057

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Db       1058 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1117

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Db       1118 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1177

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       1178 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1237

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
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Db       1238 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1297

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Db       1298 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1357

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
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Db       1358 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1417

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
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Db       1418 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1477

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
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Db       1478 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCCGCGCTAGCATTGCTTGAG 1537

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
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Db       1538 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1597

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
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Db       1598 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1657

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1658 ATGAAGGTGGGTAAAACTCGGGAGTTA 1684
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Search completed: July 14, 2005, 19:30:37
Job time : 4700 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 14, 2005, 15:51:49 ; Search time 554 Seconds
(without alignments)
5866.314 Million cell updates/sec

Title: US-09-769-066-15
Perfect score: 2813
Sequence: 1 AVAPAHDTPPVPDVDSRGAI.....QSTVAELQRLKMKVGKTREL 549

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
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9: geneseqn2003bs:*
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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2813	100.0	1647	2	AAT27109	Aat27109 Hepatitis
2	2813	100.0	1983	2	AAT96959	Aat96959 Hepatitis
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4	2813	100.0	2094	2	AAQ47129	Aaq47129 HEV third
5	2813	100.0	2094	2	AAQ46813	Aaq46813 Burma str
6	2813	100.0	7195	2	AAV66321	Aav66321 ET-NANB (
7	2813	100.0	7195	2	AAV54729	Aav54729 DNA seque
8	2813	100.0	7195	3	AAA99259	Aaa99259 Hepatitis
9	2813	100.0	7195	4	AAF83495	Aaf83495 ET-NANB v
10	2813	100.0	7195	6	AAL50386	Aal50386 Hepatitis
11	2806	99.8	1647	2	AAV61686	Aav61686 Hepatitis
12	2806	99.8	1983	2	AAV61688	Aav61688 Hepatitis
13	2806	99.8	7194	2	AAV61690	Aav61690 Hepatitis
14	2804	99.7	1984	2	AAQ86592	Aaq86592 Hepatitis
15	2804	99.7	1990	6	ABL60053	Abl60053 Hepatitis
16	2804	99.7	1990	10	ADB97808	Adb97808 HEV ORF2
17	2804	99.7	2054	4	AAS01448	Aas01448 Hepatitis
18	2800	99.5	7158	2	AAT27394	Aat27394 Hepatitis
19	2800	99.5	7168	2	AAQ45197	Aaq45197 HEV strai
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21	2800	99.5	7204	9	ADA50062	Ada50062 SK-HEV-3
22	2800	99.5	7204	9	ADA50065	Ada50065 Hepatitis
23	2800	99.5	7204	9	ADA50064	Ada50064 Hepatitis
24	2800	99.5	7204	9	ADA50063	Ada50063 SK-HEV-2
25	2798	99.5	7195	10	ADD24374	Add24374 Hepatitis
26	2778	98.8	7195	2	AAQ14412	Aaq14412 Forward s
27	2775	98.6	7099	5	ADH13466	Adh13466 Hepatitis
28	2775	98.6	7194	5	ADH13469	Adh13469 Hepatitis
29	2773	98.6	1989	6	ABL60054	Abl60054 Hepatitis
30	2773	98.6	1989	10	ADB97809	Adb97809 HEV relat
31	2696	95.8	7256	10	ADE06693	Ade06693 Hepatitis
32	2695	95.8	1980	8	ABZ23919	Abz23919 Swine HEV
33	2695	95.8	7207	2	AAX23032	Aax23032 Swine HEV
34	2694	95.8	7233	10	ADE06694	Ade06694 Hepatitis
35	2692	95.7	7277	2	AAZ00267	Aaz00267 HEV-US2 O
36	2692	95.7	7277	2	AAZ00266	Aaz00266 HEV-US2 f
37	2688	95.6	7229	10	ADE06695	Ade06695 Hepatitis
38	2686	95.5	7228	10	ADE06696	Ade06696 Hepatitis
39	2686	95.5	7230	10	ADE06697	Ade06697 Hepatitis
40	2685	95.4	7234	10	ADE06660	Ade06660 Hepatitis
41	2684	95.4	1647	2	AAT27110	Aat27110 Hepatitis
42	2684	95.4	2058	2	AAT27108	Aat27108 Hepatitis
43	2682	95.3	7202	2	AAZ00195	Aaz00195 HEV-US1 O
44	2682	95.3	7202	2	AAZ00194	Aaz00194 HEV-US1 f
45	2657.5	94.5	1980	2	AAT96960	Aat96960 Hepatitis

ALIGNMENTS

RESULT 1
AAT27109
ID AAT27109 standard; DNA; 1647 BP.
XX
AC AAT27109;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Burma strain) 62K antigen DNA.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid; ds.
XX
OS Hepatitis E virus; Burma strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;

XX
DR WPI; 1996-230608/23.
DR P-PSDB; AAR96090.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Disclosure; Page 72-73; 125pp; English.
XX
CC A DNA sequence (AAT27109) codes for 62K antigen (AAR96091) comprising the
CC C-terminal 549 amino acids of hepatitis E virus (HEV) Burma strain capsid
CC protein (AAR96089). It is obtd. by PCR amplification of HEV Burma ORF-2
CC (AAT27107) from pBET1 plasmid. The amplified fragment is inserted into
CC vector pGEX for prodn. 62K in E. coli cells. Expression of full-length
CC ORF-2 in Sf9 insect cells using a baculovirus system also results in
CC prodn. of 62K antigen (see also AAR96101 and AAR96103). 62K represents an
CC improved antigen, in comparison to bacterial expressed proteins, for use
CC in HEV diagnostic assays, and also has excellent immunogenic properties.
CC (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 1647 BP; 302 A; 533 C; 391 G; 421 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.76e-229	Length:	1647
Score:	2813.00	Matches:	549
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-09-769-066-15 (1-549) x AAT27109 (1-1647)

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Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 60

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 120

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
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Db        121 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 180

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
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Db        181 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 240

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 300

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 360

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 420

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 480

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 540

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 600

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 660

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 720

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 780

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 840

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 900

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 960

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1020

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1080

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1140

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1200

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1260

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1320

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1380

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1440

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1500

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1560

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1620

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              ||||||||||||||||||||||||||
Db       1621 ATGAAGGTGGGTAAAACTCGGGAGTTG 1647
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RESULT 2
AAT96959

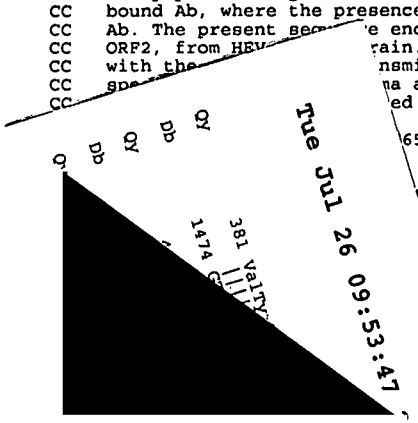
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ID   AAT96959 standard; DNA; 1983 BP.
XX
AC   AAT96959;
XX
DT   17-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   26-FEB-1998  (first entry)
XX
DE   Hepatitis E virus Burma strain ORF2.
XX
KW   Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
KW   diagnosis; HEV; ds.
XX
OS   Hepatitis E virus; - Burma strain.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1983
FT                   /*tag= a
FT                   /product= "ORF2_protein"
XX
PN   US5686239-A.
XX
PD   11-NOV-1997.
XX
PF   09-MAY-1994;   94US-00240049.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   17-JAN-1992;   92US-00822335.
PR   20-APR-1992;   92US-00870985.
PR   01-MAY-1992;   92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Tam AW,  Reyes GR,  Yarbough PO;
XX
DR   WPI; 1997-558132/51.
DR   P-PSDB; AAW35826.
XX
PT   Diagnosis of hepatitis E virus Burma and Mexico strain infection - by
PT   immunoassay with hepatitis E virus peptide antigens.
XX
PS   Disclosure; Col 23-24; 36pp; English.
XX
CC   A method has been developed for detecting hepatitis E virus (HEV)
CC   antibodies (Ab). The method comprises: (a) reacting a serum sample with a
CC   HEV peptide antigen; and (b) examining the peptide for the presence of
CC   bound Ab, where the presence of bound Ab indicates the presence of HEV
CC   Ab. The present seq[illegible]e encodes the protein from the open reading frame,
CC   ORF2, from HEV[illegible]rain. The method can be used to diagnose infection
CC   with the[illegible]nsmitted non-A/non-B viral hepatitis agent HEV,
CC   spe[illegible]a and Mexico strains. (Updated on 25-MAR-2003 to
CC   [illegible]ed on 17-OCT-2003 to standardise OS field)

     [illegible]65 C; 486 G; 492 T; 0 U; 0 Other;

                        Length:        1983
                        Matches:       549
                        Conservative:  0
                        Mismatches:    0
                        Indels:        0
                        Gaps:          0

                    (1-1983)

Qy                  rProProValProAspValAspSerArgGlyAlaIle 20
                    ||||||||||||||||||||||||||||||||||||||
Db                  CCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 393
```




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Qy          21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy          41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 513

Qy          61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy          81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy         101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy         121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy         141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy         161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873

Qy         181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         874 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy         201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy         221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1053

Qy         241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy         261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1114 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy         281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy         301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy         321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1353

Qy         341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy         361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473
```

[redacted]ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
[redacted]TTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

[redacted]01 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
Db 1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy 441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
Db 1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy 461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
Db 1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy 481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
Db 1774 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy 501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
Db 1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy 521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
Db 1894 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy 541 MetLysValGlyLysThrArgGluLeu 549
Db 1954 ATGAAGGTGGGTAAAACTCGGGAGTTG 1980

RESULT 3
AAT27107
ID AAT27107 standard; DNA; 2049 BP.
XX
AC AAT27107;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Burma strain) ORF-2.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid; ds.
XX
OS Hepatitis E virus; Burma strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
DR P-PSDB; AAR96089.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Disclosure; Page 69-70; 125pp; English.

XX
CC The hepatitis E virus (HEV) Burma strain ORF-2 (AAT27107) codes for the
CC putative capsid protein (AAR96089). PCR amplification of ORF-2 allows
CC prodn. of capsid protein or of C-terminal regions of the capsid protein
CC (see also AAR96091, AAR96093 and AAR96095) and expression in Spodoptera
CC frugiperda Sf9 insect cells using a baculovirus vector provides
CC recombinant C-terminal regions (see also AAR96101 and AAR96103) useful as
CC diagnostic reagents and in vaccines. The HEV Mexico strain ORF-2
CC (AAT27108) may similarly be used. (Updated on 16-OCT-2003 to standardise
CC OS field)
XX
SQ Sequence 2049 BP; 344 A; 686 C; 496 G; 523 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.35e-229	Length:	2049
Score:	2813.00	Matches:	549
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-09-769-066-15 (1-549) x AAT27107 (1-2049)

Qy 1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
Db 334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 393

Qy 21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
Db 394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy 41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
Db 454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 513

Qy 61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
Db 514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy 81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
Db 574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy 101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
Db 634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy 121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
Db 694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy 141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
Db 754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy 161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
Db 814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873

Qy 181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
Db 874 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy 201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
Db 934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy 221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
Db 994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1053

Qy 241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260

```
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1774 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTG 1980

RESULT 4
AAQ47129
ID   AAQ47129 standard; DNA; 2094 BP.
XX
AC   AAQ47129;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   11-JAN-1994  (first entry)
XX
DE   HEV third and second ORFs.
XX
KW   Enterically transmitted non-A non-B hepatitis; ET-NANB; vaccine; ss.
XX
OS   Hepatitis E virus; Burma strain.
XX
FH   Key             Location/Qualifiers
FT   CDS             5. .376
FT                   /*tag=  a
FT                   /label= ORF3
FT   CDS             46. .2094
FT                   /*tag=  b
FT                   /label= ORF2
FT   misc_RNA        275. .376
FT                   /*tag=  c
FT                   /label= 406.4-2
FT   misc_RNA        718. .2029
FT                   /*tag=  d
FT                   /label= C2
FT   misc_RNA        1045. .2029
FT                   /*tag=  e
FT                   /label= SG3
FT   misc_RNA        1882. .2029
FT                   /*tag=  f
FT                   /label= 406.3-2
XX
PN   WO9314116-A1.
XX
PD   22-JUL-1993.
XX
PF   15-JAN-1993;   93WO-US000459.
XX
PR   17-JAN-1992;   92US-00822335.
PR   01-MAY-1992;   92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
PA   (USSH ) US SEC DEPT HEALTH.
XX
PI   Reyes GR,  Bradley DW,  Tam AW,  Carl M;
XX
DR   WPI; 1993-243144/30.
DR   P-PSDB; AAR38784, AAR38785.
XX
PT   New immunogenic hepatitis E virus (HEV) peptide(s) - are from the ORF1,
PT   ORF2 and ORF3 regions of HEV, useful as a vaccine against HEV infection.
XX
PS   Disclosure; Fig 7; 48pp; English.
XX
CC   Immunogenic hepatitis E virus (HEV) peptides are selected from the ORF1,
CC   ORF2 and ORF3 regions of HEV. The peptides can be used in vaccines to
CC   prevent infection by HEV. The antibodies can neutralise and block HEV
CC   infection and can be used to prevent or treat HEV infection. The peptides
CC   and antibodies can also be used as diagnostic reagents. (Updated on 25-
CC   MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS
CC   field)
XX
SQ   Sequence 2094 BP; 353 A; 697 C; 508 G; 536 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.42e-229       Length:         2094
Score:                  2813.00         Matches:        549
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     2               Gaps:           0

US-09-769-066-15 (1-549) x AAQ47129 (1-2094)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 438

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        439 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 498

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 558

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 618

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 678

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 738

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 798

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 858

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 918

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 978

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 1038

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1098

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1158

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1218

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1278

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1338

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1398

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1458

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1518

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1578

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1579 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1638

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1639 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1698

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1699 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1758

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1759 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1818

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1819 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1878

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1879 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1938

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1939 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1998

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1999 ATGAAGGTGGGTAAAACTCGGGAGTTG 2025
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RESULT 5
AAQ46813
ID AAQ46813 standard; DNA; 2094 BP.
XX
AC AAQ46813;
XX
DT 25-MAR-2003 (revised)
DT 14-FEB-1994 (first entry)
XX
DE Burma strain HEV ORF2 and ORF3.
XX
KW Hepatitis E virus; vaccine; neutralising antibodies; infection; block;
KW open reading frame; antibodies; ss.
XX
OS Hepatitis E virus.
XX
FH Key   Location/Qualifiers
FT CDS   5. .311
FT   /*tag= a
FT   /note= "ORF2"
FT CDS   46. .2094
FT   /*tag= b
FT   /note= "ORF3"
XX
PN WO9314208-A2.
XX
PD 22-JUL-1993.
XX
PF 19-JAN-1993; 93WO-US000475.
XX
PR 17-JAN-1992; 92US-00822335.
PR 20-APR-1992; 92US-00870985.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Reyes GR, Bradley DW, Twu J, Purdy MA, Tam AW, Krawczynski KZ;
XX
DR WPI; 1993-243223/30.
DR P-PSDB; AAR39305, AAR39306.

```
XX
PT   Antigen and antibody vaccines against hepatitis E virus infection -
PT   contain peptide(s) derived from capsid protein C-terminal or antibodies
PT   against protein.
XX
PS   Disclosure; Fig 7; 43pp; English.
XX
CC   The sequence is that encoding Burma strain hepatitis E virus (HEV) open
CC   reading frames ORF2 and ORF3. ORF2 encodes the putative capsid protein of
CC   the virus, this protein or peptide fragments of it may be used in a
CC   vaccine composition for immunising an individual against HEV. Antibodies
CC   raised against these peptides can also be used in such vaccines. (Updated
CC   on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 2094 BP; 353 A; 697 C; 508 G; 536 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.42e-229       Length:          2094
Score:                    2813.00         Matches:         549
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       2               Gaps:            0

US-09-769-066-15 (1-549) x AAQ46813 (1-2094)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 438

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 498

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 558

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 618

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 678

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 738

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 798

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 858

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 918

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 978

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 1038

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1098

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1158

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACACGAATTGATTTCGTCGGCT 1218

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1278

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1338

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1398

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1458

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1518

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1578

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1579 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1638

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1639 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1698

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1699 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1758

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1759 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1818

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1819 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1878

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1879 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1938

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1939 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1998

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1999 ATGAAGGTGGGTAAAACTCGGGAGTTG 2025

RESULT 6
AAV66321
ID   AAV66321 standard; DNA; 7195 BP.
XX
AC   AAV66321;
XX
DT   27-AUG-2003  (revised)
DT   25-MAR-2003  (revised)
```

```
DT   23-DEC-1998  (first entry)
XX
DE   ET-NANB (HEV) Burma strain DNA sequence.
XX
KW   Enterically transmitted non A non B hepatitis virus; ET-NANB;
KW   Hepatitis E virus; HEV; Burma HEV isolate; vaccine; diagnostic probe; ds.
XX
OS   Non-A.
OS   non-B hepatitis virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             28. .5109
FT                   /*tag=  a
FT                   /note= " encodes AAW80196"
FT   CDS             5106. .5477
FT                   /*tag=  c
FT                   /note= " encodes AAW80198"
FT   CDS             5147. .7129
FT                   /*tag=  b
FT                   /note= " encodes AAW80197"
XX
PN   US5824649-A.
XX
PD   20-OCT-1998.
XX
PF   07-JUN-1995;   95US-00475807.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   25-JUL-1994;   94US-00279823.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Bradley DW,  Reyes GR,  Krawczynski KZ,  Tam A,  Fry KE,  Yarbough PO;
XX
DR   WPI; 1998-582599/49.
DR   P-PSDB; AAW80196, AAW80197, AAW80198.
XX
PT   Hepatitis E virus proteins - useful for diagnosis or vaccine production
PT   the virus.
XX
PS   Claim 1; Col 51-58; 47pp; English.
XX
CC   The present sequence represents the genome of the Burma strain of
CC   enterically transmitted non A non B hepatitis virus (ET-NANB) (hepatitis
CC   E virus (HEV)). The specification describes an isolated protein which is
CC   specifically immunoreactive with antibodies present in individuals
CC   infected with HEV and encoded by a sequence contained in an open reading
CC   frame (ORF) of an HEV genome. The genome has a sequence that is more than
CC   70% identical to the ORF1 sequence from Burma HEV isolate. The protein is
CC   used as a vaccine and a diagnostic probe for ET-NANB. (Updated on 25-MAR-
CC   2003 to correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 7195 BP; 1221 A; 2312 C; 1868 G; 1794 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.23e-228      Length:          7195
Score:                  2813.00        Matches:         549
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     2              Gaps:            0

US-09-769-066-15 (1-549) x AAV66321 (1-7195)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5480 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 5539

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5540 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 5599

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5600 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 5659

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5660 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 5719

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5720 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 5779

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5780 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 5839

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5840 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 5899

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5900 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 5959

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5960 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 6019

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6020 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 6079

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6080 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 6139

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6140 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 6199

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6200 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 6259

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6260 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 6319

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6320 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 6379

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6380 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 6439

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6440 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 6499

Qy        341 ProThrProSerProAlaProSerArgProProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6500 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 6559

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6560 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 6619

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db       6620 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 6679

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6680 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 6739

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6740 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 6799

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6800 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 6859

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6860 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 6919

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6920 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 6979

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6980 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 7039

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7040 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 7099

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       7100 ATGAAGGTGGGTAAAACTCGGGAGTTG 7126
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RESULT 7
AAV54729
ID   AAV54729 standard; DNA; 7195 BP.
XX
AC   AAV54729;
XX
DT   25-MAR-2003  (revised)
DT   30-OCT-1998  (first entry)
XX
DE   DNA sequence of the Burmese isolate of ET-NANB.
XX
KW   Enterically transmitted nonA/nonB hepatitis virus; identification; HEV;
KW   ET-NANB; detection; vaccine; ds.
XX
OS   Hepatitis virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             28. .5109
FT                   /*tag= a
FT                   /note= "see AAW71209"
FT   CDS             5106. .5477
FT                   /*tag= c
FT                   /note= "see AAW71211"
FT   CDS             5147. .7129
FT                   /*tag= b
FT                   /note= "see AAW71210"
XX
PN   US5789559-A.
XX
PD   04-AUG-1998.
XX
PF   25-JUL-1994;   94US-00279823.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   19-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Bradley DW,  Reyes GR,  Krawczynski KZ,  Tam A,  Fry KE,  Yarbough PO;
XX
DR   WPI; 1998-446186/38.
DR   P-PSDB; AAW71209, AAW71210, AAW71211.
XX
PT   Hepatitis E virus DNA - useful for e.g. virus detection and viral protein
PT   production.
XX
PS   Disclosure; Col 49-56; 45pp; English.
XX
CC   The present sequence represents the sequence of the Burmese isolate of an
CC   enterically transmitted nonA/nonB viral hepatitis agent (ET-NANB). The
CC   nucleic acid sequence may be used for identifying and sequencing the
CC   entire viral agent (also referred to as HEV), detecting ET-NANB in
CC   infected samples, e.g. by specific amplification of virus-derived DNA
CC   sequences and for producing recombinant viral proteins for use in
CC   vaccines. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 7195 BP; 1221 A; 2312 C; 1868 G; 1794 T; 0 U; 0 Other;
```

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Alignment Scores:
Pred. No.:              1.23e-228      Length:          7195
Score:                  2813.00        Matches:         549
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     2              Gaps:            0

US-09-769-066-15 (1-549) x AAV54729 (1-7195)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5480 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 5539

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5540 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 5599

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5600 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 5659

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5660 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 5719

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5720 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 5779

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5780 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 5839

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5840 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 5899

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5900 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 5959

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5960 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 6019

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6020 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 6079
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Qy       201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6080 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 6139

Qy       221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6140 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 6199

Qy       241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6200 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 6259

Qy       261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6260 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 6319

Qy       281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6320 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 6379

Qy       301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6380 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 6439

Qy       321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6440 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 6499

Qy       341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6500 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 6559

Qy       361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6560 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 6619

Qy       381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6620 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 6679

Qy       401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6680 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 6739

Qy       421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6740 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 6799

Qy       441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6800 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 6859

Qy       461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6860 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 6919

Qy       481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6920 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 6979

Qy       501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
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Db      6980 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 7039

Qy       521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7040 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 7099

Qy       541 MetLysValGlyLysThrArgGluLeu 549
            |||||||||||||||||||||||||||
Db      7100 ATGAAGGTGGGTAAAACTCGGGAGTTG 7126
```

RESULT 8

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AAA99259
ID   AAA99259 standard; DNA; 7195 BP.
XX
AC   AAA99259;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Hepatitis E virus Burma strain gene sequence SEQ ID NO:6.
XX
KW   Hepatitis E virus; HEV; non-A/non-B viral hepatitis; viral protein;
KW   immunological; diagnosis; hepatitis; infection; identification;
KW   detection; immunoreactive; hepatotropic; antiinflammatory; virucide;
KW   vaccine; antiviral; antigenic; antibody; antigen; ds.
XX
OS   Hepatitis E virus.
XX
PN   US6120988-A.
XX
PD   19-SEP-2000.
XX
PF   07-JUN-1995;   95US-00478507.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   25-JUL-1994;   94US-00279823.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
PA   (USGO ) US GOVERNMENT.
XX
PI   Yarbough PO,  Krawczynski KZ,  Fry KE,  Bradley DW,  Tam A,  Reyes GR;
XX
DR   WPI; 2000-593712/56.
DR   P-PSDB; AAB24119, AAB24120, AAB24121.
XX
PT   Identifying recombinant antigen immunoreactive with antibody induced by
PT   hepatitis E virus (HEV), for detecting HEV infection, comprises
PT   immunoreacting a polypeptide from an HEV genome with an HEV-positive
PT   antiserum.
XX
PS   Claim 5; Col 49-56; 46pp; English.
XX
CC   The present invention describes a method for identifying a recombinant
CC   antigen immunoreactive with a hepatitis E virus (HEV)-induced antibody.
CC   The method comprises producing a polypeptide derived from an HEV genome,
CC   immunoreacting the polypeptide with an HEV-positive antiserum and
CC   selecting the polypeptide as a recombinant antigen if the polypeptide
CC   reacts with the HEV-positive antiserum. The method is useful for
CC   identifying recombinant antigen immunoreactive with antibody induced by
CC   HEV. The enterically transmitted non-A/non-B hepatitis (ET-NANB (also
CC   known as HEV))-specific fragments are useful for identifying ET-NANB-
CC   derived cDNAs, which contain additional sequence information, as primers
CC   for detecting ET-NANB viral genomic material in a patient sample, for the
CC   synthesis of polypeptides for use in immunoassays, and for identifying
CC   similar antigenic regions encoded by related viral strains, e.g. Burmese
CC   strain. The antigens are especially useful in the preparation of vaccine
CC   against ET-NANB infection. These antigens may further be used to prepare
CC   antibodies to ET-NANB virus particles for use directly as antiviral
CC   agents, and to produce antiserum designed for pre- or post-exposure
CC   prophylaxis. The present sequence represents a specifically claimed HEV
CC   Burma strain gene sequence for use in the present invention
XX
SQ   Sequence 7195 BP; 1221 A; 2312 C; 1868 G; 1794 T; 0 U; 0 Other;
```

Alignment Scores:

Pred. No.:	1.23e-228	Length:	7195
Score:	2813.00	Matches:	549
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0

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DB:                 3          Gaps:          0

US-09-769-066-15 (1-549) x AAA99259 (1-7195)

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Db       5480 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 5539

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
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Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
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Db       5900 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 5959

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
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Db       6260 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 6319

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
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Db       6380 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 6439

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
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Qy        541 MetLysValGlyLysThrArgGluLeu 549
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```

RESULT 9
AAF83495
ID AAF83495 standard; DNA; 7195 BP.
XX
AC AAF83495;
XX
DT 23-JUL-2001 (first entry)
XX
DE ET-NANB viral DNA sequence from HEV-Burma strain.
XX
KW HEV; enterically transmitted nonA/nonB viral hepatitis agent; viral;
KW ET-NANB; infection; vaccine; ds.
XX
OS Hepatitis E virus.
XX

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XX
PN US6229005-B1.
XX
PD 08-MAY-2001.
XX

PF 03-AUG-1998; 98US-00128275.
XX
PR 17-JUN-1988; 88US-00208997.
PR 11-APR-1989; 89US-00336672.
PR 16-JUN-1989; 89US-00367486.
PR 13-OCT-1989; 89US-00420921.
PR 05-APR-1990; 90US-00505888.
PR 05-APR-1991; 91US-00681078.
PR 25-JUL-1994; 94US-00279823.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Reyes GR, Yarbough PO, Bradley DW, Krawczynski KZ, Tam AW;
PI Fry KE;
XX
DR WPI; 2001-342705/36.
DR P-PSDB; AAB62522, AAB62523, AAB62524.
XX
PT New DNA sequences of enterically transmitted non-A/non-B (ET-NANB)
PT hepatitis viral agent, useful in diagnosing infection by an enterically
PT transmitted agent (e.g. ET-NANB virus), as well as in vaccine production.
XX
PS Disclosure; Col 49-56; 45pp; English.
XX
CC The invention relates to an isolated DNA comprising the genome of an
CC enterically transmitted nonA/nonB (ET-NANB) viral hepatitis agent (also
CC referred as HEV). The DNA sequences or their fragments are useful in
CC preparing ET-NANB viral proteins and as probes for virus detection. These
CC are particularly useful in diagnosing infection by an enterically
CC transmitted agent (e.g. ET-NANB virus), as well as in vaccine production.
CC The present sequence represents a ET-NANB viral DNA sequence from HEV-
CC Burma strain
XX
SQ Sequence 7195 BP; 1221 A; 2312 C; 1868 G; 1794 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.23e-228	Length:	7195
Score:	2813.00	Matches:	549
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-769-066-15 (1-549) x AAF83495 (1-7195)

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Db       5480 GCGGTCGCTCCGGCCCATGACACCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 5539

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
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Db       5540 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 5599

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
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Db       5720 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 5779

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
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Db       5960 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 6019

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Db       6020 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 6079

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Db       6080 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 6139

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Db       6140 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 6199

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
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Db       6200 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 6259

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db       6440 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 6499

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Db       6500 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 6559

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Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
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Db       6860 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 6919

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Qy        541 MetLysValGlyLysThrArgGluLeu 549
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Db       7100 ATGAAGGTGGGTAAAACTCGGGAGTTG 7126

RESULT 10
AAL50386
ID   AAL50386 standard; DNA; 7195 BP.
XX
AC   AAL50386;
XX
DT   08-NOV-2002  (first entry)
XX
DE   Hepatitis E virus (Burma strain) gene sequence.
XX
KW   HEV; enterically transmitted nonA/nonB hepatitis viral agent;
KW   Burma strain; bile; ds; gene; ORF1; ORF2; ORF3.
XX
OS   Hepatitis E virus.
XX
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PD   30-APR-2002.
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PF   19-APR-2000; 2000US-00553427.
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PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   15-APR-1991;   91US-00681078.
PR   25-JUL-1994;   94US-00279823.
PR   07-JUN-1995;   95US-00478507.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Reyes GR,  Yarbough PO,  Bradley DW,  Krawczynski KZ,  Tam A,  Fry KE;
XX
DR   WPI; 2002-517277/55.
DR   P-PSDB; AAO15698, AAO15699, AAO15700.
XX
PT   Detecting the presence of enterically transmitted nonA/nonB hepatitis
PT   viral (HEV) agents in bile samples from infected humans and monkeys using
PT   polymerase chain reaction.
XX
PS   Disclosure; Col 13-24; 61pp; English.
XX
CC   The invention comprises a method for detecting the presence of
CC   enterically transmitted nonA/nonB hepatitis viral (HEV) agents in a
CC   sample and isolating HEV agents or nucleic acid fragments produced by the
CC   agent. The method utilises PCR - using bile from a human or cynomolgus
CC   monkey actively infected with HEV as a source of the agent. The method of
CC   the invention is used for detecting the presence of a viral agent in a
CC   sample of cultured cells infected with the agent and isolating
CC   enterically transmitted nonA/nonB HEV agents or nucleic acid fragments
CC   produced by the agent. The present DNA sequence was isolated from a
CC   Burmese strain of the Hepatitis E virus, the present DNA sequence has
CC   three open reading frames ORF1, ORF2 and ORF3
XX
SQ   Sequence 7195 BP; 1221 A; 2312 C; 1868 G; 1794 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.23e-228       Length:          7195
Score:                    2813.00         Matches:         549
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       6               Gaps:            0

US-09-769-066-15 (1-549) x AAL50386 (1-7195)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5480 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 5539

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5540 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 5599

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5600 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 5659

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5660 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 5719

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5720 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 5779

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5780 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 5839

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5840 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 5899

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5900 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 5959

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5960 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 6019

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6020 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 6079

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6080 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 6139

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6140 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 6199

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6200 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 6259

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6260 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 6319
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```
Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6320 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 6379

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6380 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 6439

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6440 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 6499

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6500 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 6559

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6560 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 6619

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6620 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 6679

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6680 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 6739

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6740 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 6799

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6800 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 6859

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6860 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 6919

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6920 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 6979

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6980 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 7039

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7040 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 7099

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       7100 ATGAAGGTGGGTAAAACTCGGGAGTTG 7126

RESULT 11
AAV61686
ID   AAV61686 standard; DNA; 1647 BP.
XX
AC   AAV61686;
XX
DT   03-DEC-1998  (first entry)
XX
DE   Hepatitis E virus hollow particle protein ORF2 DNA.
XX
KW   Hollow particle protein; virus; antibody; detection; immunoassay;
KW   infection; ss.
XX
OS   Hepatitis virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1647
FT                   /*tag=  a
FT                   /product= "hollow particle protein"
FT                   /note= "No start codon given for ORF2"
XX
PN   JP10234383-A.
XX
PD   08-SEP-1998.
XX
PF   28-FEB-1997;   97JP-00062445.
XX
PR   28-FEB-1997;   97JP-00062445.
XX
PA   (DENK-) DENKA SEIKEN KK.
PA   (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR   WPI; 1998-535037/46.
DR   P-PSDB; AAW76367.
XX
PT   Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids
PT   encoding it - useful for more accurate detection of HEV in samples, using
PT   immuno-assays and nucleic acid hybridisation.
XX
PS   Claim 1; Page 15-17; 29pp; Japanese.
XX
CC   This sequence encodes a Hepatitis E viral hollow particle protein
CC   described as ORF2. This polypeptide can be used to raise antibodies to
CC   detect HEV infection in samples, e.g. by immuno-assay based techniques,
CC   and the nucleic acid can be used for the same in nucleic acid
CC   hybridisation assays. The polypeptide and nucleic acid allow more
CC   accurate detection of HEV than previously possible
XX
SQ   Sequence 1647 BP; 303 A; 535 C; 390 G; 419 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.94e-229      Length:          1647
Score:                    2806.00        Matches:         548
Percent Similarity:       99.82%         Conservative:    0
Best Local Similarity:    99.82%         Mismatches:      1
Query Match:              99.75%         Indels:          0
DB:                       2              Gaps:            0

US-09-769-066-15 (1-549) x AAV61686 (1-1647)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGGTCGCTCCAGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCTCGCGGCGCCATC 60

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGCGCCGGCAGTATAATCTATCAACATCTCCCCTCACCTCTTCCGTGGCCACCGGCACT 120

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAAT 180

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 240

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTC 300

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 360

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 420

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
```

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Db        421 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 480

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180

Db        481 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAACACA 540

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        541 CCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 600

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db        601 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 660

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db        661 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAG 720

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260

Db        721 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 780

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db        781 CTGTTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 840

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db        841 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCGGCCAATGGCGAGCCGACTGTTAAG 900

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320

Db        901 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 960

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db        961 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGG 1020

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1021 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1080

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1081 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1140

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1141 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1200

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420

Db       1201 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1260

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1261 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1320

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460

Db       1321 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1380

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480

Db       1381 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1440

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500

Db       1441 CCCGTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1500

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1501 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1560

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1561 CCTCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1620

Qy        541 MetLysValGlyLysThrArgGluLeu 549

Db       1621 ATGAAGGTGGGTAAAACTCGGGAGTTA 1647
```

RESULT 12
AAV61688
ID AAV61688 standard; DNA; 1983 BP.
XX
AC AAV61688;
XX
DT 03-DEC-1998 (first entry)
XX
DE Hepatitis E virus hollow particle protein DNA #2.
XX
KW Hollow particle protein; virus; antibody; detection; immunoassay;
KW infection; ss.
XX
OS Hepatitis virus.
XX
PN JP10234383-A.
XX
PD 08-SEP-1998.
XX
PF 28-FEB-1997; 97JP-00062445.
XX
PR 28-FEB-1997; 97JP-00062445.
XX
PA (DENK-) DENKA SEIKEN KK.
PA (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR WPI; 1998-535037/46.
DR P-PSDB; AAW76369.
XX
PT Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids
PT encoding it - useful for more accurate detection of HEV in samples, using
PT immuno-assays and nucleic acid hybridisation.
XX
PS Claim 13; Page 24-26; 29pp; Japanese.
XX
CC This sequence encodes a Hepatitis E viral hollow particle protein. This
CC polypeptide can be used to raise antibodies to detect HEV infection in
CC samples, e.g. by immuno-assay based techniques, and the nucleic acid can
CC be used for the same in nucleic acid hybridisation assays. The
CC polypeptides and nucleic acids allow more accurate detection of HEV than
CC previously possible
XX
SQ Sequence 1983 BP; 342 A; 665 C; 485 G; 491 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.87e-229	Length:	1983
Score:	2806.00	Matches:	548
Percent Similarity:	99.82%	Conservative:	0
Best Local Similarity:	99.82%	Mismatches:	1
Query Match:	99.75%	Indels:	0
DB:	2	Gaps:	0

US-09-769-066-15 (1-549) x AAV61688 (1-1983)

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Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20

Db        334 GCGGTCGCTCCAGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCTCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40

Db        394 TTGCGCCGGCAGTATAATCTATCAACATCTCCCCTCACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
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Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr  80

Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db        754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180

Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAACACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        874 CCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db        934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db        994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAG 1053

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260

Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db       1114 CTGTTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCGGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320

Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProProSerValLeuArgAlaAsnAspValLeu 360

Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420

Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460

Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480

Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500

Db       1774 CCCGTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1894 CCTCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 MetLysValGlyLysThrArgGluLeu 549

Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTA 1980
```

RESULT 13
AAV61690
ID AAV61690 standard; DNA; 7194 BP.
XX
AC AAV61690;
XX
DT 03-DEC-1998 (first entry)
XX
DE Hepatitis E virus hollow particle protein DNA #4.
XX
KW Hollow particle protein; virus; antibody; detection; immunoassay;
KW infection; ss.
XX
OS Hepatitis virus.
XX
PN JP10234383-A.
XX
PD 08-SEP-1998.
XX
PF 28-FEB-1997; 97JP-00062445.
XX
PR 28-FEB-1997; 97JP-00062445.
XX
PA (DENK-) DENKA SEIKEN KK.
PA (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR WPI; 1998-535037/46.
XX
PT Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids
PT encoding it - useful for more accurate detection of HEV in samples, using
PT immuno-assays and nucleic acid hybridisation.
XX
PS Disclosure; Page 27-29; 29pp; Japanese.
XX
CC This sequence encodes a Hepatitis E viral hollow particle protein. This
CC polypeptide can be used to raise antibodies to detect HEV infection in
CC samples, e.g. by immuno-assay based techniques, and the nucleic acid can
CC be used for the same in nucleic acid hybridisation assays. The
CC polypeptides and nucleic acids allow more accurate detection of HEV than
CC previously possible
XX
SQ Sequence 7194 BP; 1217 A; 2312 C; 1871 G; 1794 T; 0 U; 0 Other;

```
Alignment Scores:
Pred. No.:                4.86e-228       Length:          7194
Score:                    2806.00         Matches:         548
Percent Similarity:       99.82%          Conservative:    0
Best Local Similarity:    99.82%          Mismatches:      1
Query Match:              99.75%          Indels:          0
DB:                       2               Gaps:            0

US-09-769-066-15 (1-549) x AAV61690 (1-7194)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5480 GCGGTCGCTCCAGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCTCGCGGCGCCATC 5539

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5540 TTGCGCCGGCAGTATAATCTATCAACATCTCCCCTCACCTCTTCCGTGGCCACCGGCACT 5599

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5600 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAAT 5659

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5660 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 5719

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5720 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTC 5779

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5780 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 5839

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5840 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 5899

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5900 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 5959

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5960 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAACACA 6019

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6020 CCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 6079

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6080 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 6139

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6140 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAG 6199

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6200 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 6259

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6260 CTGTTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 6319

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6320 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCGGCCAATGGCGAGCCGACTGTTAAG 6379

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6380 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 6439

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6440 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGG 6499

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6500 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 6559

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6560 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 6619

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6620 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 6679

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6680 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 6739

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6740 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 6799

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6800 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 6859

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6860 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 6919

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6920 CCCGTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 6979

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6980 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 7039

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7040 CCTCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 7099

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       7100 ATGAAGGTGGGTAAAACTCGGGAGTTA 7126

RESULT 14
AAQ86592
ID   AAQ86592 standard; DNA; 1984 BP.
XX
AC   AAQ86592;
XX
DT   25-MAR-2003  (revised)
DT   28-SEP-1995  (first entry)
XX
DE   Hepatitis E virus ORF2.
XX
KW   HEV; ORF2; antigen; vaccine; immunogen; ss.
XX
OS   Hepatitis E virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1983
FT                   /*tag=  a
XX
PN   WO9508632-A1.
XX
PD   30-MAR-1995.
XX
PF   23-SEP-1994;   94WO-AU000572.
```

XX
PR 24-SEP-1993; 93AU-00001423.
PR 15-DEC-1993; 93AU-00002964.
XX
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX
PI Anderson DA, Locarnini SA, Torresi J, Li F, Hui Z;
XX
DR WPI; 1995-139601/18.
DR P-PSDB; AAR70323.
XX
PT Antigens of hepatitis E virus (HEV) - selectively immuno:reactive to
PT convalescent and/or acute phase circulating antibodies to HEV.
XX
PS Disclosure; Page 39-41; 78pp; English.
XX
CC RNA from an HEV strain isolated in the Xinjiang region of China was
CC subjected to RT-PCR to obtain fragments corresp. to ORF2 (given in
CC AAQ86592) and ORF3 (AAQ86593) that encoded antigenic proteins (AAR70323-
CC 24, respectively). DNA fragments were manipulated into pGEX vectors for
CC production of GST fusion proteins in E. coli. Applications include HEV
CC infection diagnosis, therapy and vaccine development. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 1984 BP; 347 A; 666 C; 481 G; 490 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.31e-228	Length:	1984
Score:	2804.00	Matches:	547
Percent Similarity:	99.82%	Conservative:	1
Best Local Similarity:	99.64%	Mismatches:	1
Query Match:	99.68%	Indels:	0
DB:	2	Gaps:	0

US-09-769-066-15 (1-549) x AAQ86592 (1-1984)

```
Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGTCGCGGTGCAGATGGGACTGCCGAGCTTACCACCACGGCTGCTACCCGCTTCATGAAG 1053

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 1113

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGTGGCCAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 1293

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuGluGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1774 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCCGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1893

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
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Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTA 1980

RESULT 15
ABL60053
ID   ABL60053 standard; DNA; 1990 BP.
XX
AC   ABL60053;
XX
DT   16-AUG-2002  (first entry)
XX
DE   Hepatitis E virus ORF-2 DNA #1.
XX
KW   Hepatitis E virus; ORF-2; HEV; virucide; immunisation; gene; ds.
XX
OS   Hepatitis E virus.
XX
PN   WO200240681-A1.
XX
PD   23-MAY-2002.
XX
PF   30-SEP-2001; 2001WO-CN001469.
XX
PR   30-SEP-2000; 2000CN-00130634.
XX
PA   (YANG-) YANG SHENG TANG CO LTD.
XX
PI   Xia N,  Zhang J,  Li S,  Ge S,  Gu Y,  He Z;
XX
DR   WPI; 2002-427096/45.
XX
PT   Polypeptide fragments of hepatitis E virus (HEV) for vaccine compositions
PT   and diagnosis in preventing and treating HEV infection.
XX
PS   Example 1; Page 82-83; 91pp; Chinese.
XX
CC   The sequence encodes hepatitis E virus (HEV) ORF-2 polypeptide. The
CC   invention relates to novel n-mer polypeptides comprising amino acids of
CC   ORF-2 of HEV where n = 2-180. The polypeptides of the invention have
CC   virucide activity. The polypeptide of HEV, its fragments, and chimeric
CC   proteins, are useful for vaccine compositions and diagnosis in preventing
CC   and treating HEV infection by immunisation, which may also be applied in
CC   the diagnosis of HEV infection
XX
SQ   Sequence 1990 BP; 348 A; 666 C; 481 G; 495 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.32e-228       Length:         1990
Score:                  2804.00         Matches:        547
Percent Similarity:     99.82%          Conservative:   1
Best Local Similarity:  99.64%          Mismatches:     1
Query Match:            99.68%          Indels:         0
DB:                     6               Gaps:           0

US-09-769-066-15 (1-549) x ABL60053 (1-1990)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
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Db        514 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db        574 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Db        754 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
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Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
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Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 1113

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
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Db       1234 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 1293

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
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Db       1534 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Db       1594 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
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Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
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Db       1714 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
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Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
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Qy        541 MetLysValGlyLysThrArgGluLeu 549
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Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTA 1980
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Search completed: July 14, 2005, 16:55:40
Job time : 617 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 14, 2005, 16:23:19 ; Search time 3367 Seconds
(without alignments)
6206.500 Million cell updates/sec

Title: US-09-769-066-15
Perfect score: 2813
Sequence: 1 AVAPAHDTPPVPDVDSRGAI.....QSTVAELQRLKMKVGKTREL 549

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09769066/runat_13072005_133014_23069/app_query.fasta_1.1422
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	130.5	4.6	2369	3	AK032985	AK032985 Mus muscu
c 2	128.5	4.6	2391	8	BH771003	BH771003 LLMGtag72
c 3	123.5	4.4	3822	9	CL972913	CL972913 OsIFCC023
4	122	4.3	2419	3	AK049595	AK049595 Mus muscu
5	122	4.3	3612	3	AK050493	AK050493 Mus muscu
6	122	4.3	3702	9	AY404468	AY404468 Mus muscu
7	121.5	4.3	2232	9	AY417426	AY417426 Homo sapi
8	117.5	4.2	759	7	CF870156	CF870156 tric021xl
9	117.5	4.2	828	6	CB900324	CB900324 tric021xl
10	117	4.2	931	7	CR552265	CR552265 CR552265
11	115.5	4.1	9097	9	AY400949	AY400949 Mus muscu
12	115	4.1	1211	3	AK082573	AK082573 Mus muscu
13	114.5	4.1	2241	9	AY417428	AY417428 Mus muscu
c 14	111.5	4.0	630	5	BQ028470	BQ028470 UI-H-CO0-
c 15	110.5	3.9	2453	3	BC068239	BC068239 Mus muscu
16	110	3.9	747	8	BZ156047	BZ156047 CH230-312
17	110	3.9	1012	9	CNS06YMP	AL421223 T3 end of
18	110	3.9	4978	3	AK052394	AK052394 Mus muscu
19	109	3.9	711	7	CF865933	CF865933 tric004xa
20	109	3.9	765	6	CB895871	CB895871 tric004xa
c 21	109	3.9	918	2	BF535671	BF535671 602054068
22	109	3.9	2707	9	CL953164	CL953164 OsJRUA000
23	108.5	3.9	2907	9	CL948895	CL948895 OsIFSB002
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c 32	105.5	3.8	655	4	BJ796987	BJ796987 BJ796987
33	105.5	3.8	684	7	CF877297	CF877297 tric075xg
c 34	105.5	3.8	763	4	BJ818034	BJ818034 BJ818034
35	105.5	3.8	776	6	CB905612	CB905612 tric075xg
c 36	105.5	3.8	777	4	BJ811207	BJ811207 BJ811207
37	105.5	3.8	933	6	CB183940	CB183940 AGENCOURT
38	105.5	3.8	2031	9	AY410823	AY410823 Homo sapi
39	105	3.7	1409	2	BF529003	BF529003 602042057
c 40	105	3.7	1499	3	CR639300	CR639300 Tetraodon
41	104.5	3.7	769	7	CF869972	CF869972 tric021xb
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45	104.5	3.7	4917	9	CL965254	CL965254 OsIFCC012

ALIGNMENTS

RESULT 1
AK032985
LOCUS AK032985 2369 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:6720484N02 product:CDNA FLJ13589 FIS, CLONE PLACE1009308, WEAKLY SIMILAR TO GLUCOSE REPRESSION MEDIATOR PROTEIN homolog [Homo sapiens], full insert sequence.
ACCESSION AK032985
VERSION AK032985.1 GI:26328748
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,

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            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2369)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES            Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:                0.0296          Length:          2369
Score:                    130.50          Matches:         124
Percent Similarity:       33.89%          Conservative:    58
Best Local Similarity:    23.09%          Mismatches:      217
Query Match:              4.64%           Indels:          138
DB:                       3               Gaps:            24

US-09-769-066-15 (1-549) x AK032985 (1-2369)

Qy          4 ProAlaHisAspThrPro-ProValPro------------------------------ 12
              ||||||       ||| |||||||||
Db        534 CCAGCACAATGCGTCCCTTCCTGTGCCTGCAGAGACAGCAAGCAAAGACGGCGTTAGCTG 593

Qy         13 ----AspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThrSerPr 31
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Qy         51 oLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSerAsnTy 71
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Qy         71 rAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAlaVa 91
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Qy         91 lGlyGlyTyrAlaIleSerIleSerPheTrp---ProGlnThrThrThrThrProThrSe 110
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Qy        110 rValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAl 130
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Db        834 AACACAGAAGGTTATTATAGTGACCACATCACCAAGTTCAACCTTTGTGCCCAACATTCT 893

Qy        130 aSerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgServa 150
               |||                :::   |||                    :::   ||
Db        894 CTCC--------------------AAATCTCATAACTATGCAGCAGTCACTAAGCTTGT 932

Qy        150 lGluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHi 170
              |   ||||||   :::|||                  :::|||:::
Db        933 ACCAACATCAGTCATTGCCTCCACGACTCAGAAGCCACCTGTTGTTATAACTGCGTCCCA 992

Qy        170 sGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAs 190
                 |||||||||   |||   :::|||
Db        993 GGCCTCTCTGGTCACCAGTAGCAGCAAT------------------------------ 1020

Qy        190 pPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSe 210
                                                |||||:::::::::      ||
Db       1021 ----------------------------------GGCAACAGCAGTTCTACGTCATC 1043

Qy        210 rArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLe 230
              |     |||||||||
Db       1044 ACCTATTTCTAGTACAGTT-------------------------------------GC 1064

Qy        230 uThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyVa 250
                 ||||||      :::               :::      |||         |||||
Db       1065 AGTAACAACGGTGGTATCTTCCACACCGTCCGTGGTCATGTCAACAGTAGCACAAGGTGT 1124
```

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Qy        250 lGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGl 270
Db       1125 ATCCACATCAGCAATCAAAGTGGCATCGACAAGACTTCCTTCCCCCAAAAGCTTAGTGAG 1184

Qy        270 yGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSer-------- 287
Db       1185 TGGC---CCTACCCAGATTCTTGCACAGTTTCCTAAACAGCATCAGCAGTCTCCTAAGCA 1241

Qy        288 -------ArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerVa 305
Db       1242 GCAGTTACAGCAAGTACAACAACAGACACAGCAGCCA---GTGGCCCAGCCTTCTTCAGT 1298

Qy        305 lGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAsp----------- 321
Db       1299 GTCTCAGCAGCAGCAGCCTCAGCAGTCAGCATTGCCGCCTGGTATCAAACCTACCATCCA 1358

Qy        322 ----LeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspAr 340
Db       1359 GATCAAACAGGAGTCAGGTGTTAAAATCATCACACAGCAGGTTCAACCAAGTAAAATCTT 1418

Qy        340 gProThrProSerProAla---------------ProSerArgProPheSerValLeuAr 355
Db       1419 ACCCAAACCAGTGACTGCAACTCTACCCACCAGTAGCAATTCCCCAATTATGGTAGTTAG 1478

Qy        355 gAlaAsnAspValLeuTrpLeuSerLeu---------------------ThrAlaAlaGl 368
Db       1479 CAGTAATGGTGCAATTATGACAACTAAACTGGTAACCACTCCTACCGGTACTCAGGCAAC 1538

Qy        368 uTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrValSer---AspSerVa 387
Db       1539 CTATACCCGGCCAACAGTGAGCCCATCCTTAGGTCGTGTGGCTACAACCCCTGGAGCTGC 1598

Qy        387 lThrLeuValAsnValAlaThrGlyAla------GlnAlaValAlaArgSerLeuAspTr 405
Db       1599 AACCTATGTGAAAACTACCAGTGGCAGCATCATCACTGTAGTACCCAAATCATTA----- 1653

Qy        405 pThrLysValThrLeuAspGlyArgProLeuSer------------------------- 416
Db       1654 -------GCTACCTTGGGAGGCAAGATAATTAGCAGTAATATTGTTTCTGGAACGACTAC 1706

Qy        417 ----------ThrIleGlnGlnTyrSerLys------ThrPhePheValLeuProLeuAr 431
Db       1707 CAAAATCACTACAATCCCAATGACTTCCAAGCCCAATGTGATTGTTGTACAAAAGACTAC 1766

Qy        431 gGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro---TyrAsnTy 450
Db       1767 AGGAAAA-----------------GGAACGACCATTCAAGGCCTCCCTGGCAAAAACGT 1808

Qy        450 rAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIl 470
Db       1809 TGTCACAACC-----------------TTGCTAAATGCTGGAGGAGAAAAG-------- 1842

Qy        470 eSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAla 486
Db       1843 -ACTCTTCAGACAGTGCCAGCTGGAGCCAAGCCAGCTATAATTACTGCT 1890
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```
RESULT 2
BH771003/c
LOCUS       BH771003               2391 bp    DNA     linear   GSS 01-MAY-2002
DEFINITION  LLMGtag726 MG1363 Random Sequence Tag Library Lactococcus lactis
            subsp. cremoris genomic, genomic survey sequence.
ACCESSION   BH771003
VERSION     BH771003.1  GI:20373960
KEYWORDS    GSS.
SOURCE      Lactococcus lactis subsp. cremoris
  ORGANISM  Lactococcus lactis subsp. cremoris
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Lactococcus.
REFERENCE   1  (bases 1 to 2391)
  AUTHORS   Bolotin,A., Ehrlich,S.D. and Sorokin,A.
  TITLE     Studies of genomes of dairy bacteria Lactococcus lactis
  JOURNAL   Sci. Aliments (2002) In press
COMMENT     Contact: Sorokin A
            Genetique Microbienne
            INRA
            CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
            Tel: 33 1 34 65 25 16
            Fax: 33 1 34 65 25 21
            Email: sorokine@jouy.inra.fr
            best homologue in strain IL1403 is yhgD (62%)
            Class: shotgun
            High quality sequence start: 30
            High quality sequence stop: 2361.
FEATURES             Location/Qualifiers
     source          1. .2391
                     /organism="Lactococcus lactis subsp. cremoris"
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                     /strain="MG1363"
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                     /clone_lib="MG1363 Random Sequence Tag Library"
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ORIGIN
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Pred. No.:                0.0491          Length:          2391
Score:                    128.50          Matches:         112
Percent Similarity:       30.83%          Conservative:    56
Best Local Similarity:    20.55%          Mismatches:      204
Query Match:              4.57%           Indels:          173
DB:                       8               Gaps:            23

US-09-769-066-15 (1-549) x BH771003 (1-2391)

Qy          7 AspThrProProValProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsn 26
Db       1579 GATACCTCAGTCGTAACTGACAATCCTTTCGCCTCGACGACCCTTCTTAAAAACTAT--- 1523

Qy         27 LeuSerThrSerProLeuThrSerSerValAlaThrGlyThrAsnLeuValLeuTyrAla 46
Db       1522 ------GCCAGTGACTTGACAGCAGCTGTCCCTGCAGGCTACAACATTACG--------- 1478

Qy         47 AlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThr 66
Db       1477 --------------------TCTATCACTAATGGCACGAGTACTTATACTGGTGCGACA 1439

Qy         67 GluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeu 86
Db       1438 ACTGCAGCGACACTGGCAACTTTCACAGCGGCCAACCCAACAGTTAGC------------ 1391

Qy         87 ValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThr 106
Db       1390 GCAACCCAAGCAAACAATAACTATACGGTCACGCTGACAGCAGCAGCACAAACGGCAACC 1331

Qy        107 ----------------------------------------ThrProThrSerValAsp 112
Db       1330 TTCAACTATGGCTACGTCTCAGGAGCACTCAACACGCCTGCTATACCTACTAGCCTGTCA 1271

Qy        113 MetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGlu 132
Db       1270 GCGAGTGGGACGACAGGAGCAAATGTC---------ACACCACCA-------------- 1235

Qy        133 LeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThr 152
Db       1234 ----------------------------------ACTGGCTGGAATACAGCATCCACA 1211

Qy        153 SerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySer 172
Db       1210 GCGACAGTGGCT---AATAAAATCCCTTATGGATATTATATCTCTGCCATATATGCTGGA 1154

Qy        173 LeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
Db       1153 ------AACTCTGCGACAGGAACACCGATAGCCACAGGGACGGGAACAACCGGAACTGGC 1100
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Qy        193 LeuGluLeuGluPhe------ArgAsnLeuThrProGlyAsnThrAsn------------ 206
Db       1099 GCAAATGCTGCCTTCCCTGCAACTGGTCAGACTTACGGTGCAACTGGTAATCAATACTAT 1040

Qy        207 ThrArgValSerArgTyrSer---SerThrAlaArgHisArgLeuArgArgGlyAlaAsp 225
Db       1039 GTTCAACTCTCGCCATACTCAGTCAGAACTTCTTGGCACATTTCAGTATTAGGAACTGAC 980

Qy        226 GlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThr 245
Db        979 CCC---------------------------------------------------------- 977

Qy        246 SerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAla 265
Db        976 ----------------------------------------------------GATTACCTT 968

Qy        266 AspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPhe 285
Db        967 GATACT---CTTGGAGGT---------CAGTATGCGGGTTATGTGGGAGGTCAAGCCACT 920

Qy        286 TyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerVal 305
Db        919 CCTAATGCCCAAACCTTCATGATGAATGATGTTAATAATTCTACGCCTTTAACGACGACA 860

Qy        306 GluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSer 325
Db        859 GATAATATTGTCTATACAGATGGTGCAGGAATT-------------------------- 827

Qy        326 ArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerPro 345
Db        826 CGTTATATTATCACAGGCTATACCTATTCTTTGACCAGTAACTCGGCAACAGGAACGACT 767

Qy        346 AlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThr 365
Db        766 TATCCGACA------TTTACAGCTCTT-------------------------CTTGCC 740

Qy        366 AlaAlaGluTyr---AspGlnSerThrTyrGlySerSerThrGlyProVal--------- 381
Db        739 GCCAATCCTTATATGCCTGTCGGAACATACAATGCTCCGACGCAGTATGTCACGGTGAAT 680

Qy        382 TyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAla--------- 398
Db        679 ATGATTTCTGATCAGACGAGTATAACGTCTAATTTGACAAGTAGCACAACACCGTTAACC 620

Qy        399 ----------------------------ValAlaArgSerLeuAspTrpThrLysVal 408
Db        619 CCAGCAACGAACTATATGCCTATCAACGATATCACGGCAAGTACAGATATTGATGGTGTA 560

Qy        409 ThrLeuAspGlyArgProLeuSer---------------------------------- 416
Db        559 GATGATGACGGTCTACCTTATGCTATCAATGGCTATAATGCCGTGACGAATATCGTAGGC 500

Qy        417 ----------------------------------------------ThrIleGlnGlnTyr 421
Db        499 GCCACGACTAACTACTGGGGAGATGCGACAAACTCTCTGAAACTTCCGATTGGCTCATAC 440

Qy        422 SerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThr 441
Db        439 ACAGAAAATTTCTATGCGCTTAATTACTTGGGA---CTTCAGGCTTATCAAGCACAGTCA 383

Qy        442 ThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGlu 461
Db        382 ACA--------------------TACACGACAGTCGCTAGCTTTCTTCAAAGTCTGTCT 344

Qy        462 AsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyPro 481
Db        343 AGTGCCAATCTGGCAAAATACACGGTAAGTTCAACAACCACACTAACCGTCGCTGATGCA 284

Qy        482 ValSerIleSerAla 486
Db        283 ACGACTATTTCGGCA 269
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RESULT 3
CL972913/c
LOCUS       CL972913               3822 bp    DNA     linear   GSS 21-SEP-2004
DEFINITION  OsIFCC023739 Oryza sativa Express Library Oryza sativa (indica
            cultivar-group) genomic, genomic survey sequence.
ACCESSION   CL972913
VERSION     CL972913.1  GI:52400355
KEYWORDS    GSS.
SOURCE      Oryza sativa (indica cultivar-group)
  ORGANISM  Oryza sativa (indica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 3822)
  AUTHORS   Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
            Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
            Wong,G.K.S., Deng,X.W. and Wang,J.
  TITLE     An analysis of transcriptional regulation of the rice genome and
            its comparison to Arabidopsis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Chen Chen
            Department of Bioinformatic
            Beijing Institute of Genomics
            Chinese Academy of Sciences, Beijing 101300, China
            Tel: 86-10-80481559
            Fax: 86-10-80488676
            Email: chenchen@genomics.org.cn
            Rice genomic sequence.
            Class: exon-trapped.
FEATURES             Location/Qualifiers
     source          1. .3822
                     /organism="Oryza sativa (indica cultivar-group)"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:39946"
                     /clone_lib="Oryza sativa Express Library"
                     /note="Oryza sativa exon trapped genomic sequences "
ORIGIN

Alignment Scores:
Pred. No.:                0.346          Length:          3822
Score:                    123.50         Matches:         114
Percent Similarity:       34.28%         Conservative:    80
Best Local Similarity:    20.14%         Mismatches:      213
Query Match:              4.39%          Indels:          159
DB:                       9              Gaps:            27

US-09-769-066-15 (1-549) x CL972913 (1-3822)

Qy          9 ProProValProAspValAspSerArgGlyAlaIleLeu--------------ArgArg 23
Db       2792 CCGCCACCGCCGAGGCTCGACGAGAACGCCGTGCAGTTCACCTCCCCGGACCGCCGCCGC 2733

Qy         24 GlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThrAsnLeuVal 43
Db       2732 CGCACCGCGATCAGCACGAGCACGATCACCAGCAGC----------------------- 2697

Qy         44 LeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsnThrHisIle 63
Db       2696 ----------------------------------------------ACCACCGACAGCGTC 2682

Qy         64 MetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyr 83
Db       2681 ACCGCCGCCGACACCAGCGCGATCGTC---------GCCGACCGCAGCGCCGACCGGCCG 2631

Qy         84 ArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGln 103
Db       2630 CCGCCGCCGACGCCGCAGCTCACCAGCGGG--------------------TGGCCGCAG 2592

Qy        104 ThrThrThrThrProThrSerValAspMet------------AsnSerIleThrSerThr 119
Db       2591 AGCCGCGCGTTGCCGGCGAACGCGCCACGCGGCCACCGCGAGAACTCGCTCCCCAGCCTC 2532

Qy        120 AspValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArg 139
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Db       2531 CCCTGCAGCTGGTTGCTGGACAAATCCAGCTGCACCAAGCTGCTCATCCCGGCG------ 2478

Qy        140 LeuHisTyrArgAsnGlnGly----------------------TrpArgSerValGlu 151

Db       2477 -----------AGCTGCGGCGGCACAGCTCCGGCGAGCGCGTTGTGGGAGAGATTCAAG 2430

Qy        152 ThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuVal---------MetLeuCys 168

Db       2429 CTCTCCAGCTTGGAGAGCGACCCGAGCGACGCCGGGATGCTGCCGCTGAGATCGTTGCTG 2370

Qy        169 IleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGly--- 187

Db       2369 CTCAAATCCAGCAAGCTCTGCAGCTCTTGCAGCTGGCCAATGTCGGGAGGGATCGGGCCG 2310

Qy        188 ----------------------------------LeuLeuAspPheAlaLeuGluLeu 195

Db       2309 GACAAGAGATTCCGCGACAGGTTCAGCTCGTACAGGTTGATCAGCTTCGCG--------- 2259

Qy        196 GluPheArgAsnLeuThrProGlyAsn---ThrAsnThrArgValSerArgTyrSerSer 214

Db       2258 AGGGTAGCCGGAATCTCGCCGGAGAGCTGGTTGCCGGCCAGGTTGAGCACGTTGAGCGAG 2199

Qy        215 ThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAla 234

Db       2198 ACCAAGCTGCCGATC-----------TCCGATGGCACTGTTCCATTGATCTGGTTGCCG 2151

Qy        235 AlaThrArgPheMetLysAsp-----------LeuTyrPheThrSerThrAsnGlyVal 250

Db       2150 TCGAGCGAGAGCTTGATGAGCTTGGAGCAGTTGCTGAGCTGGACGGGCACCGGCCCGGTG 2091

Qy        251 GlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGly 270

Db       2090 AGCTCGTTGCCGGAGAGCGCCAGCTCACCGAGCTCCGGCAGCGCGCCGACCCACGCCGGC 2031

Qy        271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgPro--- 289

Db       2030 ACGGGGCCGGACAGCCGGTTGCCGCTGAGGGCG------ATGTGGCTGAGCCGCGCGCAC 1977

Qy        290 ValValSerAlaAsnGlyGluProThrValLysLeuTyr---------ThrSerValGlu 306

Db       1976 CGCGCGAGGGCGTCCGGGATGCCGCCGGTGAGCGCGTTCCCCGACGCGTCGAGCATCGTC 1917

Qy        307 AsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSerArg 326

Db       1916 AGCGCG--------------GCGGCGTTGCCGAGCGCCGCCGGGATCGGGCCGGACAGC 1872

Qy        327 ValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAla 346

Db       1871 GCGTTGCTCCCGAAGCGGACGCGCTGGAGCGACCGCGACCGGCCGAGCTGCGCCGGGATG 1812

Qy        347 ProSerArgProPheSerValLeuArgAlaAsnAsp---------------------- 358

Db       1811 CCGCCGGAGAAGGAGTTGTTGGTGGCGTCGAACGACAGGAGCCTCGCCGAGCCGCAGAGC 1752

Qy        359 --------------------ValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGln 371

Db       1751 GGCAGGAGGCTGCCGGCGAGCCGGTTGTGCGCGATGTTGACGCGGGTGATGTTCCGGCAC 1692

Qy        372 SerThrTyrGlySerSerThrGlyPro--------------------ValTyrValSer 384

Db       1691 TCGAACATGCCGTCGGGGACGTCGCCGGCGAGCGAGTTGTTGTACAGCATGAGCTGCTCC 1632

Qy        385 AspSerValThrLeuValAsnValAla--------------ThrGlyAlaGlnAlaVal 399

Db       1631 AGCGACCGGAGCCTCCCGAACGTCGCCGGGATCTCGCCGGAGAGCGCGTTGTCGGCTAGG 1572

Qy        400 AlaArgSerLeuAspTrpThrLysValThrLeuAspGly------ArgProLeuSerThr 417

Db       1571 TCGAGGACGGCGAGGTTCACGCAGTCGCCGAGCTCCGGCGGGATCCGGCCGGACAGCTCG 1512

Qy        418 Ile---------------GlnGlnTyrSerLysThrPhePheValLeuProLeu---Arg 431

Db       1511 TTCTGCCGGAGATGGAGGAACGCCAGCTCGGAGAGCTTC---------CCGATGGACGCC 1461

Qy        432 GlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsn------ 449

Db       1460 GGCAAGCTG-----------------------------------CCGTTGAACCGGTTC 1437

Qy        450 --------------------------TyrAsnThrThrAlaSerAspGlnLeuLeuVal 460

Db       1436 CCGAAGAAATCAACCATCTGCAAGCTCGAGCACTCCCCGATCGTCTCCGGTATCTCGCCG 1377

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThr---------ThrSerLeu 477

Db       1376 GAGAAGTCGTTCTCGTACAGGAAGAGCACCTCGAGGTTCACGAGGCGGCCGACGGCGTCC 1317

Qy        478 GlyAlaGlyProValSer 483

Db       1316 GGCAGCCGGCCGGTGAGC 1299
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RESULT 4
AK049595

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LOCUS       AK049595               2419 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 7 days embryo whole body cDNA, RIKEN full-length
            enriched library, clone:C430049D20 product:hypothetical Serine-rich
            region containing protein, full insert sequence.
ACCESSION   AK049595
VERSION     AK049595.1  GI:26340339
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2419)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
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Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1. .2419
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:C430049D20"
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/clone="C430049D20"
/tissue_type="whole body"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="7 days embryo"

CDS 40. .>2418
/note="unnamed protein product; hypothetical Serine-rich region containing protein (PROSITE|PS50324, evidence: InterPro)
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SEQKTQLDNCPESMREQLQQQLKRDADLLDVESKHFEDLEFQQLEHESRLDEEKENLT
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ORIGIN

Alignment Scores:

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Score:	122.00	Matches:	94
Percent Similarity:	35.48%	Conservative:	66
Best Local Similarity:	20.84%	Mismatches:	182
Query Match:	4.34%	Indels:	109
DB:	3	Gaps:	15

US-09-769-066-15 (1-549) x AK049595 (1-2419)

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Qy          3 AlaProAlaHisAspThrProProValPro--------------------AspValAsp 15
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Db        129 GCCCCAAAACATGATGGAGAGCCTAAGCCCGAGGAAATACTCATCAAGTCTGAAGTTTAA 188

Qy         16 SerArgGlyAlaIleLeuArgArgGlnTyrAsn-Leu---------------------- 27
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Db        189 AGCCAACGGGGACTATTCTGGCTCCTATTTAACCCTCTCCCAACCGGTGTCTGCCAAGAG 248

Qy         28 -SerThrSerProLeuThrSerSerValAlaThrGlyThrAsnLeuValLeuTyrAlaAl 47
               |||   ||||||:::   :::||||||   :::      :::|||           ||
Db        249 AAGCCCTTCTCCAATGGGCACCAGCGTCAGGAGCAGTCCCTCCTTG-----------GC 296

Qy         47 aProLeuSerProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGl 67
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Db        297 CAAAATCCAGGGAAGCAAACAGTTCTGCGATGGAATTGATAAAAATATTTCCATGAAACC 356

Qy         67 uAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuVa 87
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Db        357 TCCTATTTCTTTCCTCAGTTCTGCAGCC------------------------------ 384

Qy         87 lProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrTh 107
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Db        385 -------TCTCTTGGCGGCTATCCTCTTGGG---------------------------- 408

Qy        107 rProThrSerValAspMetAsnSerIleThrSerThrAsp------------ValArgIl 123
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Db        409 -------AAAGCAGATTTGGATCATTATACTGGTCGAGACAGTGAGAGGTCCACCAGGCT 461

Qy        123 eLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeuHisTyrAr 143
                :   :::|||                        |||      |||      ||
Db        462 CTCAGAGAAGCCT----------------------CCCTATTCCAGATACAGCTCTAG 497

Qy        143 gAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaThrSerGl 163
                |||:::         ||||||        |||      |||         ||||||||
Db        498 GAATAAATCTCATGACAGTGTCTACTTTCTAGGGGGGCTGGAAGGAAGAAAAACCTCTGG 557

Qy        163 yLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyr-- 182
                |   ::::::         :::|||:::   ::::::        ::::::|||
Db        558 CTCGCTCCTGACCATGTGGAACGGAAATTCCTTGAGCTGCACTGGCTCGTCACCCATCAG 617

Qy        183 ----ThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuTh 201
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Qy        201 rProGlyAsnThr---AsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLe 220
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Db        678 GGACCACTCGACACTTCAGCCCAGGTTAAGCAGGCACAAGGAGCCGGCCTCAGAAAACGT 737

Qy        220 u---------ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrAr 237
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Db        738 CAGTGTGAGAACAAGGAAATACTCAGGGAGCAGTCTGAGTAATATGGGTGCCTACAGCCG 797

Qy        237 gPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIl 257
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Qy        257 eAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGly------GlyLeuProThrGl 275
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Qy        275 uLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGl 295
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Qy        295 yGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAl 315
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Qy        315 aIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGl 335
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Qy        335 nHisGluGlnAspArgProThrProSerProAlaProSerArgProPheSerValLeuAr 355
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Qy        355 gAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyr-- 374
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Qy        375 -GlySerSerThrGlyProValTyrValSerAspSerValThrLeuValAsnValAlaTh 394
Db       1107 AGGGACCAGCCCAAGTCATTCCTTCATTTCTGGAGAGCCAGACCGAGTGCTTGTGGCC-- 1164

Qy        394 rGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArgPr 414
Db       1165 ----------------AGGAGGAACTTCTCTTGTGGATCAATGGAGCTTGATGACTCTGA 1208

Qy        414 oLeuSerThrIleGlnGlnTyrSerLysThr 424
Db       1209 TCTGGAAAGCCTAAGACAGTCGTCAGAAACT 1239
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RESULT 5
AK050493

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DEFINITION  Mus musculus adult pancreas islet cells cDNA, RIKEN full-length
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            region containing protein, full insert sequence.
ACCESSION   AK050493
VERSION     AK050493.1  GI:26093966
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3612)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
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            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Cells were provided by Hiroo Iwata (Department of Reparative
            Materials Field of Tissue Engineering Institute for Frontier
            Medical Sciences,Sakyo-ku,Kyoto,606-8507,Japan) whose assistance we
            gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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ORIGIN
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Score:                    122.00        Matches:         94
Percent Similarity:       35.48%        Conservative:    66
Best Local Similarity:    20.84%        Mismatches:      182
Query Match:              4.34%         Indels:          109
DB:                       3             Gaps:            15

US-09-769-066-15 (1-549) x AK050493 (1-3612)

Qy          3 AlaProAlaHisAspThrProProValPro--------------------AspValAsp 15
Db        442 GCCCCAAAACATGATGGAGAGCCTAAGCCCGAGGAAATACTCATCAAGTCTGAAGTTTAA 501

Qy         16 SerArgGlyAlaIleLeuArgArgGlnTyrAsn-Leu---------------------- 27
Db        502 AGCCAACGGGGACTATTCTGGCTCCTATTTAACCCTCTCCCAACCGGTGTCTGCCAAGAG 561

Qy         28 -SerThrSerProLeuThrSerSerValAlaThrGlyThrAsnLeuValLeuTyrAlaAl 47
Db        562 AAGCCCTTCTCCAATGGGCACCAGCGTCAGGAGCAGTCCCTCCTTG------------GC 609

Qy         47 aProLeuSerProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGl 67
Db        610 CAAAATCCAGGGAAGCAAACAGTTCTGCGATGGAATTGATAAAAATATTTCCATGAAACC 669

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Db       775 CTCAGAGAAGCCT-----------------------CCCTATTCCAGATACAGCTCTAG 810

Qy       143 gAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaThrSerGl 163
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Db       811 GAATAAATCTCATGACAGTGTCTACTTTCTAGGGGGGCTGGAAGGAAGAAAAACCTCTGG 870

Qy       163 yLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyr-- 182
             |   ::::::       :::|||:::   ::::::       ::::::|||
Db       871 CTCGCTCCTGACCATGTGGAACGGAAATTCCTTGAGCTGCACTGGCTCGTCACCCATCAG 930

Qy       183 ----ThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuTh 201
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Db       931 CAGGTCTGGGGCAGCGAGCATGCCTTCAAGTCCAAAGCAAGTCAGGAAGATGAACCTTCA 990

Qy       201 rProGlyAsnThr---AsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLe 220
                 :::|||         |||:::||||||:::         |||          ::
Db       991 GGACCACTCGACACTTCAGCCCAGGTTAAGCAGGCACAAGGAGCCGGCCTCAGAAAACGT 1050

Qy       220 u---------ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrAr 237
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Db      1051 CAGTGTGAGAACAAGGAAATACTCAGGGAGCAGTCTGAGTAATATGGGTGCCTACAGCCG 1110

Qy       237 gPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIl 257
             |   :::      ||||||     :::   |||  :::     :::
Db      1111 ATCGCTTCCCAGGTTGTATAAAGCCACAGACAACCAGATGTCGCCTCTCAGCCTGCCTCC 1170

Qy       257 eAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGly------GlyLeuProThrGl 275
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Db      1171 AAGAAGTTCCCTGGGCAATTCCAGAAGAGGTCAGTTAGGAGAAAAGGATCTACCTCATAG 1230

Qy       275 uLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGl 295
             |||:::   |||          |||   |||          :::|||:::
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Qy       295 yGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAl 315
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Db      1282 TTCACCC------------------------------------------------------ 1288

Qy       315 aIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGl 335
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Qy       335 nHisGluGlnAspArgProThrProSerProAlaProSerArgProPheSerValLeuAr 355
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Qy       355 gAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyr-- 374
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Qy       375 -GlySerSerThrGlyProValTyrValSerAspSerValThrLeuValAsnValAlaTh 394
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Db      1420 AGGGACCAGCCCAAGTCATTCCTTCATTTCTGGAGAGCCAGACCGAGTGCTTGTGGCC-- 1477

Qy       394 rGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArgPr 414
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Db      1478 ---------------AGGAGGAACTTCTCTTGTGGATCAATGGAGCTTGATGACTCTGA 1521

Qy       414 oLeuSerThrIleGlnGlnTyrSerLysThr 424
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LOCUS       AY404468               3702 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Mus musculus HCM1900 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY404468
VERSION     AY404468.1  GI:39760445
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3702)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 3702)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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ORIGIN
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Pred. No.:                0.478          Length:          3702
Score:                    122.00         Matches:         94
Percent Similarity:       35.48%         Conservative:    66
Best Local Similarity:    20.84%         Mismatches:      182
Query Match:              4.34%          Indels:          109
DB:                       9              Gaps:            15

US-09-769-066-15 (1-549) x AY404468 (1-3702)

Qy         3 AlaProAlaHisAspThrProProValPro----------------------AspValAsp 15
             ||||||   ||||||       |||   |||                    :::|||
Db       171 GCCCCAAAACATGATGGAGAGCCTAAGCCCGAGGAAATACTCATCAAGTCTGAAGTTTAA 230

Qy        16 SerArgGlyAlaIleLeuArgArgGlnTyrAsn-Leu---------------------- 27
             |||:::      :::           :::||| |||
Db       231 AGCCAACGGGGACTATTCTGGCTCCTATTTAACCCTCTCCCAACCGGTGTCTGCCAAGAG 290

Qy        28 -SerThrSerProLeuThrSerSerValAlaThrGlyThrAsnLeuValLeuTyrAlaAl 47
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Db       291 AAGCCCTTCTCCAATGGGCACCAGCGTCAGGAGCAGTCCCTCCTTG-----------GC 338

Qy        47 aProLeuSerProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGl 67
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Db       339 CAAAATCCAGGGAAGCAAACAGTTCTGCGATGGAATTGATAAAAATATTTCCATGAAACC 398

Qy        67 uAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuVa 87
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Qy        87 lProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrTh 107
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Qy        123 eLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeuHisTyrAr 143
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Db        504 CTCAGAGAAGCCT----------------------CCCTATTCCAGATACAGCTCTAG 539

Qy        143 gAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaThrSerGl 163
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Qy        183 ----ThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuTh 201
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Qy        201 rProGlyAsnThr---AsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLe 220
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Db        720 GGACCACTCGACACTTCAGCCCAGGTTAAGCAGGCACAAGGAGCCGGCCTCAGAAAACGT 779

Qy        220 u---------ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrAr 237
                :         |||      |||::::::                 |||   :::||
Db        780 CAGTGTGAGAACAAGGAAATACTCAGGGAGCAGTCTGAGTAATATGGGTGCCTACAGCCG 839

Qy        237 gPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIl 257
                |   :::      ||||||     :::   |||   :::       :::
Db        840 ATCGCTTCCCAGGTTGTATAAAGCCACAGACAACCAGATGTCGCCTCTCAGCCTGCCTCC 899

Qy        257 eAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGly------GlyLeuProThrGl 275
                  :::|||   |||                |||||||         ||||||
Db        900 AAGAAGTTCCCTGGGCAATTCCAGAAGAGGTCAGTTAGGAGAAAAGGATCTACCTCATAG 959

Qy        275 uLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGl 295
                |||:::   |||                |||   |||       :::|||:::
Db        960 CCTAGTGGATAGTGACAATTACCTTAACTTTTCTTCT---------CTAAGCTCAGGGGC 1010

Qy        295 yGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAl 315
                |||
Db       1011 TTCACCC------------------------------------------------------ 1017

Qy        315 aIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGl 335
                                                                  |||
Db       1018 ----------------------------------------------TATAAAACCTG 1028

Qy        335 nHisGluGlnAspArgProThrProSerProAlaProSerArgProPheSerValLeuAr 355
                  :::      |||      |||   |||   |||   |||   |||
Db       1029 TCTGTCAGAGGGAAATCCTTACGTAAGCTCCGCCCTCAGTGTTCCTGCCAGTCCTCGTGT 1088

Qy        355 gAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyr-- 374
                |||      :::|||      |||   ::::::   ::::::|||:::::::::|||
Db       1089 GGCTCGGAAGATGCTCCTGGCCTCCACCTCCTCTGATGACTTTGATAGGGCTTCATACTC 1148

Qy        375 -GlySerSerThrGlyProValTyrValSerAspSerValThrLeuValAsnValAlaTh 394
                 |||:::|||            ::::::|||            |||   ||||||
Db       1149 AGGGACCAGCCCAAGTCATTCCTTCATTTCTGGAGAGCCAGACCGAGTGCTTGTGGCC-- 1206

Qy        394 rGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArgPr 414
                              |||:::         :::   |||||
Db       1207 ---------------AGGAGGAACTTCTCTTGTGGATCAATGGAGCTTGATGACTCTGA 1250

Qy        414 oLeuSerThrIleGlnGlnTyrSerLysThr 424
                |||   :::::::::|||   |||:::|||
Db       1251 TCTGGAAAGCCTAAGACAGTCGTCAGAAACT 1281

RESULT 7
AY417426
LOCUS       AY417426               2232 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Homo sapiens POU2F1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY417426
VERSION     AY417426.1  GI:39773386
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2232)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2232)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .2232
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1. .>2232
                     /gene="POU2F1"
                     /locus_tag="HCM6220"
ORIGIN

Alignment Scores:
Pred. No.:                0.249          Length:          2232
Score:                    121.50         Matches:         78
Percent Similarity:       38.94%         Conservative:    40
Best Local Similarity:    25.74%         Mismatches:      136
Query Match:              4.32%          Indels:          49
DB:                       9              Gaps:            13

US-09-769-066-15 (1-549) x AY417426 (1-2232)

Qy         28 SerThrSerProLeu--------------------ThrSerSerValAlaThrGlyThr 40
                |||:::||||||:::                  ||||||   ||||||||
Db       1336 AGCAGCTCACCTATTAAAGCAATTTTCCCCAGCCCAACTTCACTGGTGGCGACCACACCA 1395

Qy         41 AsnLeuValLeuTyrAlaAla------------ProLeuSerProLeuLeuProLeuGln 56
                :::||||||      :::|||               :::||||||:::|||||||||
Db       1396 AGCCTTGTGACTAGCAGTGCAGCAACTACCCTCACAGTCAGCCCTGTCCTCCCTCTGACC 1455

Qy         57 AspGlyThrAsnThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgVal 76
                        |||::::::      |||      |||:::
Db       1456 AGTGCTGCTGTGACGAATCTTTCAGTTACAGGCACTTCAGACACCACCTCCAACAACACA 1515

Qy         77 AlaArgAlaThrIleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIle 96
                |||         |||      |||         :::||||||          ::::::
Db       1516 GCA---ACCGTGATTTCCACAGCGCCTCCAGCTTCCTCAGCAGTCACGTCCCCCTCTCTG 1572

Qy         97 SerIleSerPheTrpProGln---------ThrThrThrThrProThrSerValAspMet 113
                |||   |||      |||             :::|||:::    :::|||
Db       1573 AGTCCCTCC------CCTTCTGCCTCAGCCTCCACCTCCGAGGCATCCAGTGCCAGTGAG 1626

Qy        114 AsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGluLeu 133
                  |||   |||   |||             |||       |||         |||::::::
Db       1627 ACCAGCACAACACAGACCACCTCCACTCCTTTGTCCTCCCCTCTTGGGACCAGCCAGGTG 1686

Qy        134 ValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThrSer 153
                ::::::   :::      |||             |||         :::
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Db       1687 ATGGTGACAGCATCAGGTTTG-----------CAAACAGCAGCAGCTGCTGCCCTTCAA 1734

Qy        154 GlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeu 173
Db       1735 GGAGCTGCACAGTTGCCAGCAAATGCCAGTCTTGCTGCCATGGCAGCTGCTGCAGGACTA 1794

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
Db       1795 AACCCAAGCCTGATGGCACCCTCACAGTTTGCGGCTGGAGGTGCCTTA------------ 1842

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSer--------- 210
Db       1843 ------------CTCAGTCTGAATCCAGGGACCCTGAGCGGTGCTCTCAGCCCAGCTCTA 1890

Qy        211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
Db       1891 ATGAGCAACAGTACACTGGCAACTATTCAAGCTCTTGCTTCTGGTGGCTCTCTTCCAATA 1950

Qy        231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyVal 250
Db       1951 ACATCACTTGATGCAACT---------GGGAACCTGGTATTTGCCAATGCGGGAGGAGCC 2001

Qy        251 GlyGluIleGlyArgGlyIleAlaLeuThrLeuPhe------------AsnLeuAlaAsp 266
Db       2002 CCCAACATC---------GTGACTGCCCCTCTGTTCCTGAACCCTCAGAACCTC------ 2046

Qy        267 ThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyr 286
Db       2047 TCTCTGCTCACCAGCAACCCTGTTAGCTTGGTCTCTGCCGCCGCAGCATCTGCAGGGAAC 2106

Qy        287 SerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGlu 306
Db       2107 TCTGCACCTGTAGCCAGCCTTCACGCCACCTCC--------------ACCTCTGCTGAG 2151

Qy        307 AsnAlaGln 309
Db       2152 TCCATCCAG 2160
```

```
RESULT 8
CF870156
LOCUS       CF870156               759 bp    mRNA    linear   EST 31-OCT-2003
DEFINITION  tric021xl12.b1 T.reesei mycelial culture, Version 6 October 2003
            Hypocrea jecorina cDNA clone tric021xl12, mRNA sequence.
ACCESSION   CF870156
VERSION     CF870156.1  GI:38124838
KEYWORDS    EST.
SOURCE      Hypocrea jecorina (anamorph: Trichoderma reesei)
  ORGANISM  Hypocrea jecorina
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE   1  (bases 1 to 759)
  AUTHORS   Diener,S.E., Dunn-Coleman,N., Foreman,P., Houfek,T.D.,
            Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K.,
            Ward,M. and Dean,R.A.
  TITLE     Characterization of the protein processing and secretion pathways
            in a comprehensive set of expressed sequence tags from Trichoderma
            reesei
  JOURNAL   FEMS Microbiol. Lett. 230 (2), 275-282 (2004)
COMMENT     Contact: Ralph A. Dean
            Fungal Genomics Laboratory
            North Carolina State University
            Campus Box 7251, Raleigh, NC 27695, USA
            Tel: 919-513-0020
            Fax: 919-513-0024
            Email: ralph_dean@ncsu.edu
            Seq primer: LT-F1 primer.
FEATURES             Location/Qualifiers
     source          1. .759
                     /organism="Hypocrea jecorina"
                     /mol_type="mRNA"
                     /strain="QM6a"
                     /db_xref="taxon:51453"
                     /clone="tric021xl12"
                     /dev_stage="mycelia"
                     /clone_lib="T.reesei mycelial culture, Version 6 October
                     2003"
                     /note="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial
                     culture grown from 24 hrs to 6 days with varying Carbon
                     and Nitrogen sources and concentrations."
ORIGIN
```

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Alignment Scores:
Pred. No.:                0.129          Length:          759
Score:                    117.50         Matches:         79
Percent Similarity:       37.34%         Conservative:    36
Best Local Similarity:    25.65%         Mismatches:      105
Query Match:              4.18%          Indels:          89
DB:                       7              Gaps:            12

US-09-769-066-15 (1-549) x CF870156 (1-759)

Qy         12 ProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThrSerPro 31
Db         15 CCTGATATAGCTTCAAAATGGCCATTACCAAGGTTCACGCTCGCTCTGTCTACGACTCCC 74

Qy         32 LeuThrSerSerValAlaThrGlyThrAsnLeuValLeuTyrAla------AlaProLeu 49
Db         75 GTGGCAACCCCACCGTGGAGGTCGACCTCGTCACTGACACTGGCCTGCACCGCGCCATTG 134

Qy         50 SerProLeuLeuProLeuGlnAspGlyThr------AsnThrHisIleMetAlaThrGlu 67
Db        135 TCCCCTCCGGTGCCTCTACCGGCCAGCACGAGGCTGTCGAGCTTCGAGATGGCGACAAGG 194

Qy         68 AlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuVal 87
Db        195 CCAAGTGGG--------------GTGGCAAGGGTGTCACCAAGG-------------- 224

Qy         88 ProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThr 107
Db        225 ----------------------------------------CCGTCGAGAACGTCAACA 242

Qy        108 ProThrSerValAspMetAsnSer--------------------------------Ile 116
Db        243 CCATCATCGGCCCCGCTCTCATCAAGGAGAACCTTGATGTCAAGGACCAGTCCAAGGTCG 302

Qy        117 ThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIlePro 136
Db        303 ACGAGTTCCTGAACAGCCTTGACGGCACCCCCAACAAGGGCAAGCTCGGTGCCAACGCCA 362

Qy        137 SerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAla 156
Db        363 TCC--------------------------------TCGGTGTCAGCTTG-GCTGTTGCC 388

Qy        157 GluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSer 176
Db        389 AAGGCCGGTGCCGCTGAGAAGAACGTCCCCCTGTACGCCCACATCTCCGACCTT---GCC 445

Qy        177 TyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGlu 196
Db        446 GGAACCAAGAAGCCCTAC--------------------------GTCCTCCCCGTTCCC 478

Qy        197 PheArgAsnLeuThrProGlyAsnThrAsnThrArg---------------------- 208
Db        479 TTCATGAACGTCCTCAACGGCGGTTCCCACGCCGGTGGCCGTCTTGCCTTCCAGGAGTTC 538

Qy        209 ------ValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGly 226
Db        539 ATGATTGTTCCTTCAGAGGCTCCCAGCTTCTCCGAGGCCCTTCGCCAGGGCTCCGAGGTC 598

Qy        227 ThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSer 246
Db        599 TACCAGAAGCTGAAGACCCTGGCC--------------AAGAAGAAGTACGGCCAGTCC 643

Qy        247 ThrAsnGlyValGlyGluIleGlyArgGly-IleAlaLeuThrLeuPheAsnLeuAlaAs 266
Db        644 GCTGGCAACGTCGGCGAC------GAGGGTGGTGTCGCTCCCGATATCCAGACTGCCGAC 697
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Qy        266 pThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTy 286
              ||||||     ||||||   |||
Db        698 GAGGCTCTTGAGCTCATCACCGACGCCATTG---------------------------- 728

Qy        286 rSerArgProValValSerAla 293
               |||||||||        |||
Db        729 -AGCAGGCCGGCTACACTGGCA 749
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RESULT 9
CB900324

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LOCUS       CB900324                828 bp    mRNA    linear   EST 02-JUL-2003
DEFINITION  tric021xl12 T.reesei mycelial culture, Version 3 april Hypocrea
            jecorina cDNA clone tric021xl12, mRNA sequence.
ACCESSION   CB900324
VERSION     CB900324.1  GI:30114982
KEYWORDS    EST.
SOURCE      Hypocrea jecorina (anamorph: Trichoderma reesei)
  ORGANISM  Hypocrea jecorina
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
REFERENCE   1  (bases 1 to 828)
  AUTHORS   Foreman,P.K., Brown,D.E., Dankmeyer,L., Dean,R., Diener,S.,
            Dunn-Coleman,N.S., Goedegebuur,F., Houfek,T.D., England,G.J.,
            Kelley,A.S., Meerman,H.J., Mitchell,T., Mitchinson,C.,
            Olivares,H.A., Teunissen,P.J., Yao,J. and Ward,M.
  TITLE     Transcriptional regulation of biomass-degrading enzymes in the
            filamentous fungus Trichoderma reesei
  JOURNAL   J. Biol. Chem. 278 (34), 31988-31997 (2003)
  MEDLINE   22803314
   PUBMED   12788920
COMMENT     Contact: Pamela K. Foreman
            Genencor Intl.
            925 Page Mill Road, Palo Alto, CA 94304, USA
            Tel: (650) 846-7635
            Fax: (650) 621-7817
            Email: Pforeman@genencor.com
            Seq primer: LT-F1 primer.
FEATURES             Location/Qualifiers
     source          1. .828
                     /organism="Hypocrea jecorina"
                     /mol_type="mRNA"
                     /strain="QM6a"
                     /db_xref="taxon:51453"
                     /clone="tric021xl12"
                     /dev_stage="mycelia"
                     /clone_lib="T.reesei mycelial culture, Version 3 april"
                     /note="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial
                     culture grown from 24 hrs to 6 days with varying Carbon
                     and Nitrogen sources and concentrations."
ORIGIN
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Alignment Scores:

Pred. No.:	0.147	Length:	828
Score:	117.50	Matches:	79
Percent Similarity:	37.34%	Conservative:	36
Best Local Similarity:	25.65%	Mismatches:	105
Query Match:	4.18%	Indels:	89
DB:	6	Gaps:	12

US-09-769-066-15 (1-549) x CB900324 (1-828)

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Qy         12 ProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThrSerPro 31
              ||||||:::   |||:::      :::   |||              |||||||||:::|||
Db         84 CCTGATATAGCTTCAAAATGGCCATTACCAAGGTTCACGCTCGCTCTGTCTACGACTCCC 143

Qy         32 LeuThrSerSerValAlaThrGlyThrAsnLeuValLeuTyrAla------AlaProLeu 49
              :::  :::                 |||:::   :::      |||      |||||||||
Db        144 GTGGCAACCCCACCGTGGAGGTCGACCTCGTCACTGACACTGGCCTGCACCGCGCCATTG 203

Qy         50 SerProLeuLeuProLeuGlnAspGlyThr------AsnThrHisIleMetAlaThrGlu 67
              ||||||   :::||||||          |||      ::::::     |||||||||
Db        204 TCCCCTCCGGTGCCTCTACCGGCCAGCACGAGGCTGTCGAGCTTCGAGATGGCGACAAGG 263

Qy         68 AlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuVal 87
              |||                 |||||||||   :::   |||
Db        264 CCAAGTGGG--------------GTGGCAAGGGTGTCACCAAGG--------------- 293

Qy         88 ProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThr 107
                                                      |||      |||:::|||
Db        294 ----------------------------------------CCGTCGAGAACGTCAACA 311

Qy        108 ProThrSerValAspMetAsnSer--------------------------------Ile 116
              |||:::|||      ::::::|||
Db        312 CCATCATCGGCCCCGCTCTCATCAAGGAGAACCTTGATGTCAAGGACCAGTCCAAGGTCG 371

Qy        117 ThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIlePro 136
              ||||||:::         :::         |||      ||||||   :::      |||
Db        372 ACGAGTTCCTGAACAGCCTTGACGGCACCCCCAACAAGGGCAAGCTCGGTGCCAACGCCA 431

Qy        137 SerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAla 156
              |||                                |||||                |||||
Db        432 TCC--------------------------------TCGGTGTCAGCTTG-GCTGTTGCC 457

Qy        157 GluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSer 176
              :::      |||              |||  |||      |||  |||  :::  :::
Db        458 AAGGCCGGTGCCGCTGAGAAGAACGTCCCCCTGTACGCCCACATCTCCGACCTT---GCC 514

Qy        177 TyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGlu 196
              |||      ||||||                                |||   :::
Db        515 GGAACCAAGAAGCCCTAC-------------------------GTCCTCCCCGTTCCC 547

Qy        197 PheArgAsnLeuThrProGlyAsnThrAsnThrArg----------------------- 208
              |||   |||:::      |||   ::::::
Db        548 TTCATGAACGTCCTCAACGGCGGTTCCCACGCCGGTGGCCGTCTTGCCTTCCAGGAGTTC 607

Qy        209 ------ValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGly 226
                    |||         :::  :::            ||||||:::|||:::::
Db        608 ATGATTGTTCCTTCAGAGGCTCCCAGCTTCTCCGAGGCCCTTCGCCAGGGCTCCGAGGTC 667

Qy        227 ThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSer 246
                 :::|||   |||  |||                |||     |||     |||
Db        668 TACCAGAAGCTGAAGACCCTGGCC--------------AAGAAGAAGTACGGCCAGTCC 712

Qy        247 ThrAsnGlyValGlyGluIleGlyArgGly-IleAlaLeuThrLeuPheAsnLeuAlaAs 266
                   ||||||:::         ||| :::::::|||   :::     |||
Db        713 GCTGGCAACGTCGGCGAC------GAGGGTGGTGTCGCTCCCGATATCCAGACTGCCGAC 766

Qy        266 pThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTy 286
              ||||||     ||||||   |||
Db        767 GAGGCTCTTGAGCTCATCACCGACGCCATTG---------------------------- 797

Qy        286 rSerArgProValValSerAla 293
               |||||||||        |||
Db        798 -AGCAGGCCGGCTACACTGGCA 818
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RESULT 10
CR552265

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LOCUS       CR552265                931 bp    mRNA    linear   EST 12-JUL-2004
DEFINITION  CR552265 Normalized and Subtracted bovine embryonic and
            extraembryonic tissues (bcaz) Bos taurus cDNA clone bcaz0007a.e.20
            5', mRNA sequence.
ACCESSION   CR552265
VERSION     CR552265.1  GI:50247175
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 931)
  AUTHORS   Renard,J.P., Lewin,H.A., Yang,J., Hernandez,A., Degrelle,S.,
            Everts,R.E. and Hue,I.
  TITLE     Embryonic ESTs (bcaz)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Renard JP
```

Biologie du Developpement et Reproduction
INRA
Domaine de Vilvert 78350 Jouy en Josas, FRANCE
Email: renard@jouy.inra.fr
Funding for EST sequencing was provided by funds dedicated to J.P.RENARD (BDR, Inra). Funding for construction and subtraction of the cDNA library was provided by USDA ARS contract No 58-1275-2-020 to H. A. Lewin The cDNA library was constructed, normalized and subtracted by Dr. A. Hernandez (W.M. Keck Center, University of Illinois Urbana-Champaign) and S. Degrelle (BDR, Inra) as described in Bonaldo et al.(1996), Genome Research 6, 791-806. BE03 library is a normalized library of embryonic tissues subtracted with 7800 known EST sequences. The double-stranded cDNA was size selected (>450 bp), adaptored with EcoRI adaptors at both ends and digested with NotI. The cDNA was then directionally cloned into EcoRI-NotI digested pGEM11Zf(+) phagemid vector. Insert size was between 450-2200 bp. Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this sequence.

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FEATURES             Location/Qualifiers
     source          1. .931
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /clone="bcaz0007a.e.20"
                     /tissue_type="embryo (day 36 and day 64), extra-embryonic
                     tissue (day 14 to 25)"
                     /lab_host="DH10B"
                     /clone_lib="Normalized and Subtracted bovine embryonic and
                     extraembryonic tissues (bcaz)"
                     /note="Vector: pGEMZf11; Tagged oligo-dT was used to
                     identify the origin of the ESTs where possible. (A18)TGCGT
                     = extraembryonic tissue; (A18)TCGGT = 36-day oldfetus;
                     (A18)TGCGA = 64-day old fetus (organs); (A18)TCGGA =
                     64-day old fetus (body)"
ORIGIN
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Alignment Scores:

Pred. No.:	0.199	Length:	931
Score:	117.00	Matches:	73
Percent Similarity:	38.75%	Conservative:	39
Best Local Similarity:	25.26%	Mismatches:	139
Query Match:	4.16%	Indels:	38
DB:	7	Gaps:	11

US-09-769-066-15 (1-549) x CR552265 (1-931)

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Qy         28 SerThrSerProLeu--------------------ThrSerSerValAlaThrGlyThr 40
              |||:::||||||:::                    |||    |||||||||
Db         83 AGCAGCTCGCCTATCAAAGCAGTTTTCCCCAGCCCAGCCTCACTGGTGGCAACCACACCA 142

Qy         41 AsnLeuValLeuTyrAlaAla------------ProLeuSerProLeuLeuProLeuGln 56
              :::||||||      :::|||               ::::::|||:::|||||||||||
Db        143 AGCCTTGTGACAAGCAGTGCAGCAACTACCCTCACGGTCAATCCAGTCCTTCCTTTAACC 202

Qy         57 AspGlyThrAsnThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgVal 76
                  |||::::::      |||      ::::::
Db        203 AGCGCTGCGGTAACTAATCTCTCTGTTACAGGCACTACAGATACCACCGCCAACAACACT 262

Qy         77 AlaArgAlaThrIleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIle 96
              |||    |||      |||      |||:::||||||          |||:::
Db        263 GCA---ACCGTGATTTCCACGGCGCCTCCGGCCCCCTCGGCGGTCACCTCCCCCGCCCTG 319

Qy         97 SerIleSerPheTrpProGln---------ThrThrThrThrProThrSerValAspMet 113
              |||   |||      |||               |||:::      :::|||
Db        320 AGCCCCTCC------CCTTCCGCCTCAGCCGCCACCTCCGAGGCGTCCAGCGCCAGCGAG 373

Qy        114 AsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGluLeu 133
                 |||   |||   |||              |||      |||          |||::::::
Db        374 ACCAGCACCACACAGACCACCTCTGCTCCTCTGTCCTCTCCTCTTGGGACCAGCCAGGTG 433

Qy        134 ValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThrSer 153
              ::::::   :::      |||             |||         :::
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Db        434 ATGGTGACAGCATCAGGGTTG-----------CAAACAGCAGCAGCTGCCGCCCTCCAA 481

Qy        154 GlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeu 173
              |||   |||:::   |||   :::   |||      :::                |||
Db        482 GGAGCTGCCCAGTTGCCAGCAAATGCCAGTCTCGCTGCCATGGCTGCTGCTGCAGGACTA 541

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
                                          |||   :::             ||||||
Db        542 ----------------------AACCCAGGCCTGATGGCACCCTCACAGTTTGCAGCT 577

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSer--------- 210
                        :::|||   ||||||               :::|||
Db        578 GGAGGTGCCTTACTCAGTCTCAATCCGGGAACCCTTGGTGGTGCTCTCAGCCCAGCTCTG 637

Qy        211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
                 :::||||||                    :::   |||:::      :::
Db        638 ATGAGCAACAGTACACTGGCAACTATTCAAGCTCTTGCTTCTGGTGGCTCTCTGCCAATA 697

Qy        231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyVal 250
              |||:::      ||||||           :::|||   |||   :::      |||
Db        698 ACGTCACTGGACGCGACT---------GGGAACCTGGTATTCGCCAACGCAGGAGGAGCC 748

Qy        251 GlyGluIleGlyArgGly---IleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeu 269
                 |||            :::   ||||||      ||||||      :::||||||
Db        749 CCCAACATCGTGACCGCCCCTCTCTTCCTGACCCCTCAGAACCTC------TCTCTGCTC 802

Qy        270 GlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgPro 289
                       |||      |||:::|||:::|||                |||   |||
Db        803 ACCAGCAATCCAGTTAGCTTGGTCTCTGCCGCTGCAACCTCTGCAGGGAATTCTGGACCT 862

Qy        290 ValValSerAlaAsnGlyGluProThr 298
              |||   |||   :::      |||
Db        863 GTAGCCAGCCTTCATGCCACCTCCACC 889
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RESULT 11
AY400949
LOCUS       AY400949               9097 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Mus musculus HCM0727 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY400949
VERSION     AY400949.1  GI:39756938
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 9097)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 9097)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .9097
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1. .>9097
                     /locus_tag="HCM0727"
ORIGIN
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Alignment Scores:
Pred. No.:              9.41          Length:         9097
Score:                  115.50        Matches:        117
Percent Similarity:     37.16%        Conservative:   77
Best Local Similarity:  22.41%        Mismatches:     193
Query Match:            4.11%         Indels:         136
DB:                     9             Gaps:           27

US-09-769-066-15 (1-549) x AY400949 (1-9097)

Qy          2 ValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle--- 20
Db       4969 ATCTCTGAAACTAATAACACTACCCTTGTAACATCTACCCAGTCTACAGCCACTGTGAAC 5028

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
Db       5029 CTTACCAAAACTACTGGGATAACTACTAGCCCTGTGGCTTCA------------------- 5070

Qy         41 AsnLeuValLeuTyrAlaAlaProLeu------SerPro------LeuLeuProLeuGln 56
Db       5071 ------GTTTCATTTGCTAAACCATTGGTAGCATCTCCAACCATAACTCTTCCTGTTGCT 5124

Qy         57 AspGlyThrAsnThrHisIle---MetAlaThrGluAlaSerAsnTyrAlaGlnTyrArg 75
Db       5125 TCCACTGCCTCCACCTCCATAGTCATGGTGACCACAGCTGCATCTTCCTCCGTGGTGACC 5184

Qy         76 ValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAla 95
Db       5185 ACACCTACTTCATCACTGAGTTCTGTACCTATTATACTCTCAGGAATTAATGGA---AGT 5241

Qy         96 IleSerIleSerPheTrpProGlnThr---------------ThrThrThrProThrSer 110
Db       5242 CCACCCGTGAGCCAGAGACCAGAAAATGCCCCTCAAATTCCAGTGACTACTCCA---CAG 5298

Qy        111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeu---------ValGlnPro 127
Db       5299 ATCTCTTCTAACAACGTGAAACGTACTGGACCTCGATTGTTGTTGATTCCAGTGCAGCAG 5358

Qy        128 GlyIleAlaSerGluLeuValIlePro-SerGluArgLeuHisTyrArgAsnGlnGlyTr 147
Db       5359 GGT------TCTCCTACGCTTAGACCAATCCAAAACCCACAGCTTCAGGGACAGCGGATG 5412

Qy        147 pArgSerValGluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLe 167
Db       5413 G---TCTTGCAACCTGTTAGGGGTCCAAGTGGAATGAACCTATTCAGGCACCCCAATG-- 5467

Qy        167 uCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGl 187
Db       5468 ----------GGCAGATTGTCCAACTCCTACCTTTACATCAGATTCGAGGCTCTAATGCC 5517

Qy        187 yLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGly---------- 203
Db       5518 CAGCCCAGCTTACAGCCTGTG-GTA---TTTCGGAAC------CCAGGATCTATGGTGGG 5567

Qy        204 ------------------------AsnThrAsnThrArgValSerArgTyrSerSerTh 215
Db       5568 AATCCGACTACCAGCTCCTTGCAAATCTTCAGAGACTCCATCATCTTCTGCTTCATCCTC 5627

Qy        215 rAlaArgHisArgLeuArgArg--------------GlyAlaAspGlyThrAlaGluLe 230
Db       5628 TGCCTTCTCTGTCATGAGTCCTGTGATTCAGGCTGTTGGGTCTTCTCCAACAGTAAATGT 5687

Qy        230 uThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyVa 250
Db       5688 CATTTCTCAGGCACCTTCACTGCTTTCCTCTGGATCTAGTTTTGTCTCTCAGGCTGGT-- 5745

Qy        250 lGlyGluIleGlyArgGlyIleAlaLeuThrLeu--------------------PheAs 263
Db       5746 ----------------------ACACTGACTCTGAGGATCTCTCCTCCTGAAACTCAAAA 5783

Qy        263 nLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly-- 282
Db       5784 CCTTGCAAGTAAAACA------GGCTCTGAAAGCAAAATAACACCCAGCACTGGAGGACA 5837

Qy        283 ----------------------------------------------------------GlnLe 284
Db       5838 GCCTGTAGGCACTGCTAGCCTCATTCCTCTGCAGTCAGGTAGTTTTGCCTTGTTGCAGCT 5897

Qy        284 uPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSe 304
Db       5898 CCCAGGACAAAAGCCTATCCCTAGCTCTGTTCTTCAGCATGTTGCTTCCCTTCAAATAAA 5957

Qy        304 rValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGl 324
Db       5958 AAAGGAATCTCAGAGTACAGACCAG---------------------------------- 5982

Qy        324 uSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSe 344
Db       5983 ---------------AAAGATGAAACAAACTCTATCAAAAGAGAGGAGGAAACTAAGAA 6026

Qy        344 rProAlaProSerArg-----------------ProPheSerValLeuArgAlaAsnAs 358
Db       6027 AGCTCTACCATCAAAAGATAAAGCTCTAGACTCTGAGGCTAATATAATGAAGCAAAACTC 6086

Qy        358 pValLeuTrpLeuSerLeuThrAlaAlaGlu--------------------------Ty 369
Db       6087 AGGAATTATTGCCTCAGAAAATACCTCGAATAATTCATTGGATGATGGGGGTGATCTTTT 6146

Qy        369 rAspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAspSer-ValThrL 389
Db       6147 GGATGAAGAAACCCTTAGGGAAGATGCCAGACCTTATGAATACTCTTATAGCACTGGGTC 6206

Qy        389 euValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValT 409
Db       6207 TCATACAGATGAAGACA------AAGATGGTGATGAGGACTCTG---------------- 6244

Qy        409 hrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuP 429
Db       6245 --------GGAACAAGAATCAGAACAGTCCAAAAGAAAAACAAACTGTTCCAGAAGTTAG 6296

Qy        429 roLeuArgGlyLys---LeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProT 448
Db       6297 AGCTGGCTCTAAAAACATTGATATTATGGCAC---------TCCAAAGCATCAGAAGTAT 6347

Qy        448 yr 448
Db       6348 AC 6349

RESULT 12
AK082573
LOCUS       AK082573                1211 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length
            enriched library, clone:C230064N08 product:POU domain, class 2,
            transcription factor 1, full insert sequence.
ACCESSION   AK082573
VERSION     AK082573.1  GI:26349790
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
```

REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 1211)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
FEATURES Location/Qualifiers
source 1. .1211
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:C230064N08"
/db_xref="taxon:10090"
/clone="C230064N08"
/tissue_type="cerebellum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
CDS 515. .1057
/note="unnamed protein product; POU domain, class 2, transcription factor 1 (MGD|MGI:101898, GB|NM_011137, evidence: BLASTN, 99%, match=2629) putative"
/codon_start=1
/protein_id="BAC38535.1"
/db_xref="GI:26349791"
/translation="MVTTPGLQTAATALQGAAQLPANASLAAMAAAAGLSPGLMAPSQ

FAAGGALLSLSPGTLGSALSPALMSNSTLATIQALASSGSLPITSLDATGNLVFANAG
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FTVASASGPASTTTAASKAQ"
ORIGIN

Alignment Scores:

Pred. No.:	0.487	Length:	1211
Score:	115.00	Matches:	72
Percent Similarity:	40.86%	Conservative:	51
Best Local Similarity:	23.92%	Mismatches:	122
Query Match:	4.09%	Indels:	56
DB:	3	Gaps:	13

US-09-769-066-15 (1-549) x AK082573 (1-1211)

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Qy         27 LeuSerThrSerPro------LeuThrSerSerValAlaThrGlyThrAsnLeuValLeu 44
              ::::::|||:::|||      :::|||||||||   ||||||
Db        205 GTGGCAACCACTCCAAGCCTTGTGACAAGCAGTACGGCAACT----------------- 246

Qy         45 TyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMet 64
                      ::::::|||:::|||||||||                 |||:::::::
Db        247 ---ACCCTCACAGTCAACCCTGTCCTCCCTTTAACCAGTGCTGCTGTGACTAATCTCTCT 303

Qy         65 AlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArg 84
                 |||      ::::::                                  |||
Db        304 CTTACAGGCACTACAGACTCGACGTCCAACAACAACACGGCCACGGTGATTTCCACAGCA 363

Qy         85 ProLeuValProAsnAlaValGlyGlyTyrAlaIle--SerIleSerPheTrpProGln- 103
                 |||          ::::|||||          ::::::  |||:::|||   ||||||:::
Db        364 CCCCCTGCTTCCTCAGCAGTCACATCCCCTTCCTTGAGTCCCTCTCCCTCTGGCCTCGGC 423

Qy        104 -ThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAspValArgIl 123
                :::|||:::      :::|||            :::   |||   |||
Db        424 CTCCACCTCAGAGGCCTCCAGTGCCAGTGAGACCAACACGACACAGACCACCTCCACGCC 483

Qy        123 eLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeuHisTyrAr 143
                |||      |||          ||||||:::::::::::::   :::
Db        484 TCTTCCCTCCCCTCTCGGAGCCAGCCAGGTGATGGTGACCACG---------------- 526

Qy        143 gAsnGlnGlyTrpArgSerValGluThrSer------GlyValAlaGluGluGluAlaTh 161
                   |||   ::::::       |||:::      |||   |||:::      |||
Db        527 ----CCCGGCTTACAGACAGCAGCCACCGCTCTCCAAGGAGCGGCACAGTTGCCAGCAAA 582

Qy        161 rSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrPr 181
                :::   |||      :::                 |||                  :::||
Db        583 CGCCAGTCTTGCTGCTATGGCTGCTGCTGCGGGACTC-----------------AGCCC 624

Qy        181 oTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuTh 201
                |      |||   :::              ||||||                 :::|||::
Db        625 A------GGCCTCATGGCACCCTCACAGTTTGCTGCTGGAGGTGCCTTACTCAGTCTCAG 678

Qy        201 rProGlyAsnThrAsnThrArgValSer---------ArgTyrSerSerThrAlaArgHi 218
                :||||||          :::   :::|||              :::|||||||
Db        679 TCCGGGGACTCTGGGCAGTGCTCTCAGCCCAGCCCTAATGAGCAACAGTACACTGGCAAC 738

Qy        218 sArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPh 238
                        :::   |||:::      :::|||:::      ||||||
Db        739 GATTCAAGCTCTTGCTTCTAGTGGCTCTCTTCCAATAACGTCTCTGGATGCAACT----- 793

Qy        238 eMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAl 258
                  :::|||   |||   :::       |||         |||          :::
Db        794 ----GGGAACCTGGTATTTGCCAATGCAGGAGGAGCCCCGAACATC---------GTGAC 840

Qy        258 aLeuThrLeuPhe------------AsnLeuAlaAspThrLeuLeuGlyGlyLeuProTh 274
                |||||             ||||||      :::||||||          |||
Db        841 TGCACCTCTGTTCCTGAACCCTCAGAACCTC------TCTCTGCTCACCAGCAACCCAGT 894

Qy        274 rGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAs 294
                  |||:::|||:::|||                                    :::   ||
Db        895 AAGCTTGGTTTCTGCCGCTGCAGCCTCC----------------------ACAGGGAA 930

Qy        294 nGlyGluProThrValLysLeuTyr---------ThrSerValGluAsnAlaGln 309
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Db        931 CTCTGCACCTACAGCCAGCCTTCATGCCTCCTCCACCTCAACTGAGTCCATCCAG 985

RESULT 13
AY417428
LOCUS       AY417428               2241 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Mus musculus POU2F1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY417428
VERSION     AY417428.1  GI:39773388
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2241)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2241)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .2241
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1. .>2241
                     /gene="POU2F1"
                     /locus_tag="HCM6220"
ORIGIN

Alignment Scores:
Pred. No.:              1.41          Length:         2241
Score:                  114.50        Matches:        70
Percent Similarity:     39.26%        Conservative:   47
Best Local Similarity:  23.49%        Mismatches:     128
Query Match:            4.07%         Indels:         53
DB:                     9             Gaps:           14

US-09-769-066-15 (1-549) x AY417428 (1-2241)

Qy          27 LeuSerThrSerPro------LeuThrSerSerValAlaThrGlyThrAsnLeuValLeu 44
               :::::::|||:::|||      :::|||||||||   ||||||
Db        1390 GTGGCAACCACTCCAAGCCTTGTGACAAGCAGTACGGCAACT----------------- 1431

Qy          45 TyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMet 64
                     ::::::|||:::|||||||||                 |||::::::
Db        1432 ---ACCCTCACAGTCAACCCTGTCCTCCCTTTAACCAGTGCTGCTGTGACTAATCTCTCT 1488

Qy          65 AlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArg 84
               |||      ::::::                  |||
Db        1489 CTTACAGGCACTACAGACTCGACGTCCAACAACAACACGGCCACGGTGATTTCCACAGCA 1548

Qy          85 ProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGln--- 103
               |||         :::||||||        ::::::|||   |||      |||
Db        1549 CCCCCTGCTTCCTCAGCAGTCACATCCCCTTCCTTGAGTCCCTCT------CCCTCTGCC 1602

Qy         104 ------ThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAspVal 121
                   :::|||:::     :::|||          :::   |||   |||
Db        1603 TCGGCCTCCACCTCAGAGGCCTCCAGTGCCAGTGAGACCAACACGACACAGACCACCTCC 1662

Qy         122 ArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeuHis 141
               |||      |||      ||||||:::::::::::   :::      |||
Db        1663 ACGCCTCTTCCCTCCCCTCTCGGAGCCAGCCAGGTGATGGTGACCACGCCCGGCTTACAG 1722

Qy         142 TyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaThr 161
                        :::              |||   |||:::      |||
Db        1723 --------------ACAGCAGCCGCCGCTCTCCAAGGAGCGGCACAGTTGCCAGCAAAC 1767

Qy         162 SerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrPro 181
               :::   |||      :::              |||                 :::|||
Db        1768 GCCAGTCTTGCTGCTATGGCTGCTGCTGCGGGACTC-----------------AGCCCA 1809

Qy         182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
               |||   :::              ||||||                 :::|||:::
Db        1810 ------GGCCTCATGGCACCCTCACAGTTTGCTGCTGGAGGTGCCTTACTCAGTCTCAGT 1863

Qy         202 ProGlyAsnThrAsnThrArgValSer---------ArgTyrSerSerThrAlaArgHis 218
               ||||||         :::   :::|||              :::||||||
Db        1864 CCGGGGACTCTGGGCAGTGCTCTCAGCCCAGCCCTAATGAGCAACAGTACACTGGCAACG 1923

Qy         219 ArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPhe 238
                        :::   |||:::      :::|||:::      ||||||
Db        1924 ATTCAAGCTCTTGCTTCTAGTGGCTCTCTTCCAATAACGTCTCTGGATGCAACT------ 1977

Qy         239 MetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAla 258
               :::|||   |||   :::      |||      |||         :::
Db        1978 ---GGGAACCTGGTATTTGCCAATGCAGGAGGAGCCCCGAACATC---------GTGACT 2025

Qy         259 LeuThrLeuPhe------------AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThr 274
               ||||||            ||||||      :::||||||          |||
Db        2026 GCACCTCTGTTCCTGAACCCTCAGAACCTC------TCTCTGCTCACCAGCAACCCAGTA 2079

Qy         275 GluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsn 294
               |||:::|||:::|||                                  :::   |||
Db        2080 AGCTTGGTTTCTGCCGCTGCAGCCTCC----------------------ACAGGGAAC 2115

Qy         295 GlyGluProThrValLysLeuTyr---------ThrSerValGluAsnAlaGln 309
               ||||||      |||:::      ||||||   |||:::   |||
Db        2116 TCTGCACCTACAGCCAGCCTTCATGCCTCCTCCACCTCAACTGAGTCCATCCAG 2169

RESULT 14
BQ028470/c
LOCUS       BQ028470               630 bp    mRNA    linear   EST 27-MAR-2002
DEFINITION  UI-H-CO0-arl-g-06-0-UI.s1 NCI_CGAP_Sub9 Homo sapiens cDNA clone
            IMAGE:3107098 3', mRNA sequence.
ACCESSION   BQ028470
VERSION     BQ028470.1  GI:19763749
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 630)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .630
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3107098"
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/tissue_type="mixed"
/dev_stage="mixed"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Sub9"
/note="Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; tissues: Cholonic mucosa with Crohns disease, Cholonic mucosa with ulcerative colitis, Fetal thymus, Cervix, Cervical adenosquamous carcinoma, Ligament cells, Prostate carcinoma, Bladder carcinoma, Brain oligodenroga ; NCI_CGAP_Sub9 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are CGTC, AACG, GGGCC, GGAAG, TAGC, TAAGC, ATGG, AGACA, ATCAC. For additional information, contact: Bento Soares, bento-soares@uiowa.edu
TAG_TISSUE=colonic mucosa with Crohns disease
TAG_LIB=UI-H-CO0
TAG_SEQ=CGTC"

ORIGIN

Alignment Scores:

Pred. No.:	0.426	Length:	630
Score:	111.50	Matches:	68
Percent Similarity:	36.82%	Conservative:	34
Best Local Similarity:	24.55%	Mismatches:	88
Query Match:	3.96%	Indels:	87
DB:	5	Gaps:	14

US-09-769-066-15 (1-549) x BQ028470 (1-630)

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Qy        149 SerValGluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCys 168
              |||      :::|||||||||:::||||||      ||||||
Db        589 AGCACGACAAGCTCAGGCGTCAGTGAAGAATCCACCACCTCC----------------- 548

Qy        169 IleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeu 188
               |||           :::::::::|||   |||   :::   |||:::     :::
Db        547 ---CACAGCCGACCAGGCTCAACGCACACA---ACAGCATTCCCTGGCAGTACCACCATG 494

Qy        189 LeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArg 208
                  :::   |||        :::   :::||||||:::|||:::|||
Db        493 CCAGGCGTCAGTCAGGAATCTACAGCTTCCCACAGCAGCCCAGGCTCCACAGACACAACA 434

Qy        209 ValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAla 228
              :::|||      |||:::||||||                |||   :::   |||
Db        433 CTGTCCCCTGGCAGTACCACAGCATCA---------TCCCTTGGTCCAGAATCTACT--- 386

Qy        229 GluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsn 248
                                                          |||      :::
Db        385 ------------------------------------------------ACCTTCCACAGC 374

Qy        249 GlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeu 268
              |||   |||                                      :::|||
Db        373 GGCCCAGGCTCC-----------------------------------ACTGAAACAACA 350

Qy        269 LeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArg 288
              |||      ||||||           :::::|||   |||   |||      |||
Db        349 CTC------TTACCTGACAAC------ACCACAGCCTCAGGCCTCCTTGAAGCATCTACG 302

Qy        289 ProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAla 308
              ||||||   |||:::   |||   |||          |||      :::
Db        301 CCCGTCCACAGCAGCACTGGATCGCCACACACAACACTGTCCCCTGCCGGCTCTACAACC 242

Qy        309 GlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSerArgValVal 328
              :::|||                                  |||||||||
Db        241 CGTCAG----------------------------------GGAGAATCT---ACCACC 221
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Qy        329 IleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSer 348
                 |||   :::   |||      :::                  :::|||||||||
Db        220 TTCCAGAGCTGGCCTAACTCGAAGGAC--------------ACTACCCCTGCACCTCCT 176

Qy        349 ArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGlu 368
                  |||                                                |||
Db        175 ACTACCACATCAGCCTTT-----------------------------------GTTGAG 152

Qy        369 TyrAspGlnSerThrTyrGly------SerSerThrGlyProValTyrValSerAspSer 386
                     :::::::::|||      |||||||||         :::   |||   |||
Db        151 CTATCTACAACCTCCCACGGCAGCCCGAGCTCAACTCCAACAACCCACTTTTCTGCCAGC 92

Qy        387 ValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThr 406
                 |||                                 :::   ||||||   :::   |||
Db         91 TCCACA--------------------------ACCTTGGGCCGTAGTGAGGAATCGACA 59

Qy        407 LysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLys 423
                    |||:::          |||:::|||||||||   |||       |||
Db         58 ------ACAGTCCACAACAGCCCAATATCTACAATCAACCAACAAGAAAAA 14
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RESULT 15
BC068239/c

LOCUS	BC068239 2453 bp mRNA linear HTC 02-APR-2004
DEFINITION	Mus musculus cDNA clone IMAGE:5324518.
ACCESSION	BC068239
VERSION	BC068239.1 GI:46189234
KEYWORDS	HTC.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 2453)
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
REFERENCE	2 (bases 1 to 2453)
AUTHORS	Strausberg,R.
TITLE	Direct Submission
JOURNAL	Submitted (31-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,

Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 92 Row: n Column: 23
This clone has the following problem: clone inconsistent with known gene structure.

FEATURES Location/Qualifiers
source 1. .2453
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NMRI"
/db_xref="taxon:10090"
/clone="IMAGE:5324518"
/tissue_type="Mammary tumor. WAP-Tag model. 5 months old, gross tissue."
/clone_lib="NCI_CGAP_Mam4"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Alignment Scores:

Pred. No.:	4.36	Length:	2453
Score:	110.50	Matches:	126
Percent Similarity:	33.33%	Conservative:	64
Best Local Similarity:	22.11%	Mismatches:	232
Query Match:	3.93%	Indels:	150
DB:	3	Gaps:	24

US-09-769-066-15 (1-549) x BC068239 (1-2453)

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Qy         10 ProValProAsp-----------------ValAspSerArgGlyAlaIleLeuArgArg  23
              |||:::|||                     :::   :::      ||||||   |||
Db       2070 CCGCTTCCTCCTCAGGTGCACATCATCAGACTTTCGGCGGAGGATGCCATCTGCAGGCAC 2011

Qy         24 GlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThrAsnLeuVal  43
                 :::   :::          |||   |||   |||:::   |||   |||
Db       2010 CTTTTTGGGGTGCTCGTCTGACCTCCGACGGGGAGCCTCTTCACACTCACT--------- 1960

Qy         44 LeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsnThrHisIle  63
                    :::||||||      |||||||||                    |||:::
Db       1959 ---------TCTCCGCTTGGCAGGCTCTTGCCCTTCCTT---GTTGTCCCGGTTCATCTT 1912

Qy         64 MetAlaThrGlu------AlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIle  81
              :::      |||      |||                  ||||||||||||:::
Db       1911 CTGCTCCTTGAGCAAGGAGCCAGGCAGGTTGGAGGCATACTTAAAGCCAGGGCCACGCTT 1852

Qy         82 ArgTyrArgProLeuValProAsnAlaValGly--GlyTyrAlaIleSerIleSerPheT  101
                    |||   |||          |||  ||||||
Db       1851 -----------TTGTTTCCCGGTCTTGCCGGCATGGTTAC------------------- 1823

Qy        101 rpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAspV  121
               |||:::   ||||||:::|||   :::   :::|||:::|||:::
Db       1822 --------ACTTCGGACACTCCCAGCAGTTGGGAAGC-TCATCGTTGACCACA------- 1779

Qy        121 alArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeuH  141
                                                    ||||||:::   |||
Db       1778 ----------------------------------------------CCCTCCGATTCCTTAA 1763

Qy        141 isTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaT  161
               |||:::   ||||||                  :::      |||   :::
Db       1762 TCTTAAGGCATCCAGGGTGG------------ATGATCTCGTTGCAGATGGAGCATTCCA 1715

Qy        161 hrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrP  181
                 |||      :::   |||                |||   |||:::|||:::      :::|
Db       1714 TGAGCATGAGGTTAAACTTGCCTTCTTCCTCTTCCACTGTGTCCTCCTTCCCTGCCTCGC 1655

Qy        181 roTyrThr-----------------GlyAlaLeuGlyLeuLeuAspPheAlaLeuGluL  195
              ||:::|||                 |||:::   |||   :::          :::   :
Db       1654 CACACACAAGGCACACGGCGGTGTGGGGCAGCACTGGCGCGATGCACTGCCGCATG---A 1598

Qy        195 euGluPheArgAsnLeuThrProGlyAsnThrAsn------------------------  206
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                :::::          :::   ||||||      |||
Db       1597 TGCAGCTCTGCTTCATGCGCCCAGGACCTCCAAACTTCTTCATGTCCTTGCAAAAGTGGC 1538

Qy        207 --------ThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyA  224
                        |||   |||   :::|||      |||||||||:::||||||
Db       1537 ACTCTCCACACTCCGTCCGCAGGCAGGCCTCGCACTTGCGGCATCGCGTCCGGCGC---- 1482

Qy        224 laAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrP  244
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Qy        244 heThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnL  264
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Db       1454 -----GCAGCCAACTTCACCGCTGAGGCCGGGCCCAACTTGCCC---------------- 1416

Qy        264 euAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnL  284
                          ||||||          |||          :::          |||||||
Db       1415 -------------TTAGGCCGACCCACCACCCGGTTCTTTGCAGTTTTCTTTGGCCAGC 1370

Qy        284 euPheTyrSerArgProValValSerAlaAsnGly---GluProThrValLysLeuTyrT  303
              ||          ||||||::::::      |||          |||           |
Db       1369 TGACCACAGGGACCCCGGTGATGGCCAGGGTGGGGTCGTCATCCACGTGCTCTTTCAGTA 1310

Qy        303 hrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeuG  323
              ||          :::::::::      |||   :::||||||
Db       1309 CATTCTTTACACCTTCCAGGAGGGCCTGGGGGTCCTCGATTCCC---------------T 1265

Qy        323 lyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrP  343
                 :::   :::                 |||:::
Db       1264 CAGGGACACACTTCTTATTCTCCGGAAGGGACTCTAGCTTT------------------- 1224

Qy        343 roSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuS  363
               |||          :::|||||||||                        |||      :::
Db       1223 --TCAACCAGGGCTTTCAAGCCCTTCAGTTCAAATTCGGTAAGGTGAGTCCACTTGGTAG 1166

Qy        363 erLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrV  383
                 :::   |||                    |||||||||   |||   :::   |
Db       1165 AAACCTCGGTGGCCGGGGAGCCCGTGGGCGTCTTGGGATCGTCCGTGGGC---ATCGAGG 1109

Qy        383 alSer-----------------------AspSerValThrLeuValAsnValAlaThrG  395
              ||                        |||:::|||   |||   |||      |
Db       1108 TCGACTTGACACTTTCCTCTGACTCATTGGACAACGTCCTCTTGAGGAACCGTATGGCAG 1049

Qy        395 lyAlaGlnAlaValAlaArgSerLeuAspTrpThrLys---------------------  407
              |||||                  |||   |||:::
Db       1048 GGGCTTTAGGCTTCTTCCCTGTGCTGTCCTGGTCTTCGGGCGGGGTGCTGGTGGGTGAGG 989

Qy        408 -------------------------ValThrLeuAspGlyArgProLeuSerThrIleG  419
                                        |||          |||   |||::::::
Db        988 TGGGGTCATCGGTGGGTGGCTTGGGTGTTTTATCTGCACCATCTCCTTCCTCCTCCTTGT 929

Qy        419 lnGlnTyrSerLysThrPhePheVal---LeuProLeuArgGlyLysLeuSerPheTrpG  438
                 |||      |||   :::   |||   |||   |||   |||          :
Db        928 CCTCCTCCTCCTCCTC-TTCCTCCTGTGGCTGCTGCTCGCAGGACTCCTCCTCCATGTCC 870

Qy        438 luAlaGly------------ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrA  454
              ::  |||                 |||:::   :::       |||
Db        869 AGCCAGGAGTCGGATGAAAAGCCGTCTACACTGGTTTTTCTTGGGGCATCAATAAGCATT 810

Qy        454 laSerAspGlnLeuLeuValGlu------AsnAlaAlaGlyHisArgValAlaIleSerT  472
                       :::   :::          |||   ||||||   |||   ||||||
Db        809 AATTCTCTCTGGTATTCCTGAGTGAGGTAGGAGCGCTGGGTCACACAGTACACATATCTC 750

Qy        472 hrTyr-----------------------------ThrThrSerLeuGlyAlaGlyProV  482
                                              |||   ||||||      |||
Db        749 TCCAAGACATACCAGCACATCTCATAGTAGAAGGGGTAACGGAACTTGGGCTGAACCCGG 690

Qy        482 alSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuGluAspT  502
                    :::      :::                |||      :::      ::::::|||
Db        689 GTCCTGTCCTCGATCTCGTAGATCCGCAGCTGCATGGGCACGTTGAAGCTATGCAGGATG 630

Qy        502 hrLeuAspTyrProAlaArgAlaHis 510
                             |||   |||
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Db 629 TTCCCGCCGAACACCAGAGAGTCCAC 604

Search completed: July 14, 2005, 21:22:48
Job time : 3404 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 14, 2005, 00:29:03 ; Search time 43.4198 Seconds
(without alignments)
4676.418 Million cell updates/sec

Title: US-09-769-066-15_COPY_1_525
Perfect score: 2694
Sequence: 1 AVAPAHDTPPVPDVDSRGAI.....PARAHTFDDFCPECRPLGLQ 525

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2694	100.0	525	2	AAR96103	Aar96103 Hepatitis
2	2694	100.0	540	2	AAR96101	Aar96101 Hepatitis
3	2694	100.0	549	2	AAR96091	Aar96091 Hepatitis
4	2694	100.0	660	2	AAR38785	Aar38785 HEV ORF2
5	2694	100.0	660	2	AAR39306	Aar39306 Burma str
6	2694	100.0	660	2	AAR96089	Aar96089 Hepatitis
7	2694	100.0	660	2	AAW35826	Aaw35826 Hepatitis
8	2694	100.0	660	2	AAW80197	Aaw80197 Protein e
9	2694	100.0	660	2	AAW93389	Aaw93389 Human HEV
10	2694	100.0	660	3	AAB24120	Aab24120 Hepatitis
11	2694	100.0	660	4	AAB62523	Aab62523 HEV-Burma
12	2694	100.0	660	5	AAO15699	Aao15699 Hepatitis
13	2694	100.0	660	7	ADD24376	Add24376 Hepatitis
14	2687	99.7	549	2	AAW76367	Aaw76367 Hepatitis
15	2687	99.7	660	2	AAW76369	Aaw76369 Hepatitis
16	2687	99.7	660	2	AAW71210	Aaw71210 Protein e
17	2685	99.7	660	2	AAR70323	Aar70323 Hepatitis
18	2685	99.7	660	4	AAE12980	Aae12980 Hepatitis
19	2681	99.5	660	2	AAR91814	Aar91814 Hepatitis
20	2681	99.5	660	2	AAW93386	Aaw93386 Human HEV
21	2681	99.5	660	2	AAW93388	Aaw93388 Human HEV
22	2681	99.5	660	5	ABB81670	Abb81670 Hepatitis
23	2681	99.5	660	6	ADA50060	Ada50060 Hepatitis
24	2681	99.5	660	7	ADB97807	Adb97807 HEV ORF2
25	2679	99.4	660	5	ABJ04803	Abj04803 Hepatitis
26	2677	99.4	660	2	AAW93390	Aaw93390 Human HEV
27	2676	99.3	660	2	AAW93395	Aaw93395 Human HEV
28	2672	99.2	660	2	AAR51265	Aar51265 HEV strai
29	2672	99.2	660	2	AAW81520	Aaw81520 Hepatitis
30	2670	99.1	660	5	ABJ04811	Abj04811 Hepatitis
31	2669	99.1	660	2	AAW93391	Aaw93391 Human HEV
32	2668	99.0	660	5	ABJ04820	Abj04820 Hepatitis
33	2668	99.0	660	5	ABJ04819	Abj04819 Hepatitis
34	2666	99.0	660	2	AAW93392	Aaw93392 Human HEV
35	2666	99.0	660	5	ABJ04807	Abj04807 Hepatitis
36	2666	99.0	660	5	ABJ04809	Abj04809 Hepatitis
37	2663	98.8	660	5	ABJ04822	Abj04822 Hepatitis
38	2662	98.8	660	5	ABJ04818	Abj04818 Hepatitis
39	2662	98.8	660	5	ABJ04805	Abj04805 Hepatitis
40	2661	98.8	660	5	ABJ04806	Abj04806 Hepatitis
41	2659	98.7	660	2	AAR14619	Aar14619 Protein e
42	2659	98.7	660	5	ABJ04821	Abj04821 Hepatitis
43	2658	98.7	660	2	AAW93394	Aaw93394 Human HEV
44	2656	98.6	660	2	AAW93393	Aaw93393 Human HEV
45	2656	98.6	660	4	ADH13471	Adh13471 Hepatitis

ALIGNMENTS

RESULT 1
AAR96103
ID AAR96103 standard; protein; 525 AA.
XX
AC AAR96103;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Burma strain) recombinant 62K antigen.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid.
XX
OS Hepatitis E virus; Burma strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Claim 7; Page 95-97; 125pp; English.
XX
CC DNA (AAT27109) coding for the 62K antigen (AAR96091) of hepatitis E virus
CC (HEV) Burma strain capsid protein was cloned into baculovirus expression
CC vector pBluBacIII and recombinant 62K was expressed in Sf9 insect cells.
CC High levels of expression were obtd. and the recombinant 62K was obtd. in
CC over 95% purity. However, C-terminal processing resulted in the deletion
CC of 9 or 23 amino acids from 62K, giving 2 related polypeptide species
CC (AAR96101 and AAR96103). Similar results were obtd. with HEV Mexico 62K
CC antigen (see also AAR96102 and AAR96104). Recombinant 62K represents an
CC improved antigen, in comparison to bacterial expressed proteins, for use
CC in HEV diagnostic assays, and also has excellent immunogenic properties.
CC (Updated on 16-OCT-2003 to standardise OS field)

```
XX
SQ   Sequence 525 AA;

  Query Match             100.0%;  Score 2694;  DB 2;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-218;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525


RESULT 2
AAR96101
ID   AAR96101 standard; protein; 540 AA.
XX
AC   AAR96101;
XX
DT   16-OCT-2003  (revised)
DT   06-AUG-1996  (first entry)
XX
DE   Hepatitis E virus (Burma strain) recombinant 62K antigen.
XX
KW   HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW   diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW   capsid.
XX
OS   Hepatitis E virus; Burma strain.
XX
PN   WO9612807-A2.
XX
PD   02-MAY-1996.
XX
PF   23-OCT-1995;   95WO-US013703.
XX
PR   24-OCT-1994;   94US-00327952.
PR   13-OCT-1995;   95US-00542634.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fuerst TR,  Mcatee CP,  Yarbough PO,  Zhang Y;
XX
DR   WPI; 1996-230608/23.
XX
PT   Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT   diagnostic reagents for determining HEV infection and in vaccines.
XX
PS   Claim 5; Page 92-93; 125pp; English.
XX
CC   DNA (AAT27109) coding for the 62K antigen (AAR96091) of hepatitis E virus
CC   (HEV) Burma strain capsid protein was cloned into baculovirus expression
CC   vector pBluBacIII and recombinant 62K was expressed in Sf9 insect cells.
CC   High levels of expression were obtd. and the recombinant 62K was obtd. in
CC   over 95% purity. However, C-terminal processing resulted in the deletion
CC   of 9 or 23 amino acids from 62K, giving 2 related polypeptide species
CC   (AAR96101 and AAR96103). Similar results were obtd. with HEV Mexico 62K
CC   antigen (see also AAR96102 and AAR96104). Recombinant 62K represents an
CC   improved antigen, in comparison to bacterial expressed proteins, for use
CC   in HEV diagnostic assays, and also has excellent immunogenic properties.
CC   (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 540 AA;

  Query Match             100.0%;  Score 2694;  DB 2;  Length 540;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-218;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525


RESULT 3
AAR96091
ID   AAR96091 standard; protein; 549 AA.
XX
AC   AAR96091;
XX
DT   16-OCT-2003  (revised)
DT   06-AUG-1996  (first entry)
XX
DE   Hepatitis E virus (Burma strain) 62K antigen.
```

```
XX
KW   HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW   diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW   capsid.
XX
OS   Hepatitis E virus; Burma strain.
XX
PN   WO9612807-A2.
XX
PD   02-MAY-1996.
XX
PF   23-OCT-1995;   95WO-US013703.
XX
PR   24-OCT-1994;   94US-00327952.
PR   13-OCT-1995;   95US-00542634.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fuerst TR,  Mcatee CP,  Yarbough PO,  Zhang Y;
XX
DR   WPI; 1996-230608/23.
DR   N-PSDB; AAT27109.
XX
PT   Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT   diagnostic reagents for determining HEV infection and in vaccines.
XX
PS   Claim 3; Page 83-84; 125pp; English.
XX
CC   62K antigen (AAR96091) comprises the C-terminal 549 amino acids of
CC   hepatitis E virus (HEV) Burma strain capsid protein (see also AAR96089).
CC   It is obtd. by PCR amplification of HEV Burma ORF-2 (AAT27107), insertion
CC   of amplified DNA (AAT27109) into vector pGEX and expression in E. coli
CC   cells. Expression of full-length ORF-2 in Sf9 insect cells using a
CC   baculovirus system also results in prodn. of 62K antigen (see also
CC   AAR96101 and AAR96103). 62K represents an improved antigen, in comparison
CC   to bacterial expressed proteins, for use in HEV diagnostic assays, and
CC   also has excellent immunogenic properties. (Updated on 16-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 549 AA;

  Query Match             100.0%;  Score 2694;  DB 2;  Length 549;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-218;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525


RESULT 4
AAR38785
ID   AAR38785 standard; protein; 660 AA.
XX
AC   AAR38785;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   11-JAN-1994  (first entry)
XX
DE   HEV ORF2 protein.
XX
KW   Enterically transmitted non-A non-B hepatitis; ET-NANB; vaccine.
XX
OS   Hepatitis E virus; Burma strain.
XX
FH   Key             Location/Qualifiers
FT   Peptide          225. .660
FT                    /label= C2
FT   Peptide          334. .660
FT                    /label= SG3
FT   Peptide          613. .660
FT                    /label= 406.3-2
XX
PN   WO9314116-A1.
XX
PD   22-JUL-1993.
XX
PF   15-JAN-1993;   93WO-US000459.
XX
PR   17-JAN-1992;   92US-00822335.
PR   01-MAY-1992;   92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
PA   (USSH ) US SEC DEPT HEALTH.
XX
PI   Reyes GR,  Bradley DW,  Tam AW,  Carl M;
XX
DR   WPI; 1993-243144/30.
DR   N-PSDB; AAQ47129.
XX
PT   New immunogenic hepatitis E virus (HEV) peptide(s) - are from the ORF1,
PT   ORF2 and ORF3 regions of HEV, useful as a vaccine against HEV infection.
XX
PS   Disclosure; Fig 8; 48pp; English.
XX
CC   Immunogenic hepatitis E virus (HEV) peptides are selected from the ORF1,
CC   ORF2 and ORF3 regions of HEV. The peptides can be used in vaccines to
CC   prevent infection by HEV. The antibodies can neutralise and block HEV
CC   infection and can be used to prevent or treat HEV infection. The peptides
CC   and antibodies can also be used as diagnostic reagents. (Updated on 25-
CC   MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS
CC   field)
XX
SQ   Sequence 660 AA;

  Query Match             100.0%;  Score 2694;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1e-217;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171
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Qy          61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy         121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy         181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy         241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy         301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy         361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy         421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy         481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
               |||||||||||||||||||||||||||||||||||||||||||||
Db         592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 5
AAR39306
ID AAR39306 standard; protein; 660 AA.
XX
AC AAR39306;
XX
DT 25-MAR-2003 (revised)
DT 14-FEB-1994 (first entry)
XX
DE Burma strain HEV ORF2 puative virus capsid protein.
XX
KW Hepatitis E virus; vaccine; neutralising antibodies; infection; block;
KW open reading frame; antibodies.
XX
OS Hepatitis E virus.
XX
PN WO9314208-A2.
XX
PD 22-JUL-1993.
XX
PF 19-JAN-1993; 93WO-US000475.
XX
PR 17-JAN-1992; 92US-00822335.
PR 20-APR-1992; 92US-00870985.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Reyes GR, Bradley DW, Twu J, Purdy MA, Tam AW, Krawczynski KZ;
XX
DR WPI; 1993-243223/30.
DR N-PSDB; AAQ46813.
XX
PT Antigen and antibody vaccines against hepatitis E virus infection -
PT contain peptide(s) derived from capsid protein C-terminal or antibodies
PT against protein.
XX
PS Disclosure; Fig 7; 43pp; English.
XX
CC The sequence is that of the putative virus capsid protein encoded by
CC Burma strain hepatitis E virus (HEV) open reading frame ORF2. This
CC protein or peptide fragments of it may be used in a vaccine composition
CC for immunising an individual against HEV. Antibodies raised against these
CC peptides can also be used in such vaccines. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 660 AA;

Query Match 100.0%; Score 2694; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 1e-217;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy           1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy          61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy         121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy         181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy         241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy         301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy         361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy         421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy         481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
               |||||||||||||||||||||||||||||||||||||||||||||
Db         592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
```

RESULT 6
AAR96089
ID AAR96089 standard; protein; 660 AA.
XX
AC AAR96089;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Burma strain) capsid protein.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid.
XX
OS Hepatitis E virus; Burma strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.

```
PR   13-OCT-1995;   95US-00542634.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fuerst TR,  Mcatee CP,  Yarbough PO,  Zhang Y;
XX
DR   WPI; 1996-230608/23.
DR   N-PSDB; AAT27107.
XX
PT   Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT   diagnostic reagents for determining HEV infection and in vaccines.
XX
PS   Disclosure; Page 78-80; 125pp; English.
XX
CC   The putative capsid protein (AAR96089) of hepatitis E virus (HEV) Burma
CC   strain is encoded by ORF-2 (AAT27107) of the virus. PCR amplification of
CC   ORF-2 allows prodn. of capsid protein or of C-terminal regions of the
CC   capsid protein (see also AAR96091, AAR96093 and AAR96095) and expression
CC   in Spodoptera frugiperda Sf9 insect cells using a baculovirus vector
CC   provides recombinant C-terminal regions (see also AAR96101 and AAR96103)
CC   useful as diagnostic reagents and in vaccines. The HEV Mexico strain
CC   capsid protein (AAR96090) may similarly be used. (Updated on 16-OCT-2003
CC   to standardise OS field)
XX
SQ   Sequence 660 AA;

  Query Match             100.0%;  Score 2694;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1e-217;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 7
AAW35826
ID   AAW35826 standard; protein; 660 AA.
XX
AC   AAW35826;
XX
DT   17-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   26-FEB-1998  (first entry)
XX
DE   Hepatitis E virus Burma strain protein from ORF2.
XX
KW   Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
KW   diagnosis; HEV.
XX
OS   Hepatitis E virus; - Burma strain.
XX
PN   US5686239-A.
XX
PD   11-NOV-1997.
XX
PF   09-MAY-1994;   94US-00240049.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   17-JAN-1992;   92US-00822335.
PR   20-APR-1992;   92US-00870985.
PR   01-MAY-1992;   92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Tam AW,  Reyes GR,  Yarbough PO;
XX
DR   WPI; 1997-558132/51.
DR   N-PSDB; AAT96959.
XX
PT   Diagnosis of hepatitis E virus Burma and Mexico strain infection - by
PT   immunoassay with hepatitis E virus peptide antigens.
XX
PS   Disclosure; Col 39-42; 36pp; English.
XX
CC   A method has been developed for detecting hepatitis E virus (HEV)
CC   antibodies (Ab). The method comprises: (a) reacting a serum sample with a
CC   HEV peptide antigen; and (b) examining the peptide for the presence of
CC   bound Ab, where the presence of bound Ab indicates the presence of HEV
CC   Ab. The present sequence represents the protein from the open reading
CC   frame, ORF2, from HEV Burma strain. The method can be used to diagnose
CC   infection with the enterically transmitted non-A/non-B viral hepatitis
CC   agent HEV, specifically the HEV Burma and Mexico strains. (Updated on 25-
CC   MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to standardise OS
CC   field)
XX
SQ   Sequence 660 AA;

  Query Match             100.0%;  Score 2694;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1e-217;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
                |||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
```

RESULT 8
AAW80197
ID AAW80197 standard; protein; 660 AA.
XX
AC AAW80197;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 23-DEC-1998 (first entry)
XX
DE Protein encoded by ORF2 of ET-NANB (HEV) Burma strain DNA sequence.
XX
KW Enterically transmitted non A non B hepatitis virus; ET-NANB;
KW Hepatitis E virus; HEV; Burma HEV isolate; vaccine; diagnostic probe.
XX
OS Non-A.
OS non-B hepatitis virus.
XX
PN US5824649-A.
XX
PD 20-OCT-1998.
XX
PF 07-JUN-1995; 95US-00475807.
XX
PR 17-JUN-1988; 88US-00208997.
PR 11-APR-1989; 89US-00336672.
PR 16-JUN-1989; 89US-00367486.
PR 13-OCT-1989; 89US-00420921.
PR 05-APR-1990; 90US-00505888.
PR 25-JUL-1994; 94US-00279823.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Bradley DW, Reyes GR, Krawczynski KZ, Tam A, Fry KE, Yarbough PO;
XX
DR WPI; 1998-582599/49.
DR N-PSDB; AAV66321.
XX
PT Hepatitis E virus proteins - useful for diagnosis or vaccine production
PT the virus.
XX
PS Claim 6; Col 65-70; 47pp; English.
XX
CC AAW80196-98 are encoded by the genome of the Burma strain of enterically
CC transmitted non A non B hepatitis virus (ET-NANB) (hepatitis E virus
CC (HEV)). The specification describes an isolated protein which is
CC specifically immunoreactive with antibodies present in individuals
CC infected with HEV and encoded by a sequence contained in an open reading
CC frame (ORF) of an HEV genome. The genome has a sequence that is more than
CC 70% identical to the ORF1 sequence from Burma HEV isolate. The protein is
CC used as a vaccine and a diagnostic probe for ET-NANB. (Updated on 25-MAR-
CC 2003 to correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)
XX

SQ Sequence 660 AA;

  Query Match   100.0%; Score 2694; DB 2; Length 660;
  Best Local Similarity 100.0%; Pred. No. 1e-217;
  Matches 525; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
```

RESULT 9
AAW93389
ID AAW93389 standard; protein; 660 AA.
XX
AC AAW93389;
XX
DT 11-JUN-1999 (first entry)
XX
DE Human HEV ORF 2 protein from strain Burma.
XX
KW Swine hepatitis E virus; HEV; cross-reaction; antibody; human; therapy;
KW vaccine; immunise; infection; detection; diagnosis; prevention.
XX
OS Hepatitis E virus.
XX
PN WO9904029-A2.
XX
PD 28-JAN-1999.
XX
PF 17-JUL-1998; 98WO-US014665.
XX
PR 18-JUL-1997; 97US-0053069P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Meng X, Emerson SU, Purcell RH;
XX
DR WPI; 1999-132270/11.
XX
PT New isolated swine hepatitis E virus - used to develop products for the

```
PT   diagnosis, prevention and treatment of hepatitis E virus infection in
PT   mammals, particularly humans.
XX
PS   Example 1; Fig 3A; 70pp; English.
XX
CC   This invention describes a swine hepatitis E virus (HEV) and its natural
CC   mutants which are capable of cross-reacting with antibodies reactive with
CC   a human HEV strain or natural mutants. The HEV and the proteins can be
CC   used in vaccines for immunising against HEV infection. The swine HEV can
CC   be used in humans to prevent possible infection by human HEV. The swine
CC   HEV can also be used as a therapeutic treatment for infection by other
CC   strains of HEV. The swine HEV can also be used for the production of
CC   antibodies which can be used in therapy, detection and diagnosis. The
CC   products can also be used for determining the susceptibility of cells or
CC   organs to infection with swine HEV. The swine HEV is particularly useful
CC   for the development of agents for the prevention, treatment and detection
CC   of human HEV because it is not a human virus and thus can be handled both
CC   experimentally and clinically without fear of severe infection and/or
CC   contamination
XX
SQ   Sequence 660 AA;

  Query Match             100.0%;  Score 2694;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1e-217;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 10
AAB24120
ID   AAB24120 standard; protein; 660 AA.
XX
AC   AAB24120;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Hepatitis E virus Burma strain ORF2 protein sequence SEQ ID NO:8.
XX
KW   Hepatitis E virus; HEV; non-A/non-B viral hepatitis; viral protein;
KW   immunological; diagnosis; hepatitis; infection; identification;
KW   detection; immunoreactive; hepatotropic; antiinflammatory; virucide;
KW   vaccine; antiviral; antigenic; antibody; antigen.
XX
OS   Hepatitis E virus.
XX
PN   US6120988-A.
XX
PD   19-SEP-2000.
XX
PF   07-JUN-1995;   95US-00478507.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   25-JUL-1994;   94US-00279823.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
PA   (USGO ) US GOVERNMENT.
XX
PI   Yarbough PO,  Krawczynski KZ,  Fry KE,  Bradley DW,  Tam A,  Reyes GR;
XX
DR   WPI; 2000-593712/56.
DR   N-PSDB; AAA99259.
XX
PT   Identifying recombinant antigen immunoreactive with antibody induced by
PT   hepatitis E virus (HEV), for detecting HEV infection, comprises
PT   immunoreacting a polypeptide from an HEV genome with an HEV-positive
PT   antiserum.
XX
PS   Claim 6; Col 63-68; 46pp; English.
XX
CC   The present invention describes a method for identifying a recombinant
CC   antigen immunoreactive with a hepatitis E virus (HEV)-induced antibody.
CC   The method comprises producing a polypeptide derived from an HEV genome,
CC   immunoreacting the polypeptide with an HEV-positive antiserum and
CC   selecting the polypeptide as a recombinant antigen if the polypeptide
CC   reacts with the HEV-positive antiserum. The method is useful for
CC   identifying recombinant antigen immunoreactive with antibody induced by
CC   HEV. The enterically transmitted non-A/non-B hepatitis (ET-NANB (also
CC   known as HEV))-specific fragments are useful for identifying ET-NANB-
CC   derived cDNAs, which contain additional sequence information, as primers
CC   for detecting ET-NANB viral genomic material in a patient sample, for the
CC   synthesis of polypeptides for use in immunoassays, and for identifying
CC   similar antigenic regions encoded by related viral strains, e.g. Burmese
CC   strain. The antigens are especially useful in the preparation of vaccine
CC   against ET-NANB infection. These antigens may further be used to prepare
CC   antibodies to ET-NANB virus particles for use directly as antiviral
CC   agents, and to produce antiserum designed for pre- or post-exposure
CC   prophylaxis. The present sequence represents a specifically claimed HEV
CC   Burma strain protein sequence for use in the present invention
XX
SQ   Sequence 660 AA;

  Query Match             100.0%;  Score 2694;  DB 3;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1e-217;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291
```

```
Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
```

RESULT 11
AAB62523
ID AAB62523 standard; protein; 660 AA.
XX
AC AAB62523;
XX
DT 23-JUL-2001 (first entry)
XX
DE HEV-Burma strain viral protein ORF2.
XX
KW HEV; enterically transmitted nonA/nonB viral hepatitis agent; viral;
KW ET-NANB; infection; vaccine.
XX
OS Hepatitis E virus.
XX
PN US6229005-B1.
XX
PD 08-MAY-2001.
XX
PF 03-AUG-1998; 98US-00128275.
XX
PR 17-JUN-1988; 88US-00208997.
PR 11-APR-1989; 89US-00336672.
PR 16-JUN-1989; 89US-00367486.
PR 13-OCT-1989; 89US-00420921.
PR 05-APR-1990; 90US-00505888.
PR 05-APR-1991; 91US-00681078.
PR 25-JUL-1994; 94US-00279823.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Reyes GR, Yarbough PO, Bradley DW, Krawczynski KZ, Tam AW;
PI Fry KE;
XX
DR WPI; 2001-342705/36.
DR N-PSDB; AAF83495.
XX
PT New DNA sequences of enterically transmitted non-A/non-B (ET-NANB)
PT hepatitis viral agent, useful in diagnosing infection by an enterically
PT transmitted agent (e.g. ET-NANB virus), as well as in vaccine production.
XX
PS Disclosure; Col 63-68; 45pp; English.
XX
CC The invention relates to an isolated DNA comprising the genome of an
CC enterically transmitted nonA/nonB (ET-NANB) viral hepatitis agent (also
CC referred as HEV). The DNA sequences or their fragments are useful in
CC preparing ET-NANB viral proteins and as probes for virus detection. These
CC are particularly useful in diagnosing infection by an enterically
CC transmitted agent (e.g. ET-NANB virus), as well as in vaccine production.
CC The present sequence represents a ORF2 protein encoded by a ET-NANB viral
CC DNA sequence from HEV-Burma strain
XX
SQ Sequence 660 AA;

Query Match 100.0%; Score 2694; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 1e-217;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
```

RESULT 12
AAO15699
ID AAO15699 standard; protein; 660 AA.
XX
AC AAO15699;
XX
DT 08-NOV-2002 (first entry)
XX
DE Hepatitis E virus (Burma strain) ORF2 protein.
XX
KW HEV; enterically transmitted nonA/nonB hepatitis viral agent;
KW Burma strain; bile; ORF2.
XX
OS Hepatitis E virus.
XX
PN US6379891-B1.
XX
PD 30-APR-2002.
XX
PF 19-APR-2000; 2000US-00553427.
XX
PR 17-JUN-1988; 88US-00208997.
PR 11-APR-1989; 89US-00336672.
PR 16-JUN-1989; 89US-00367486.

PR 13-OCT-1989; 89US-00420921.
PR 05-APR-1990; 90US-00505888.
PR 15-APR-1991; 91US-00681078.
PR 25-JUL-1994; 94US-00279823.
PR 07-JUN-1995; 95US-00478507.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Reyes GR, Yarbough PO, Bradley DW, Krawczynski KZ, Tam A, Fry KE;
XX
DR WPI; 2002-517277/55.
DR N-PSDB; AAL50386.
XX
PT Detecting the presence of enterically transmitted nonA/nonB hepatitis
PT viral (HEV) agents in bile samples from infected humans and monkeys using
PT polymerase chain reaction.
XX
PS Disclosure; Col 19-24; 61pp; English.
XX
CC The invention comprises a method for detecting the presence of
CC enterically transmitted nonA/nonB hepatitis viral (HEV) agents in a
CC sample and isolating HEV agents or nucleic acid fragments produced by the
CC agent. The method utilises PCR - using bile from a human or cynomolgus
CC monkey actively infected with HEV as a source of the agent. The method of
CC the invention is used for detecting the presence of a viral agent in a
CC sample of cultured cells infected with the agent and isolating
CC enterically transmitted nonA/nonB HEV agents or nucleic acid fragments
CC produced by the agent. The present amino acid sequence represents the
CC protein encoded by open reading frame 2 (ORF2) of a DNA sequence isolated
CC from a Burmese strain of the Hepatitis E virus
XX
SQ Sequence 660 AA;

Query Match 100.0%; Score 2694; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 1e-217;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
```

RESULT 13
ADD24376
ID ADD24376 standard; protein; 660 AA.
XX
AC ADD24376;
XX
DT 15-JAN-2004 (first entry)
XX
DE Hepatitis E virus strain Burma ORF 2.
XX
KW non-A/non-B viral hepatitis; ET-NANB; HEV; vaccine.
XX
OS Hepatitis E virus; strain Burma.
XX
PN US2003124510-A1.
XX
PD 03-JUL-2003.
XX
PF 07-MAY-2001; 2001US-00851410.
XX
PR 17-JUN-1988; 88US-00208997.
PR 11-APR-1989; 89US-00336672.
PR 16-JUN-1989; 89US-00367486.
PR 13-OCT-1989; 89US-00420921.
PR 05-APR-1990; 90US-00505888.
PR 05-APR-1991; 91US-00681078.
PR 25-JUL-1994; 94US-00279823.
PR 03-AUG-1998; 98US-00128275.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Reyes GR, Yarbough PO, Bradley DW, Krawczynski KZ, Tam AW;
PI Fry KE;
XX
DR WPI; 2003-810978/76.
DR N-PSDB; ADD24374.
XX
PT New proteins derived from an enterically transmitted non-A/non-B (ET-
PT NANB) viral hepatitis agent, useful for diagnosing ET-NANB infection and
PT producing vaccines for immunizing an individual against ET-NANB hepatitis
PT viral agent.
XX
PS Disclosure; SEQ ID NO 8; 81pp; English.
XX
CC The invention relates to a protein derived from an enterically
CC transmitted non-A/non-B viral hepatitis agent. The viral proteins are
CC useful for detecting infection by the enterically transmitted non-A/non-B
CC (ET-NANB/HEV) hepatitis viral agent. The proteins are also useful for
CC producing vaccines for immunising an individual against HEV hepatitis
CC viral agent. The DNA fragments are useful for identifying and sequencing
CC the entire viral agent and for assaying the viral agent in an infected
CC sample. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 660 AA;

Query Match 100.0%; Score 2694; DB 7; Length 660;
Best Local Similarity 100.0%; Pred. No. 1e-217;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291
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Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
```

RESULT 14
AAW76367
ID AAW76367 standard; protein; 549 AA.
XX
AC AAW76367;
XX
DT 03-DEC-1998 (first entry)
XX
DE Hepatitis E virus hollow particle protein ORF2.
XX
KW Hollow particle protein; virus; antibody; detection; immunoassay;
KW infection.
XX
OS Hepatitis virus.
XX
FH Key Location/Qualifiers
FT Protein 1. .549
FT /label= ORF2
FT /note= "partial sequence"
XX
PN JP10234383-A.
XX
PD 08-SEP-1998.
XX
PF 28-FEB-1997; 97JP-00062445.
XX
PR 28-FEB-1997; 97JP-00062445.
XX
PA (DENK-) DENKA SEIKEN KK.
PA (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR WPI; 1998-535037/46.
DR N-PSDB; AAV61686.
XX
PT Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids
PT encoding it - useful for more accurate detection of HEV in samples, using
PT immuno-assays and nucleic acid hybridisation.
XX
PS Claim 1; Page 15-17; 29pp; Japanese.
XX
CC This sequence represents a Hepatitis E viral hollow particle protein
CC described as ORF2. This polypeptide can be used to raise antibodies to
CC detect HEV infection in samples, e.g. by immuno-assay based techniques,
CC and the nucleic acid can be used for the same in nucleic acid
CC hybridisation assays. The polypeptide and nucleic acid allow more
CC accurate detection of HEV than previously possible
XX

SQ Sequence 549 AA;

Query Match 99.7%; Score 2687; DB 2; Length 549;
Best Local Similarity 99.8%; Pred. No. 3.1e-217;
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
```

RESULT 15
AAW76369
ID AAW76369 standard; protein; 660 AA.
XX
AC AAW76369;
XX
DT 03-DEC-1998 (first entry)
XX
DE Hepatitis E virus hollow particle protein #2.
XX
KW Hollow particle protein; virus; antibody; detection; immunoassay;
KW infection.
XX
OS Hepatitis virus.
XX
PN JP10234383-A.
XX
PD 08-SEP-1998.
XX
PF 28-FEB-1997; 97JP-00062445.
XX
PR 28-FEB-1997; 97JP-00062445.
XX
PA (DENK-) DENKA SEIKEN KK.
PA (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR WPI; 1998-535037/46.
DR N-PSDB; AAV61688.
XX
PT Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids

PT encoding it - useful for more accurate detection of HEV in samples, using
PT immuno-assays and nucleic acid hybridisation.
XX
PS Claim 13; Page 24-26; 29pp; Japanese.
XX
CC This sequence represents a Hepatitis E viral hollow particle protein.
CC This polypeptide can be used to raise antibodies to detect HEV infection
CC in samples, e.g. by immuno-assay based techniques, and the nucleic acid
CC can be used for the same in nucleic acid hybridisation assays. The
CC polypeptides and nucleic acids allow more accurate detection of HEV than
CC previously possible
XX
SQ Sequence 660 AA;

Query Match 99.7%; Score 2687; DB 2; Length 660;
Best Local Similarity 99.8%; Pred. No. 4e-217;
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
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Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
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Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
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Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
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Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
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Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
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Search completed: July 14, 2005, 15:46:26
Job time : 47.4198 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 14, 2005, 02:26:53 ; Search time 9.08019 Seconds
(without alignments)
5563.078 Million cell updates/sec

Title: US-09-769-066-16_COPY_1_525
Perfect score: 2701
Sequence: 1 AVAPAHDTSPVPDVDSRGAI.....PGRAHTFDDFCPECRALGLQ 525

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2674.5	99.0	659	1	B44212	structural protein
2	2569	95.1	660	1	VHWWH2	structural protein
3	128.5	4.8	5188	2	B85547	probable RTX famil
4	128.5	4.8	5291	2	F90696	hypothetical prote
5	127	4.7	1367	1	S48478	glucan 1,4-alpha-g
6	125	4.6	3282	2	E82750	hemagglutinin-like
7	125	4.6	3442	2	E82589	hemagglutinin-like
8	125	4.6	3455	2	B82519	hemagglutinin-like
9	122.5	4.5	1077	2	H96007	probable acriflavi
10	121	4.5	725	2	A41258	a-agglutinin core
11	120	4.4	1041	2	S55862	probable membrane
12	118.5	4.4	547	2	T41213	probable zinc fing
13	118.5	4.4	2130	2	AB0821	probable exported
14	118	4.4	1104	2	S59310	probable membrane
15	116.5	4.3	583	2	S67571	hypothetical prote
16	116	4.3	351	1	VCVETC	coat protein - tur
17	116	4.3	1975	2	B81192	hemagglutinin/hemo
18	116	4.3	1995	2	G81044	hemagglutinin/hemo
19	115.5	4.3	2054	2	T46612	multi PDZ domain p
20	115	4.3	2015	2	B81989	hypothetical prote
21	115	4.3	3083	2	AH2493	hypothetical prote
22	113.5	4.2	1213	2	T51032	hypothetical prote
23	113.5	4.2	1483	2	C97012	probably celluloso
24	113	4.2	797	1	VGBEX1	glycoprotein X pre
25	113	4.2	1350	2	AF2005	RNA polymerase bet
26	112.5	4.2	1643	2	D71630	outer membrane pro
27	112	4.1	1180	2	E86719	hypothetical prote
28	112	4.1	1345	2	H90975	hypothetical prote
29	112	4.1	1377	2	I54632	tsh protein - Esch
30	112	4.1	2505	1	XYRTFA	enoyl-[acyl-carrie
31	112	4.1	2660	2	B85822	probable invasin Z
32	111.5	4.1	962	2	S03818	carboxymethylcellu
33	111.5	4.1	1374	2	AE3259	extracellular seri
34	111.5	4.1	3570	2	T45025	mucin MUC5B, trach
35	111	4.1	3972	2	S75251	hypothetical prote
36	110.5	4.1	1014	1	NMCLSS	exo-alpha-sialidas
37	110.5	4.1	1306	2	S25370	MSB2 protein - yea
38	110.5	4.1	1746	1	S19694	tenascin precursor
39	110.5	4.1	3624	2	AD0835	large repetitive p
40	110	4.1	1112	2	T32733	AMPA glutamate rec
41	110	4.1	1131	2	T41144	hypothetical serin
42	109.5	4.1	1016	2	H71460	probable outer mem
43	109.5	4.1	1802	2	S69703	HKR1 protein precu
44	109.5	4.1	4199	2	S76412	hypothetical prote
45	109	4.0	973	2	B86547	polymorphic outer.

ALIGNMENTS

RESULT 1
B44212
structural protein 2 precursor - hepatitis E virus (strain Mexico)
C;Species: hepatitis E virus
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: B44212
R;Huang, C.C.; Nguyen, D.; Fernandez, J.; Yun, K.Y.; Fry, K.E.; Bradley, D.W.; Tam, A.W.
Virology 191, 550-558, 1992
A;Title: Molecular cloning and sequencing of the Mexico isolate of hepatitis E virus (HE\
A;Reference number: A44212; MUID:93079857; PMID:1448913
A;Accession: B44212
A;Molecule type: genomic RNA
A;Residues: 1-659 <HUA>
A;Cross-references: UNIPROT:Q03500; GB:M74506; NID:g330017; PIDN:AAA45732.1; PID:g330020
C;Superfamily: hepatitis E virus structural protein 2
C;Keywords: structural protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-659/Product: structural protein 2 #status predicted <SP2>

Query Match 99.0%; Score 2674.5; DB 1; Length 659;
Best Local Similarity 99.4%; Pred. No. 4.4e-179;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
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Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
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Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 635


RESULT 2
VHWWH2
structural protein 2 precursor - hepatitis E virus (strain Burma)
C;Species: hepatitis E virus
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: C40778
R;Tam, A.W.; Smith, M.M.; Guerra, M.E.; Huang, C.C.; Bradley, D.W.; Fry, K.E.; Reyes, G.
Virology 185, 120-131, 1991
A;Title: Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length vi
A;Reference number: A40778; MUID:92024067; PMID:1926770
A;Accession: C40778
A;Molecule type: genomic RNA
A;Residues: 1-660 <TAM>
A;Cross-references: UNIPROT:P29326; GB:M73218; NID:g330023; PIDN:AAA45736.1; PID:g330026
A;Note: the authors translated the codon CGC for residue 2 as Ala
C;Superfamily: hepatitis E virus structural protein 2
C;Keywords: structural protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-660/Product: structural protein 2 #status predicted <SP2>

  Query Match             95.1%;  Score 2569;  DB 1;  Length 660;
  Best Local Similarity   94.7%;  Pred. No. 1.1e-171;
  Matches  497;  Conservative   13;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| ||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              |||||||||||||||||||||||||||||||||||:|:||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| ||||||||| ||| |||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 3
B85547
probable RTX family exoprotein [imported] - Escherichia coli (strain O157:H7, substrain
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85547
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85547
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5188 <STO>
A;Cross-references: UNIPROT:Q8X4H5; GB:AE005174; NID:g12513368; PIDN:AAG54838.1; GSPDB:GN
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z0615

  Query Match             4.8%;  Score 128.5;  DB 2;  Length 5188;
  Best Local Similarity   21.2%;  Pred. No. 8.1;
  Matches  122;  Conservative   70;  Mismatches  242;  Indels  141;  Gaps   27;

Qy         11 VPDVDSRGAILRRQYNLSTS--PLTSSVASGTNLVLYAAPLNPPLPLQDG-----TNTHI 63
              | |          |  ::|    :| :  || | :| |     || :  |     |   :
Db       2215 VTDAGGNSGSATHQVTVNTGLPTITFNAISGDN-ILNADEKGQPLTISGGSTGLATGAQV 2273

Qy         64 MAT-EASNYAQYRVARA----TIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITS 118
                |    ||:    |       |:    |       | :| |          ||   |:  |
Db       2274 TVTLNGHNYSATTDASGNWTLTVPVSDLAALGQANYTVSAS--------ATSAAGNT-AS 2324

Qy        119 TDVRILVQPGIASELV--IPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNS 176
              :  :|| |:    :  :  : :    :        |||     |    | : : |   |:
Db       2325 SQANLLVDSGLPDVTINTVAGDDIINAAEAGADQTISGVVTRAAAGDTVTVTLGG---NT 2381

Qy        177 YTNTPYTG------------ALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRG 223
              || |  :              |||  |  :    ::|  | ||
Db       2382 YTATVQSNLSWSVSVPTADLQALGNGDLTIT---ASVTNANGNT---------------- 2422

Qy        224 ADGTAELTTTAATRFMKDLHFTGLNGVGEVGRGIALTLLNLADTL-LGGLPTELISSAGG 282
               || ::|  |    ::     | : |  :  | || :   :  |  | : |  |:|
Db       2423 GSGTRDITIDANLPGLRVDTVAGDDIVNSIEHGQALVITGGSSGLNAGAVLTVTINSVA- 2481

Qy        283 QLFYSRPVVSANGEPTVKLYTSVENAQQDKGVAIP-HDIDLGDSRVVIQDYDNQHEQDRP 341
                              |::   |     | ||  ::    :  :  : | |   : |
Db       2482 -------------------YSATVQADGSWSVGIPAANVSAWPAGPLTVEVDGQSSANNP 2522

Qy        342 TPSPAPSRPFSV-----------LRANDVLWLSLTAAEYDQS-TYGSSTGPVYISDSVTL 389
                : | ||:|           : ::||    : |||   : |   ||  :     :|||:
Db       2523 V---SVSHPFTVDLTAVAISINTVASDDV----INAAEKGTNLTLSGSTSGIESGQTVTV 2575

Qy        390 V-NVATGAQAVARSLDWSKVTLDGRPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPY 448
               |   :|| :  || | :    | |: : :       ::  :|     :  | |
Db       2576 TFGGKTYTASVAANGSWS-VNVPAADLATLPEGAAN-----VQASVSSASGNSASATHAY 2629

Qy        449 N---------YNTTASDQILIENAAGHRVAIS-TYTTRLG-----------AGPV-AIS 485
              :           || ||| ||     ||  : || | |   |              | | |
Db       2630 SVDASAPTLTINTIASDDILNAAEAGSPLTISGTSTAETGQTVTVTLNGATYTGTVQADG 2689

Qy        486 AAAVLAPRSAL----------ALLEDTFDYPGRA 509
              : :|  | |||           | :  |    || |
Db       2690 SWSVSVPTSALGALNASNYTVSATVNDKAGNPGSA 2724


RESULT 4
F90696
hypothetical protein ECs0542 [imported] - Escherichia coli (strain O157:H7, substrain RIM
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F90696
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90696
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5291 <HAY>
A;Cross-references: UNIPROT:Q8X2T1; GB:BA000007; PIDN:BAB33965.1; PID:g13360000; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0542

  Query Match             4.8%;  Score 128.5;  DB 2;  Length 5291;
  Best Local Similarity   21.2%;  Pred. No. 8.4;
  Matches  122;  Conservative   70;  Mismatches  242;  Indels  141;  Gaps   27;

Qy         11 VPDVDSRGAILRRQYNLSTS--PLTSSVASGTNLVLYAAPLNPPLPLQDG-----TNTHI 63
              | |           |  ::|    :| :  || | :| |      || :  |      |   :
Db       2215 VTDAGGNSGSATHQVTVNTGLPTITFNAISGDN-ILNADEKGQPLTISGGSTGLATGAQV 2273

Qy         64 MAT-EASNYAQYRVARA----TIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITS 118
                |   ||:     |     |:    |       | :| |          ||   |:  |
Db       2274 TVTLNGHNYSATTDASGNWTLTVPVSDLAALGQANYTVSAS--------ATSAAGNT-AS 2324

Qy        119 TDVRILVQPGIASELV--IPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNS 176
              :   :||  |:    :  :  : :    :        |||     |     | : : |   |:
Db       2325 SQANLLVDSGLPDVTINTVAGDDIINAAEAGADQTISGVVTRAAAGDTVTVTLGG---NT 2381

Qy        177 YTNTPYTG------------ALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRG 223
              || |  :              ||| |  :     ::|  | ||
Db       2382 YTATVQSNLSWSVSVPTADLQALGNGDLTIT---ASVTNANGNT---------------- 2422

Qy        224 ADGTAELTTTAATRFMKDLHFTGLNGVGEVGRGIALTLLNLADTL-LGGLPTELISSAGG 282
                || ::|  |    ::     | : |  :  | || :  :   |  | : |  |:|
Db       2423 GSGTRDITIDANLPGLRVDTVAGDDIVNSIEHGQALVITGGSSGLNAGAVLTVTINSVA- 2481

Qy        283 QLFYSRPVVSANGEPTVKLYTSVENAQQDKGVAIP-HDIDLGDSRVVIQDYDNQHEQDRP 341
                                |::   |     | ||  ::    :  :  : | |   : |
Db       2482 -------------------YSATVQADGSWSVGIPAANVSAWPAGPLTVEVDGQSSANNP 2522

Qy        342 TPSPAPSRPFSV-----------LRANDVLWLSLTAAEYDQS-TYGSSTGPVYISDSVTL 389
              :  | ||:|              : ::||    : |||   :  |   ||  :    :||:
Db       2523 V---SVSHPFTVDLTAVAISINTVASDDV----INAAEKGTNLTLSGSTSGIESGQTVTV 2575

Qy        390 V-NVATGAQAVARSLDWSKVTLDGRPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPY 448
                |   :|| :  || | :    | |: : :      ::  :|    :   | : |
Db       2576 TFGGKTYTASVAANGSWS-VNVPAADLATLPEGAAN-----VQASVSSASGNSASATHAY 2629

Qy        449 N---------YNTTASDQILIENAAGHRVAIS-TYTTRLG------------AGPV-AIS 485
              :           || ||| ||    ||  : || | |   |              | | |
Db       2630 SVDASAPTLTINTIASDDILNAAEAGSPLTISGTSTAETGQTVTVTLNGATYTGTVQADG 2689

Qy        486 AAAVLAPRSAL-----------ALLEDTFDYPGRA 509
              : :|  | |||           | : |    || |
Db       2690 SWSVSVPTSALGALNASNYTVSATVNDKAGNPGSA 2724


RESULT 5
S48478
glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae)
N;Alternate names: extracellular glucoamylase; mucin-like protein MUC1; protein YIR019c
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S48478; A26877; B26877; S27281; JC6123
R;Rowley, K.
submitted to the EMBL Data Library, October 1994
A;Reference number: S48478
A;Accession: S48478
A;Molecule type: DNA
A;Residues: 1-1367 <ROW>
A;Cross-references: UNIPROT:P08640; GB:Z47047; EMBL:Z38061; NID:g603997; PID:g763364; GS
R;Yamashita, I.; Nakamura, M.; Fukui, S.
J. Bacteriol. 169, 2142-2149, 1987
A;Title: Gene fusion is a possible mechanism underlying the evolution of STA1.
A;Reference number: A91831; MUID:87194600; PMID:3106330
A;Accession: A26877
A;Molecule type: DNA
A;Residues: 1-242 <YAM>
A;Cross-references: EMBL:M16164; NID:g172522; PIDN:AAA35014.1; PID:g172525
A;Accession: B26877
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A;Residues: 762-1331 <YA2>
A;Cross-references: EMBL:M16165; NID:g172523; PIDN:AAA35015.1; PID:g172526
R;Pardo, J.M.; Ianez, E.; Zalacain, M.; Claros, M.G.; Jimenez, A.
FEBS Lett. 239, 179-184, 1988
A;Title: Similar short elements in the 5' regions of the STA2 and SGA genes from Saccharc
A;Reference number: S27281; MUID:89031230; PMID:3141213
A;Accession: S27281
A;Molecule type: DNA
A;Residues: 1-31 <PAR>
A;Cross-references: EMBL:X13857; NID:g4551; PIDN:CAA32069.1; PID:g4552
R;Lambrechts, M.G.; Bauer, F.F.; Marmur, J.; Pretorius, I.S.
Proc. Natl. Acad. Sci. U.S.A. 93, 8419-8424, 1996
A;Title: Muc1, a mucin-like protein that is regulated by Mss10, is critical for pseudohyp
A;Reference number: JC6123; MUID:96323237; PMID:8710886
A;Accession: JC6123
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1367 <LAM>
A;Cross-references: GB:U30626; NID:g1304386; PIDN:AAC49609.1; PID:g1304387
C;Genetics:
A;Gene: SGD:MUC1; STA2; MAL5; DEX2; SGD:S0001458
A;Cross-references: MIPS:YIR019c; SGD:S0001458
A;Map position: 9R
C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase h
C;Keywords: glycosidase; hydrolase; polysaccharide degradation; transmembrane protein
F;5-21/Domain: transmembrane #status predicted <TM1>
F;1350-1366/Domain: transmembrane #status predicted <TM2>

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              :|||     | |                |:| :|||  | |          : |:|    :
Db        805 SVAPV----PTPS-------------SSSNITSSAPSSTPFSSSTESSSVPVPTPSSST 846

Qy         61 TH------IMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDM- 113
              |         :|  |: |       ::       |:::   : : ||   || ||:|
Db        847 TESSSAPVSSSTTESSVAPVPTPSSSSNITSSAPSSIPFSSTTESFSTGTTVTPSSSKYP 906

Qy        114 -----NSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLC 168
                  |::||    :|     : :  ||              ::|    | |||    |
Db        907 GSQTETSVSSTTETTIVPTKTTTSVTTPSTTTITTTVCSTGTNSAG----ETTSG----C 958

Qy        169 IHGSPVNSYTNTPYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADG-- 226
              ||     |  | |                ::|| :| |  :   ||  :        |
Db        959 ---SPKTVTTTVPTTTT-----------TSVTTSSTTTITTTVCSTGTNSAGETTSGCS 1003

Qy        227 -------------------------TAELTTTAATRFMKDLHFTGLNGVGE-----VGR 255
                                      |  :||  :|  :   : |      ||      | :
Db       1004 PKTITTTVPCSTSPSETASESTTTSPTTPVTTVVSTTVVTTEYSTSTKPGGEITTTFVTK 1063

Qy        256 GIALTLLNL------ADTLLGGLPTEL--------ISSAG--------GQLFYSRPVVSA 293
              | | |          |:    || :          :|||         :  : | :
Db       1064 NIPTTYLTTIAPTPSVTTVTNFTPTTITTTVCSTGTNSAGETTSGCSPKTVTTTVPCSTG 1123

Qy        294 NGEPTVKLYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSV 353
              || | :  | | |       |           :     |  :       : ||| | |  |
Db       1124 TGEYTTEATTLVTTAVTTTVVTTESSTGTNSAGKTTTGYTTKSVPTTYVTTLAPSAP--V 1181

Qy        354 LRANDVLWLSLTAAEYDQST--YGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLD 411
              | : :  ::|  |   :|   | :|    :  : |:|: |:  :  | |       |
Db       1182 TPATNAVPTTITTTECSAATNAAGETTS---VCSAKTIVSSASAGENTAPSATTPVTT-- 1236

Qy        412 GRPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGY-----PYNYNTTASDQILIENAAGH 466
              :||       |:     :   || | ||     |  | ||      ||  : |
Db       1237 --AIPTT--------VITTESSVGTNSAGETTTGYTTKSIPTTYITT-----LIPGSNGA 1281

Qy        467 R-----------VAISTYTTRLGAGPVAISAAAVLAPRSALALLED-------TFDYPGR 508
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Db       1282 KNYETVATATNPISIKT-TSQLATTASASSVAPVVTSPSLTGPLQSASGSAVATYSVPSI 1340

Qy        509 AHTF 512
Db       1341 SSTY 1344
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RESULT 6
E82750
hemagglutinin-like secreted protein XF0889 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82750
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82750
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3282 <SIM>
A;Cross-references: UNIPROT:Q9PEY9; GB:AE003928; GB:AE003849; NID:g9105798; PIDN:AAF8369
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0889

Query Match 4.6%; Score 125; DB 2; Length 3282;
Best Local Similarity 21.2%; Pred. No. 7.3;
Matches 128; Conservative 63; Mismatches 212; Indels 200; Gaps 27;

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Qy          1 AVAPAHD------TSPVP-----------------DVDSRGAILRRQYNLSTSPLTSSV 36
Db        439 SVPPATDTPPSTGTMPIPSHPQTAPVLAAGRLTLENDIDNRGGHITAGGAIDAILTTLDN 498

Qy         37 ASGTNLVLYAAPLNPPLPLQDG--TNTH---IMATEA-------SNYAQYRVARATIRYR 84
Db        499 RDGT------AALN-RLTLQGQRLDNQHGILTLATEATIHTHTLNNAAGQLHVNGTLDLT 551

Qy         85 PLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRN 144
Db        552 AQHLNNASGHLLTTG--PQSATL-TIADLLDNTSGTL------ASAGSLTLTAATL---- 598

Qy        145 QGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTTCN 204
Db        599 -------------DTTDGTVQSGQGPLHMDAATLTAHRGTLTSQD--------TLTLTG 636

Qy        205 TNTRVSRYSSTARHRLRRGADGTAELTT-------------------------TAATRF 238
Db        637 THTDLSHATTTAQQITLH----TGDLTTAGGHLTAYGTHTLQLEARTRLDNTGGTIATNG 692

Qy        239 MKDLHFTGLNGVGEVGRGIAL---------TLLNLADTLLGGLPTELI----SSAGGQLF 285
Db        693 TLDLHTAALDNTGGTLHSTATGPNRLDITDTLTNTAGHLLLNGPTTLTTGTWTNTGGHLQ 752

Qy        286 YSRPVV--------------SANGEPTVKLYTSVENAQQDKGVAIPHD-IDLGDSRVVIQ 330
Db        753 ITGPATLHATTLDNRGGILHTATGPLDLRITGTLNN--QDNGLLTTTDALTLTAASLL-- 808

Qy        331 DYDNQH-EQDRPTPSPAP-----SRPFSVLRANDVLWL----------SLTAAEYDQST- 373
Db        809 ---NQHGTLDAAGPAHLTLTGLLDNTAGLLQTAHTLWLTSAGLTNRSGTLTASQLTLDTQ 865

Qy        374 ----------YGSSTGPVYI--------------------SDSVTLVNVATGAQAVARS 402
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Qy        463 AAG 465
Db        977 TGG 979
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RESULT 7
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hemagglutinin-like secreted protein XF2196 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82589
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82589
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3442 <SIM>
A;Cross-references: UNIPROT:Q9PBE8; GB:AE004032; GB:AE003849; NID:g9107324; PIDN:AAF8499
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2196

Query Match 4.6%; Score 125; DB 2; Length 3442;
Best Local Similarity 21.2%; Pred. No. 7.9;
Matches 128; Conservative 63; Mismatches 212; Indels 200; Gaps 27;

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Qy         37 ASGTNLVLYAAPLNPPLPLQDG--TNTH---IMATEA-------SNYAQYRVARATIRYR 84
Db        499 RDGT------AALN-RLTLQGQRLDNQHGILTLATEATIHTHTLNNAAGQLHVNGTLDLT 551

Qy         85 PLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRN 144
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Qy        286 YSRPVV--------------SANGEPTVKLYTSVENAQQDKGVAIPHD-IDLGDSRVVIQ 330

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Qy        331 DYDNQH-EQDRPTPSPAP-----SRPFSVLRANDVLWL----------SLTAAEYDQST- 373

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Qy        374 ----------YGSSTGPVYI--------------------SDSVTLVNVATGAQAVARS 402

Db        866 GHTLDNTRGRLGTTTGNLTLHSGPLDNTAGLLQTAAALTIDTGAATLTNRDGGALLAATA 925

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Db        926 LDLTTATLDNRG-GTIDSQTAT--------HLHTTTLDNTTAGHISSSGTLQIDGTTLTN 976

Qy        463 AAG 465

Db        977 TGG 979
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RESULT 8
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82519
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: B82519
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3455 <SIM>
A;Cross-references: UNIPROT:Q9P9U6; GB:AE004082; GB:AE003849; NID:g9108003; PIDN:AAF8556
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laign
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
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A;Contents: annotation
C;Genetics:
A;Gene: XF2775

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Db        439 SVPPATDTPPSTGTMPIPSHPQTAPVLAAGRLTLENDIDNRGGHITAGGAIDAILTTLDN 498

Qy         37 ASGTNLVLYAAPLNPPLPLQDG--TNTH---IMATEA-------SNYAQYRVARATIRYR 84

Db        499 RDGT------AALN-RLTLQGQRLDNQHGILTLATEATIHTHTLNNAAGQLHVNGTLDLT 551

Qy         85 PLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRN 144

Db        552 AQHLNNASGHLLTTG--PQSATL-TIADLLDNTSGTL------ASAGSLTLTAATL---- 598

Qy        145 QGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTTCN 204

Db        599 -------------DTTDGTVQSGQGPLHMDAATLTAHRGTLTSQD--------TLTLTG 636

Qy        205 TNTRVSRYSSTARHRLRRGADGTAELTT-------------------------TAATRF 238

Db        637 THTDLSHATTTAQQITLH----TGDLTTAGGHLTAYGTHTLQLEARTRLDNTGGTIATNG 692

Qy        239 MKDLHFTGLNGVGEVGRGIAL---------TLLNLADTLLGGLPTELI----SSAGGQLF 285

Db        693 TLDLHTAALDNTGGTLHSTATGPNRLDITDTLTNTAGHLLLNGPTTLTTGTWTNTGGHLQ 752

Qy        286 YSRPVV--------------SANGEPTVKLYTSVENAQQDKGVAIPHD-IDLGDSRVVIQ 330

Db        753 ITGPATLHATTLDNRGGILHTATGPLDLRITGTLNN--QDNGLLTTTDALTLTAASLL-- 808

Qy        331 DYDNQH-EQDRPTPSPAP-----SRPFSVLRANDVLWL----------SLTAAEYDQST- 373

Db        809 ---NQHGTLDAAGPAHLTLTGLLDNTAGLLQTAHTLWLTSAGLTNRSGTLTASQLTLDTQ 865

Qy        374 ----------YGSSTGPVYI--------------------SDSVTLVNVATGAQAVARS 402

Db        866 GHTLDNTRGRLGTTTGNLTLHSGPLDNTAGLLQTAAALTIDTGAATLTNRDGGALLAATA 925

Qy        403 LDWSKVTLDGRPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIEN 462

Db        926 LDLTTATLDNRG-GTIDSQTAT--------HLHTTTLDNTTAGHISSSGTLQIDGTTLTN 976

Qy        463 AAG 465

Db        977 TGG 979
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RESULT 9
H96007
probable acriflavin resistence protein [imported] - Sinorhizobium meliloti (strain 1021)
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: H96007
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernanc
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endos
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: H96007
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1077 <KUR>
A;Cross-references: UNIPROT:Q92U15; GB:AL591985; PIDN:CAC49728.1; PID:g15141215; GSPDB:GN
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: acrF; SMb21498
A;Genome: plasmid
C;Superfamily: acriflavin resistance protein

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Db        375 PVALVGTFAVILAMGFSLNTVSLLALVLAIGIVVDDAIVVVENVERVMEENPGMSAAQAA 434

Qy         70 NYAQYRVARATIRYRPLVPNAVGGYAISISFWP-------QTTTTPTSVDMNSITSTDVR 122

Db        435 RLAMGEITGAIVAITLVLLSVF----VPVAFIPGLSGQLFQQFAVAVSVSM--VISAINA 488

Qy        123 ILVQPGIASELVIPSERLHYRNQGWRS----------VETSGVAEEEATSGLVMLCIH-G 171

Db        489 LTLSPALCAILLKPHHGPKRGILGWISRGIDRTRNGYAHVAGSIARRAIIGVILLAVAIG 548

Qy        172 SPVNSYTNTPYTGALGLLD---FALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTA 228

Db        549 ASGWLFRIVP-TGFLPSEDQGAFFAEIRLPEGASFNRTDAVVREVET----MLGGIEGVA 603

Qy        229 ELTTTAATRFMKDL---------------------------------------------- 242

Db        604 NVTTVTGYSFLDGIAKSSSAFAIVTMKPFAERQDESASVNAAIGTVMAKGAAIRNAQVFA 663

Qy        243 -HFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGE----P 297

Db        664 FNLPPIIGLG-TGSGFEYQLLDLQ----GRSPAELAATAGGLM------VAANQNPQLGP 712

Qy        298 TVKLYTSVE-----NAQQDKGVAIPHDIDLGDSRVVIQD-----YDNQHEQDRPTPSPAP 347

Db        713 TFSTYSASSPQLYLNLDRDRLQAL--GVSVSDLFATLQGTLGSYYVND------------ 758

Qy        348 SRPFSVLRANDVLW-LSLTAAEYDQSTYG--------SSTGPVYISDSVTLVNVATGAQA 398

Db        759 ---FNLFGRS---WKVTMQAAEADRDAVDDISRLHVRNAAGDMVPVASVARVDYIVGPQS 812

Qy        399 VARSLDWSKVTLDGRPLP---------TVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPYN 449

Db        813 IVRYNNYRSITLNGQPAPGISSGQALAAMEQVS----------------AATLPPGYSFE 856

Qy        450 YNTTASDQILIENAAGHRVAI 470

Db        857 WTGTALQEL---EAAGQTTVI 874


RESULT 10
A41258
a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: a-agglutinin attachment protein AGA1; protein N3431; protein YNR044w
C;Species: Saccharomyces cerevisiae
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C;Accession: A41258; S63375; S17031
R;Roy, A.; Lu, C.F.; Marykwas, D.L.; Lipke, P.N.; Kurjan, J.
Mol. Cell. Biol. 11, 4196-4206, 1991
A;Title: The AGA1 product is involved in cell surface attachment of the Saccharomyces ce
A;Reference number: A41258; MUID:91304412; PMID:2072914
A;Accession: A41258
A;Molecule type: DNA
A;Residues: 1-725 <ROY>
A;Cross-references: UNIPROT:P32323; GB:M60590; NID:g170963; PIDN:AAA34382.1; PID:g170964
R;Pohl, T.M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63346
A;Accession: S63375
A;Molecule type: DNA
A;Residues: 1-725 <POH>
A;Cross-references: EMBL:Z71659; NID:g1302551; PIDN:CAA96325.1; PID:e239834; PID:g130255
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:AGA1
A;Cross-references: SGD:S0005327; MIPS:YNR044w
A;Map position: 14R
C;Keywords: glycoprotein; transmembrane protein
F;8-24/Domain: transmembrane #status predicted <TM1>
F;708-724/Domain: transmembrane #status predicted <TM2>

  Query Match             4.5%;  Score 121;  DB 2;  Length 725;
  Best Local Similarity   19.3%;  Pred. No. 1.6;

  Matches  106;  Conservative   84;  Mismatches  187;  Indels  172;  Gaps   22;

Qy          8 TSPVPDVDSRGAILRRQYNLSTSP-LTSSVASGTNLVLYAAPLNPPLPLQDGTNTHIMAT 66

Db        275 TSPSSKSTSASSTSTSSYSTSTSPSLTSS-------------SPTLASTSPSSTSISST 320

Qy         67 EASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTT------TTPTSVDMNSITSTD 120

Db        321 FTDSTSS-------------LGSSIASSSTSVSLYSPSTPVYSVPSTSSNVATPSMTSST 367

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVET-------------SGV----------A 156

Db        368 VETTVSSQSSSEYITKS-----------SISTTIPSFSMSTYFTTVSGVTTMYTTWCPYS 416

Qy        157 EEEATSGLVML----------CIHGSPVNSYTNTPYTGALGLLDFALELEFRNL-TTCNT 205

Db        417 SESETSTLTSMHETVTTDATVCTHESCMPSQTTS-------LITSSIKMSTKNVATSVST 469

Qy        206 NTRVSRY-------SSTARHRLRRGADGTAELTTTAATRFMKDL---------HFTGLNG 249

Db        470 STVESSYACSTCAETSHSYSSVQTASSSSVTQQTTSTKSWVSSMTTSDEDFNKHATGKYH 529

Qy        250 VGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSA-------NGEPTVKLY 302

Db        530 VTSSGTSTISTSVSEA-TSTSSIDSE--SQEQSSHLLSTSVLSSSSLSATLSSDSTILLF 586

Qy        303 TSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWL 362

Db        587 SSVSS------------LSVEQSPVTTLQISSTSEILQPTSSTA---------------- 618

Qy        363 SLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQYS 422

Db        619 --------IATISAST------SSLSATSISTPSTSVESTIESSSLT------PTVSSIF 658

Qy        423 KTFFVLP--LRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480

Db        659 LSSSSAPSSLQTSVTTTEVSTTSISIQYQ----TSSMVTISQYMG-----SGSQTRLPLG 709

Qy        481 PVAISAAAV 489

Db        710 KLVFAIMAV 718


RESULT 11
S55862
probable membrane protein YNL327w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N0320
C;Species: Saccharomyces cerevisiae
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55862; S63308; S51288
R;Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin, C.
Yeast 11, 567-572, 1995
A;Title: Sequencing analysis of a 15.4 kb fragment of yeast chromosome XIV identifies the
A;Reference number: S55859; MUID:95373280; PMID:7645347
A;Accession: S55862
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1041 <MAF>
A;Cross-references: UNIPROT:P42835; EMBL:Z46259; NID:g633655; PIDN:CAA86371.1; PID:g6336
R;Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin, C.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63287
A;Accession: S63308
A;Molecule type: DNA
A;Residues: 1-1041 <MAW>
A;Cross-references: EMBL:Z71603; NID:g1302444; PID:e239572; PID:g1302445; MIPS:YNL327w
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:EGT2
A;Cross-references: SGD:S0005271; MIPS:YNL327w
A;Map position: 14L
C;Keywords: transmembrane protein
F;4-20/Domain: transmembrane #status predicted <TM1>
```

```
F;1025-1041/Domain: transmembrane #status predicted <TM2>

  Query Match             4.4%;  Score 120;  DB 2;  Length 1041;
  Best Local Similarity   19.1%;  Pred. No. 3.1;
  Matches  121;  Conservative   89;  Mismatches  219;  Indels  206;  Gaps   27;

Qy         29 TSPLTSSVASGTNLVLYAAPLNPPLPLQDGTNTHIMATEASNYAQYRVAR---ATIRYRP 85
              |:| :|  |: |  :: :| ::         :|    |::::      |    :|: |
Db        405 TTPSSSLSATETYSIISSASISVTQASYIDNSTTTAVTQSTSTIAVSSAEKLSSTLSY-- 462

Qy         86 LVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQ 145
                    ||:|   | ||||: |  || | :   :|
Db        463 -----TSNVTISVSSATQHTTTPSYVS-NSTTLSSSSVL---------------------- 495

Qy        146 GWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTPY---------TGALGLLDFALELE 196
                 || :|       ||        |  :  || ||        |    :  ||: :
Db        496 --ESVISSPYLANTTVSG-------ASSASQSTNPPYVSNSTTSSATQLATIAPFAINIT 546

Qy        197 FRNLTTCNTNTRVSRYSSTARHRLRRG--------ADGTAELTTTAATRFMKDL------ 242
               ::::  |||  |  |||     |  |         | |:  ||||  :  : ::
Db        547 GTSISSSITNT--SSVSSTT-SSLSSGPFVSNTAVASGSYILTTTTESAQLTEIGSLIPI 603

Qy        243 ----HFTGLNGVGEVGRG-------IALTLLNLADTLLGGLPTELISSA----------- 280
                   |  :|  : |          || :::| :   :  : |  ::|
Db        604 STITTSTTTSGTDKTGSNKVASSTEIAQSIVNNSSLSVSTINTNAATAAANARNATFTHA 663

Qy        281 --GGQL---FYSRPVVSANGEPTVKLYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQ 335
                 | |   ::|  ::|:  :   |: |:  :  :|   ::      |  | |   |
Db        664 THSGSLQPSYHSSSLLSSTID--TKVTTATTSTSRDGSSSLAFTTGLNQSVVTGTD---- 717

Qy        336 HEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQ----STY------GSSTGPVYISD 385
                     |  :||: : :     |    |||     ||        |:|    :
Db        718 -----------KSDTYSVISSTE----SAQVTEYDSLLPISTLKPTVVTGTSRNSTFSMV 762

Qy        386 SVTLVNVATG-----AQAVARSLDWSKVTLDGRPLP--TVE------------------- 419
              | | :  ||      | :|  |   ::||  |  ||  |:|
Db        763 SSTKLTEATATDKGDAYSVISSTQSAQVTEYGSMLPISTLETPTVIMSTDESGYFTLTTC 822

Qy        420 -------QYSKTFFVLPLRGKLSFWEAG--------TTKAGYPYNYNTTASDQILIENAA 464
                    :|     :  | | : :   |         ||      | :|:    : :
Db        823 TESGQATEYGSLIPISTLDGSVIYTFTGESVVVGYSTTVGAAQYAQHTSL---VPVSTIK 879

Qy        465 GHRVAIST-------YTTRLGAGPVA-----ISAAAVLAPRSALALLE----------DT 502
              | : ::||        |:| :||   |      :  : :   :::|:  |          |:
Db        880 GSKTSLSTEESVVAGYSTTVGAAQYAQHTSLVPVSTIKGSKTSLSTEESVVAGYSTTVDS 939

Qy        503 FDYPGRAH---------------TFDDFCPECRAL 522
                 |    :                |  : |  | ||
Db        940 AQYAEHTNLVAIDTLKTSTFQKATATEVCVTCTAL 974


RESULT 12
T41213
probable zinc finger protein SPCC1906.05 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 20-Oct-2000 #sequence_revision 08-Dec-2000 #text_change 09-Jul-2004
C;Accession: T41213; T41109
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z21969
A;Accession: T41213
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-379 <LYN1>
A;Cross-references: UNIPROT:O74463; EMBL:AL031538; NID:g3581923; PIDN:CAA20774.1; PID:g3
A;Experimental source: strain 972h-; cosmid c1906
A;Accession: T41109
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 320-547 <LYN2>
A;Cross-references: EMBL:AL031540; NID:g3581876; PIDN:CAA20775.1; PID:g3581877; GSPDB:GN
A;Experimental source: strain 972h-; cosmid c1739
C;Genetics:
A;Gene: SPDB:SPCC1906.05; SPDB:SPCC1739.01
A;Map position: 3

  Query Match             4.4%;  Score 118.5;  DB 2;  Length 547;
  Best Local Similarity   21.8%;  Pred. No. 1.6;
  Matches  109;  Conservative   66;  Mismatches  187;  Indels  139;  Gaps   21;

Qy         45 YAAPLNPPLPLQDGTNTHIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQT 104
              :| | |  ||  :||:|:  ||: |:|     ||              :|   || |   :|
Db         92 HALPGNTNLP--NGTSTNTMASMAANGGASSVA----------SKQMGANQISPSLSSKT 139

Qy        105 TTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVE---------TSGV 155
                 |    |: |:||||       |:     |   |   |: |  ::           :|||
Db        140 MKNPAD-KANNTTATDVR----GNTATSPYFPFSRSPGRHSGNSTINGMMTTPNFLSSGV 194

Qy        156 AE------EEATSGLVMLCIHGSPV--------------NSYTNTPYTGALGLLDFALE 194
                      ::||      ::| |:                :| ::|   |: |||
Db        195 NSRSVDEFNNSSSGFPS-SLNGIPIASPPLATSPTSFSLASSASSTNLGGSKGLL----- 248

Qy        195 LEFRNLTTCNT-----------NTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLH 243
                |: :|: |             ||  :| |||             : ||:    :    |
Db        249 --FQQMTSENNRDYFSRRPTLLNTYGNRCSSTDT------LSSLSRLTSQDPLKASLPLQ 300

Qy        244 FTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYT 303
                |    : |  ::   | | |  || |      | |  :   | | :|     :
Db        301 SPPL--APKTGVSLSRPRLTL-DQSLGNL------SLGSGINQRRQVPRSNS--YAGAFP 349

Qy        304 SVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLS 363
              || :|     | : | :|: |             |: |   :|  |   |:| :: :  ||
Db        350 SVVSASLPTKVDLNHQMDVSD-----------EEQRFLSTPLGSFDESILGSSPINRLS 397

Qy        364 LTAAEYDQS----------------------TYGSSTGPVYISDSVTLVNVATGAQ--- 397
               :  :|  |                      | | :  |  | |::   :||
Db        398 SSFKQYTSSLKSPGLSTRTSSTMNSLNSSRFGAYFSKSRYVEGSGSMSTTPLATSVNNSY 457

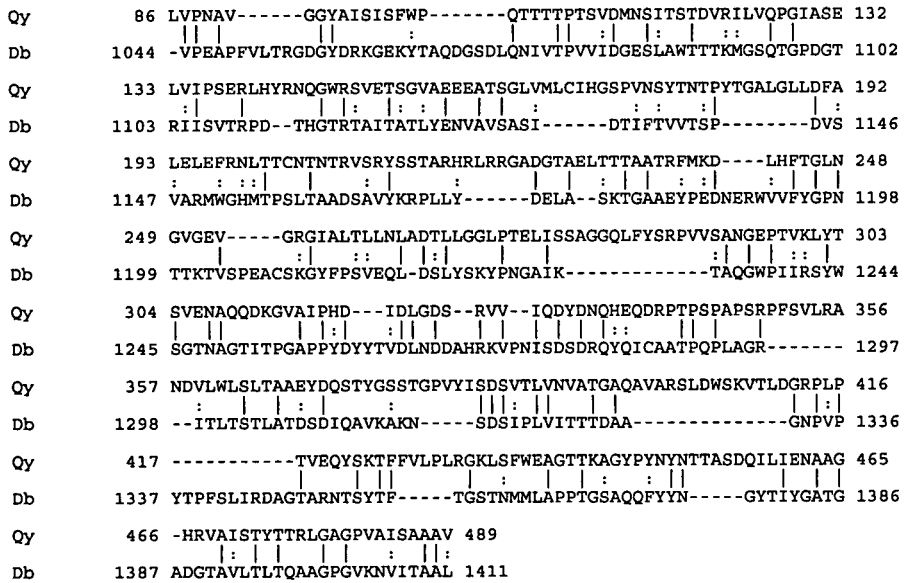
Qy        398 ------AVARSLDWSKVTLDG-RPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNY 450
                   :|     :|  | :| ||:      |:  |       |   :  | ||
Db        458 KLPSGFSVREEAVFSSPTTEGSRPVSLARLKSEPIF-------RSDTASPETIAG----L 506

Qy        451 NTTASDQILIENAAGHRVAIS 471
                | :| ::  |  :  |: ::
Db        507 GDTKNDPVVSTNNSVSRITVA 527


RESULT 13
AB0821
probable exported protein STY2760 [imported] - Salmonella enterica subsp. enterica serova
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB0821
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0821
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2130 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02718.1; PID:g16503731; GSPDB:GN00176
C;Genetics:
A;Gene: STY2760

  Query Match             4.4%;  Score 118.5;  DB 2;  Length 2130;
  Best Local Similarity   22.6%;  Pred. No. 11;
  Matches  114;  Conservative   55;  Mismatches  215;  Indels  121;  Gaps   24;

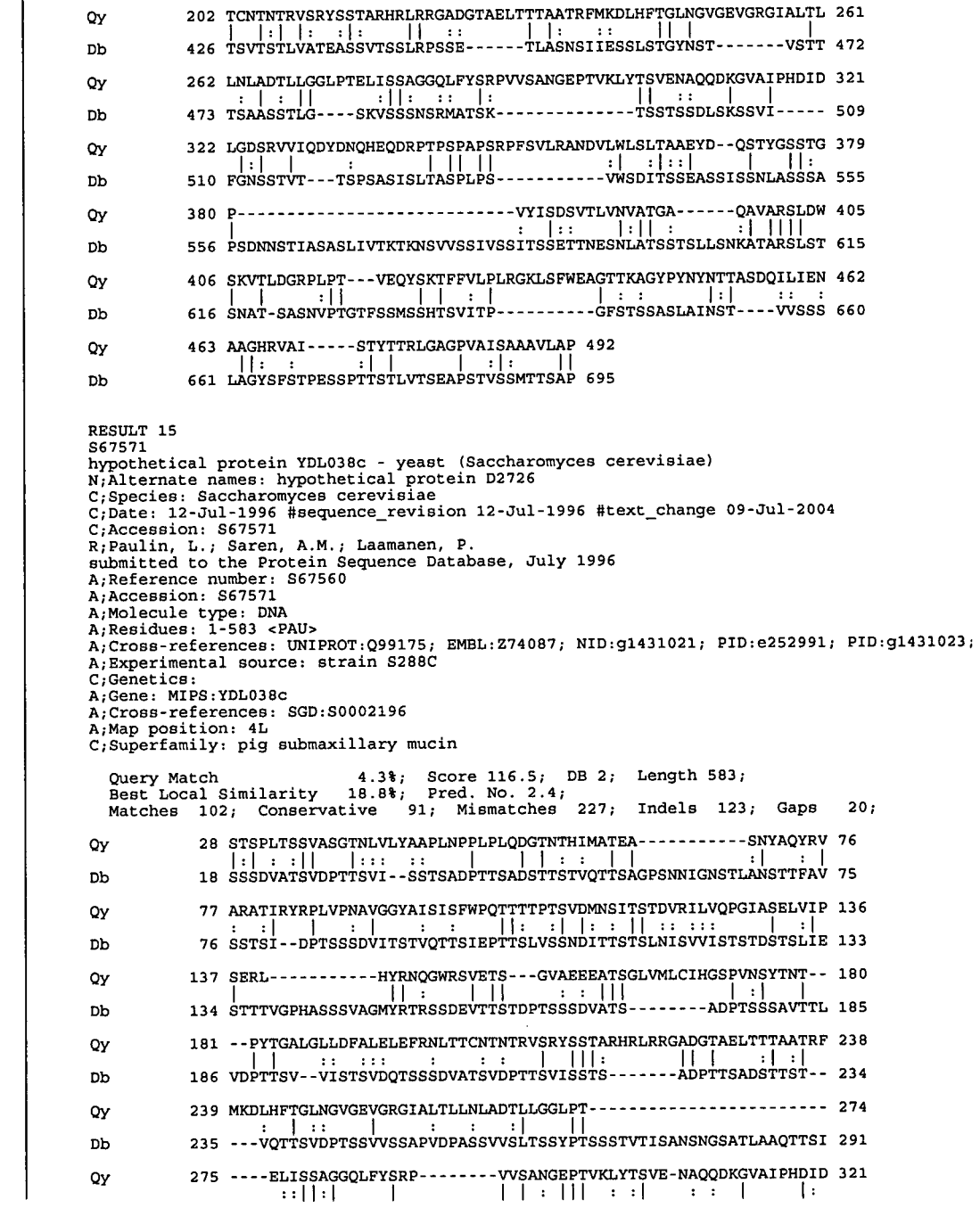
Qy         28 STSPLTSSVASGTNLVLYAAPLNPPLPLQ--DGTNTHIMATEASNYAQYRVARATIRYRP 85
              :||  || :||  | |  |  : |  | |  ||:  | :  :  :  | :|      :|
Db        985 NTSVYTSCLAS-DNPVPAAITIEPVDPSQWYDGSGVHALKVKKGDTLQLKVTVKDASGKP 1043
```



RESULT 14
S59310
probable membrane protein YMR317w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YM9924.09
C;Species: Saccharomyces cerevisiae
C;Date: 29-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 19-Apr-2002
C;Accession: S59310
R;Churcher, C.M.
submitted to the EMBL Data Library, September 1995
A;Reference number: S59302
A;Accession: S59310
A;Molecule type: DNA
A;Residues: 1-1104 <CHU>
A;Cross-references: EMBL:Z54141; GSPDB:GN00013; MIPS:YMR317w
A;Experimental source: strain AB972
C;Genetics:
A;Gene: MIPS:YMR317w
A;Cross-references: SGD:S0004936
A;Map position: 13R

Query Match 4.4%; Score 118; DB 2; Length 1104;
Best Local Similarity 19.0%; Pred. No. 4.7;
Matches 109; Conservative 92; Mismatches 214; Indels 160; Gaps 23;





RESULT 15
S67571
hypothetical protein YDL038c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein D2726
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C;Accession: S67571
R;Paulin, L.; Saren, A.M.; Laamanen, P.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67560
A;Accession: S67571
A;Molecule type: DNA
A;Residues: 1-583 <PAU>
A;Cross-references: UNIPROT:Q99175; EMBL:Z74087; NID:g1431021; PID:e252991; PID:g1431023;
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YDL038c
A;Cross-references: SGD:S0002196
A;Map position: 4L
C;Superfamily: pig submaxillary mucin

Query Match 4.3%; Score 116.5; DB 2; Length 583;
Best Local Similarity 18.8%; Pred. No. 2.4;
Matches 102; Conservative 91; Mismatches 227; Indels 123; Gaps 20;

```
Db        292 DPVSSIVSSSGATTIISSASIDPASSVVSSTSSEPTSFIVSSTSVYSTRPSGPTTSTDLA 351

Qy        322 LGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPV 381
                  ::::       ||  | | : :   |   : |:   |:  :: | ||:  |  ||
Db        352 TFSDTIILRVSTTSTSQDTQTVSSSLTDMVSSTGSADLSVSSIQRSQVDPSTFAVSNSPV 411

Qy        382 YISDSVTLVNVATGAQAVARSLDWSK-----------VTLDGRPLPTVEQYSKTFFVLP 429
              | : |    : :||    : ||  |:            |||      :  : | |  : |
Db        412 YPTASTG--STSTGIPIASESLSLSRQQGISATSSSSIVTLTPVDSASSSRSSATSIIKP 469

Qy        430 ----------LRGKLSFWEA-GTTKAGYP----YNYNTTASDQILI-ENAAGHRVAIS-T 472
                       :  :|  :|  :||: ||     :  | ||:  |:  ::: | : :  |
Db        470 NMPVSSNDSKTQSSVSVVDAFQSTKSSYPSITSADPTTLASENGLVGSSSSAHPITLDRT 529

Qy        473 YTT 475
              | :
Db        530 YAS 532

Search completed: July 14, 2005, 15:51:36
Job time : 11.0802 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 14, 2005, 00:29:03 ; Search time 43.4198 Seconds
(without alignments)
4676.418 Million cell updates/sec

Title: US-09-769-066-16_COPY_1_525
Perfect score: 2701
Sequence: 1 AVAPAHDTSPVPDVDSRGAI.....PGRAHTFDDFCPECRALGLQ 525

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2701	100.0	525	2	AAR96104	Aar96104 Hepatitis
2	2701	100.0	540	2	AAR96102	Aar96102 Hepatitis
3	2701	100.0	549	2	AAR96092	Aar96092 Hepatitis
4	2701	100.0	660	2	AAR96090	Aar96090 Hepatitis
5	2674.5	99.0	659	2	AAR38787	Aar38787 HEV ORF2
6	2674.5	99.0	659	2	AAW35827	Aaw35827 Hepatitis
7	2674.5	99.0	659	2	AAW93387	Aaw93387 Human HEV
8	2671.5	98.9	659	2	AAR39308	Aar39308 Mexico st
9	2638.5	97.7	659	5	ABJ04808	Abj04808 Hepatitis
10	2579	95.5	549	2	AAW76367	Aaw76367 Hepatitis
11	2579	95.5	660	2	AAR70323	Aar70323 Hepatitis
12	2579	95.5	660	2	AAW76369	Aaw76369 Hepatitis
13	2575	95.3	660	2	AAR91814	Aar91814 Hepatitis
14	2575	95.3	660	2	AAW93386	Aaw93386 Human HEV
15	2575	95.3	660	2	AAW93388	Aaw93388 Human HEV
16	2575	95.3	660	5	ABB81670	Abb81670 Hepatitis
17	2575	95.3	660	6	ADA50060	Ada50060 Hepatitis
18	2575	95.3	660	7	ADB97807	Adb97807 HEV ORF2
19	2569	95.1	525	2	AAR96103	Aar96103 Hepatitis
20	2569	95.1	540	2	AAR96101	Aar96101 Hepatitis
21	2569	95.1	549	2	AAR96091	Aar96091 Hepatitis
22	2569	95.1	660	2	AAR38785	Aar38785 HEV ORF2
23	2569	95.1	660	2	AAR39306	Aar39306 Burma str
24	2569	95.1	660	2	AAR96089	Aar96089 Hepatitis
25	2569	95.1	660	2	AAW35826	Aaw35826 Hepatitis
26	2569	95.1	660	2	AAW80197	Aaw80197 Protein e
27	2569	95.1	660	2	AAW93389	Aaw93389 Human HEV
28	2569	95.1	660	2	AAW93390	Aaw93390 Human HEV
29	2569	95.1	660	3	AAB24120	Aab24120 Hepatitis
30	2569	95.1	660	4	AAB62523	Aab62523 HEV-Burma
31	2569	95.1	660	5	AAO15699	Aao15699 Hepatitis
32	2569	95.1	660	7	ADD24376	Add24376 Hepatitis
33	2568	95.1	660	2	AAW93392	Aaw93392 Human HEV
34	2566	95.0	660	2	AAR51265	Aar51265 HEV strai
35	2566	95.0	660	2	AAW81520	Aaw81520 Hepatitis
36	2564	94.9	660	5	ABJ04811	Abj04811 Hepatitis
37	2563	94.9	660	2	AAW93391	Aaw93391 Human HEV
38	2562	94.9	660	2	AAW71210	Aaw71210 Protein e
39	2560	94.8	660	4	AAE12980	Aae12980 Hepatitis
40	2560	94.8	660	5	ABJ04820	Abj04820 Hepatitis
41	2560	94.8	660	5	ABJ04807	Abj04807 Hepatitis
42	2560	94.8	660	5	ABJ04809	Abj04809 Hepatitis
43	2560	94.8	660	5	ABJ04819	Abj04819 Hepatitis
44	2557	94.7	660	5	ABJ04822	Abj04822 Hepatitis
45	2556	94.6	660	7	ADE06700	Ade06700 Hepatitis

ALIGNMENTS

RESULT 1
AAR96104
ID AAR96104 standard; protein; 525 AA.
XX
AC AAR96104;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Mexico strain) recombinant 62K antigen.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid.
XX
OS Hepatitis E virus; Mexico strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Claim 8; Page 97-98; 125pp; English.
XX
CC DNA (AAT27110) coding for the 62K antigen (AAR96092) of hepatitis E virus
CC (HEV) Mexico strain capsid protein was cloned into baculovirus expression
CC vector pBluBacIII and recombinant 62K was expressed in Sf9 insect cells.
CC High levels of expression were obtd. and the recombinant 62K was obtd. in
CC over 95% purity. However, C-terminal processing resulted in the deletion
CC of 9 or 23 amino acids from 62K, giving 2 related polypeptide species
CC (AAR96102 and AAR96104). Similar results were obtd. with HEV Burma 62K
CC antigen (see also AAR96101 and AAR96103). Recombinant 62K represents an
CC improved antigen, in comparison to bacterial expressed proteins, for use
CC in HEV diagnostic assays, and also has excellent immunogenic properties.
CC (Updated on 16-OCT-2003 to standardise OS field)

XX
SQ Sequence 525 AA;

Query Match 100.0%; Score 2701; DB 2; Length 525;
Best Local Similarity 100.0%; Pred. No. 1.4e-225;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
```

RESULT 2
AAR96102
ID AAR96102 standard; protein; 540 AA.
XX
AC AAR96102;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Mexico strain) recombinant 62K antigen.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid.
XX
OS Hepatitis E virus; Mexico strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Claim 6; Page 93-95; 125pp; English.
XX
CC DNA (AAT27110) coding for the 62K antigen (AAR96092) of hepatitis E virus
CC (HEV) Mexico strain capsid protein was cloned into baculovirus expression
CC vector pBluBacIII and recombinant 62K was expressed in Sf9 insect cells.
CC High levels of expression were obtd. and the recombinant 62K was obtd. in
CC over 95% purity. However, C-terminal processing resulted in the deletion
CC of 9 or 23 amino acids from 62K, giving 2 related polypeptide species
CC (AAR96102 and AAR96104). Similar results were obtd. with HEV Burma 62K
CC antigen (see also AAR96101 and AAR96103). Recombinant 62K represents an
CC improved antigen, in comparison to bacterial expressed proteins, for use
CC in HEV diagnostic assays, and also has excellent immunogenic properties.
CC (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 540 AA;

Query Match 100.0%; Score 2701; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.5e-225;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
```

RESULT 3
AAR96092
ID AAR96092 standard; protein; 549 AA.
XX
AC AAR96092;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Mexico strain) 62K antigen.

```
XX
KW   HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW   diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW   capsid.
XX
OS   Hepatitis E virus; Mexico strain.
XX
PN   WO9612807-A2.
XX
PD   02-MAY-1996.
XX
PF   23-OCT-1995;   95WO-US013703.
XX
PR   24-OCT-1994;   94US-00327952.
PR   13-OCT-1995;   95US-00542634.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fuerst TR,  Mcatee CP,  Yarbough PO,  Zhang Y;
XX
DR   WPI; 1996-230608/23.
DR   N-PSDB; AAT27110.
XX
PT   Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT   diagnostic reagents for determining HEV infection and in vaccines.
XX
PS   Claim 4; Page 84-86; 125pp; English.
XX
CC   62K antigen (AAR96092) comprises the C-terminal 549 amino acids of
CC   hepatitis E virus (HEV) Mexico strain capsid protein (see also AAR96090).
CC   It is obtd. by PCR amplification of HEV Mexico ORF-2 (AAT27108),
CC   insertion of amplified DNA (AAT27110) into vector pGEX and expression in
CC   E. coli cells. Expression of full-length ORF-2 in Sf9 insect cells using
CC   a baculovirus system also results in prodn. of 62K antigen (see also
CC   AAR96102 and AAR96104). 62K represents an improved antigen, in comparison
CC   to bacterial expressed proteins, for use in HEV diagnostic assays, and
CC   also has excellent immunogenic properties. (Updated on 16-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 549 AA;

  Query Match             100.0%;  Score 2701;  DB 2;  Length 549;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-225;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525


RESULT 4
AAR96090
ID   AAR96090 standard; protein; 660 AA.
XX
AC   AAR96090;
XX
DT   16-OCT-2003  (revised)
DT   06-AUG-1996  (first entry)
XX
DE   Hepatitis E virus (Mexico strain) capsid protein.
XX
KW   HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW   diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW   capsid.
XX
OS   Hepatitis E virus; Mexico strain.
XX
PN   WO9612807-A2.
XX
PD   02-MAY-1996.
XX
PF   23-OCT-1995;   95WO-US013703.
XX
PR   24-OCT-1994;   94US-00327952.
PR   13-OCT-1995;   95US-00542634.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fuerst TR,  Mcatee CP,  Yarbough PO,  Zhang Y;
XX
DR   WPI; 1996-230608/23.
DR   N-PSDB; AAT27108.
XX
PT   Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT   diagnostic reagents for determining HEV infection and in vaccines.
XX
PS   Disclosure; Page 80-82; 125pp; English.
XX
CC   The putative capsid protein (AAR96090) of hepatitis E virus (HEV) Mexico
CC   strain is encoded by ORF-2 (AAT27108) of the virus. PCR amplification of
CC   ORF-2 allows prodn. of capsid protein or of C-terminal regions of the
CC   capsid protein (see also AAR96092, AAR96094 and AAR96096) and expression
CC   in Spodoptera frugiperda Sf9 insect cells using a baculovirus vector
CC   provides recombinant C-terminal regions (see also AAR96102 and AAR96104)
CC   useful as diagnostic reagents and in vaccines. The HEV Burma strain
CC   capsid protein (AAR96089) may similarly be used. (Updated on 16-OCT-2003
CC   to standardise OS field)
XX
SQ   Sequence 660 AA;

  Query Match             100.0%;  Score 2701;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2e-225;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 636
```

RESULT 5
AAR38787
ID AAR38787 standard; protein; 659 AA.
XX
AC AAR38787;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 11-JAN-1994 (first entry)
XX
DE HEV ORF2 protein.
XX
KW Enterically transmitted non-A non-B hepatitis; ET-NANB; vaccine.
XX
OS Hepatitis E virus; Mexico strain.
XX
FH Key Location/Qualifiers
FT Peptide 225. .659
FT /label= C2
FT Peptide 333. .659
FT /label= SG3
FT Peptide 612. .659
FT /label= 406.3-2
XX
PN WO9314116-A1.
XX
PD 22-JUL-1993.
XX
PF 15-JAN-1993; 93WO-US000459.
XX
PR 17-JAN-1992; 92US-00822335.
PR 01-MAY-1992; 92US-00876941.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
PA (USSH) US SEC DEPT HEALTH.
XX
PI Reyes GR, Bradley DW, Tam AW, Carl M;
XX
DR WPI; 1993-243144/30.
DR N-PSDB; AAQ47130.
XX
PT New immunogenic hepatitis E virus (HEV) peptide(s) - are from the ORF1,
PT ORF2 and ORF3 regions of HEV, useful as a vaccine against HEV infection.
XX
PS Disclosure; Fig 8; 48pp; English.
XX
CC Immunogenic hepatitis E virus (HEV) peptides are selected from the ORF1,
CC ORF2 and ORF3 regions of HEV. The peptides can be used in vaccines to
CC prevent infection by HEV. The antibodies can neutralise and block HEV
CC infection and can be used to prevent or treat HEV infection. The peptides
CC and antibodies can also be used as diagnostic reagents. (Updated on 25-
CC MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 659 AA;

Query Match 99.0%; Score 2674.5; DB 2; Length 659;
Best Local Similarity 99.4%; Pred. No. 4e-223;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 635
```

RESULT 6
AAW35827
ID AAW35827 standard; protein; 659 AA.
XX
AC AAW35827;
XX
DT 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 26-FEB-1998 (first entry)
XX
DE Hepatitis E virus Mexico strain protein from ORF2.
XX
KW Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
KW diagnosis; HEV.
XX
OS Hepatitis E virus; - Mexico strain.
XX
PN US5686239-A.
XX
PD 11-NOV-1997.
XX
PF 09-MAY-1994; 94US-00240049.

```
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   17-JAN-1992;   92US-00822335.
PR   20-APR-1992;   92US-00870985.
PR   01-MAY-1992;   92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Tam AW,  Reyes GR,  Yarbough PO;
XX
DR   WPI; 1997-558132/51.
DR   N-PSDB; AAT96960.
XX
PT   Diagnosis of hepatitis E virus Burma and Mexico strain infection - by
PT   immunoassay with hepatitis E virus peptide antigens.
XX
PS   Disclosure; Col 43-46; 36pp; English.
XX
CC   A method has been developed for detecting hepatitis E virus (HEV)
CC   antibodies (Ab). The method comprises: (a) reacting a serum sample with a
CC   HEV peptide antigen; and (b) examining the peptide for the presence of
CC   bound Ab, where the presence of bound Ab indicates the presence of HEV
CC   Ab. The present sequence represents the protein from the open reading
CC   frame, ORF2, from HEV Mexico strain. The method can be used to diagnose
CC   infection with the enterically transmitted non-A/non-B viral hepatitis
CC   agent HEV, specifically the HEV Burma and Mexico strains. (Updated on 25-
CC   MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to standardise OS
CC   field)
XX
SQ   Sequence 659 AA;

  Query Match             99.0%;  Score 2674.5;  DB 2;  Length 659;
  Best Local Similarity   99.4%;  Pred. No. 4e-223;
  Matches  522;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 635


RESULT 7
AAW93387
ID   AAW93387 standard; protein; 659 AA.
XX
AC   AAW93387;
XX
DT   11-JUN-1999  (first entry)
XX
DE   Human HEV ORF 2 protein from strain Mexico.
XX
KW   Swine hepatitis E virus; HEV; cross-reaction; antibody; human; therapy;
KW   vaccine; immunise; infection; detection; diagnosis; prevention.
XX
OS   Hepatitis E virus.
XX
PN   WO9904029-A2.
XX
PD   28-JAN-1999.
XX
PF   17-JUL-1998;   98WO-US014665.
XX
PR   18-JUL-1997;   97US-0053069P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Meng X,  Emerson SU,  Purcell RH;
XX
DR   WPI; 1999-132270/11.
XX
PT   New isolated swine hepatitis E virus - used to develop products for the
PT   diagnosis, prevention and treatment of hepatitis E virus infection in
PT   mammals, particularly humans.
XX
PS   Example 1; Fig 3A; 70pp; English.
XX
CC   This invention describes a swine hepatitis E virus (HEV) and its natural
CC   mutants which are capable of cross-reacting with antibodies reactive with
CC   a human HEV strain or natural mutants. The HEV and the proteins can be
CC   used in vaccines for immunising against HEV infection. The swine HEV can
CC   be used in humans to prevent possible infection by human HEV. The swine
CC   HEV can also be used as a therapeutic treatment for infection by other
CC   strains of HEV. The swine HEV can also be used for the production of
CC   antibodies which can be used in therapy, detection and diagnosis. The
CC   products can also be used for determining the susceptibility of cells or
CC   organs to infection with swine HEV. The swine HEV is particularly useful
CC   for the development of agents for the prevention, treatment and detection
CC   of human HEV because it is not a human virus and thus can be handled both
CC   experimentally and clinically without fear of severe infection and/or
CC   contamination
XX
SQ   Sequence 659 AA;

  Query Match             99.0%;  Score 2674.5;  DB 2;  Length 659;
  Best Local Similarity   99.4%;  Pred. No. 4e-223;
  Matches  522;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
```

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                ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 635


RESULT 8
AAR39308
ID   AAR39308 standard; protein; 659 AA.
XX
AC   AAR39308;
XX
DT   25-MAR-2003  (revised)
DT   14-FEB-1994  (first entry)
XX
DE   Mexico strain HEV ORF2 puative virus capsid protein.
XX
KW   Hepatitis E virus; vaccine; neutralising antibodies; infection; block;
KW   open reading frame; antibodies.
XX
OS   Hepatitis E virus.
XX
PN   WO9314208-A2.
XX
PD   22-JUL-1993.
XX
PF   19-JAN-1993;   93WO-US000475.
XX
PR   17-JAN-1992;   92US-00822335.
PR   20-APR-1992;   92US-00870985.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Reyes GR,  Bradley DW,  Twu J,  Purdy MA,  Tam AW,  Krawczynski KZ;
XX
DR   WPI; 1993-243223/30.
DR   N-PSDB; AAQ46814.
XX
PT   Antigen and antibody vaccines against hepatitis E virus infection -
PT   contain peptide(s) derived from capsid protein C-terminal or antibodies
PT   against protein.
XX
PS   Disclosure; Fig 7; 43pp; English.
XX
CC   The sequence is that of the putative virus capsid protein encoded by
CC   Mexico strain hepatitis E virus (HEV) open reading frame ORF2. This
CC   protein or peptide fragments of it may be used in a vaccine composition
CC   for immunising an individual against HEV. Antibodies raised against these
CC   peptides can also be used in such vaccines. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 659 AA;

  Query Match             98.9%;  Score 2671.5;  DB 2;  Length 659;
  Best Local Similarity   99.2%;  Pred. No. 7.4e-223;
  Matches  521;  Conservative    1;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKLTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 635


RESULT 9
ABJ04808
ID   ABJ04808 standard; protein; 659 AA.
XX
AC   ABJ04808;
XX
DT   07-NOV-2002  (first entry)
XX
DE   Hepatitis E virus Mexico strain ORF2 capsid gene.
XX
KW   Avian hepatitis E virus; vaccine; hepatitis E; ORF2; zoonosis; virucide;
KW   avian hepatitis-splenomegaly syndrome; HEV; HS syndrome.
XX
OS   Hepatitis E virus.
XX
PN   WO200253712-A2.
XX
PD   11-JUL-2002.
XX
PF   04-JAN-2002; 2002WO-US000215.
XX
PR   05-JAN-2001; 2001US-0259846P.
PR   31-DEC-2001; 2001US-00029840.
XX
PA   (VIRG ) VIRGINIA TECH INTELLECTUAL PROPERTIES.
XX
PI   Meng X,  Haqshenas G,  Huang F;
XX
DR   WPI; 2002-548085/58.
XX
PT   Novel isolated avian hepatitis E virus useful in a vaccine for protecting
PT   an avian or mammalian species from viral infection or hepatitis-
PT   splenomegaly syndrome caused by the avian or mammalian hepatitis E virus.
```

```
XX
PS   Example 11; Fig 5; 95pp; English.
XX
CC   The present invention relates to an isolated avian hepatitis E virus
CC   having the nucleic acid sequence shown in ABT05872. Vaccines against the
CC   virus are also described, and can be used for protecting an avian or
CC   mammalian species from viral infection or hepatitis-splenomegaly syndrome
CC   caused by the avian or mammalian HEV. The present sequence is a hepatitis
CC   E virus protein described in the exemplification of the invention
XX
SQ   Sequence 659 AA;

  Query Match             97.7%;  Score 2638.5;  DB 5;  Length 659;
  Best Local Similarity   97.9%;  Pred. No. 5.4e-220;
  Matches  514;  Conservative    3;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||| ||||||||||||||||   |||||||||||||||| |
Db        292 PYTGALGLLDFALELEFRMLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFHK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              |||||| |||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGTNGVGEIGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWTKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| ||||||||||||||||||||||||||||||||
Db        591 PVSISAVAVLAPHSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 635


RESULT 10
AAW76367
ID   AAW76367 standard; protein; 549 AA.
XX
AC   AAW76367;
XX
DT   03-DEC-1998  (first entry)
XX
DE   Hepatitis E virus hollow particle protein ORF2.
XX
KW   Hollow particle protein; virus; antibody; detection; immunoassay;
KW   infection.
XX
OS   Hepatitis virus.
XX
FH   Key             Location/Qualifiers
FT   Protein         1. .549
FT                   /label= ORF2
FT                   /note= "partial sequence"
XX
PN   JP10234383-A.
XX
PD   08-SEP-1998.
XX
PF   28-FEB-1997;   97JP-00062445.
XX
PR   28-FEB-1997;   97JP-00062445.
XX
PA   (DENK-) DENKA SEIKEN KK.
PA   (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR   WPI; 1998-535037/46.
DR   N-PSDB; AAV61686.
XX
PT   Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids
PT   encoding it - useful for more accurate detection of HEV in samples, using
PT   immuno-assays and nucleic acid hybridisation.
XX
PS   Claim 1; Page 15-17; 29pp; Japanese.
XX
CC   This sequence represents a Hepatitis E viral hollow particle protein
CC   described as ORF2. This polypeptide can be used to raise antibodies to
CC   detect HEV infection in samples, e.g. by immuno-assay based techniques,
CC   and the nucleic acid can be used for the same in nucleic acid
CC   hybridisation assays. The polypeptide and nucleic acid allow more
CC   accurate detection of HEV than previously possible
XX
SQ   Sequence 549 AA;

  Query Match             95.5%;  Score 2579;  DB 2;  Length 549;
  Best Local Similarity   94.9%;  Pred. No. 6.2e-215;
  Matches  498;  Conservative   13;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| ||||||||||||||||||||||||:|||||||||:| ||||||||
Db          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||  |||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||:|||||||||:|||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||:|||||||||||||||||||||||:|||||||| |::|
Db        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| ||||||||| ||| ||||||||||||| ||||
Db        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525


RESULT 11
AAR70323
ID   AAR70323 standard; protein; 660 AA.
```

```
XX
AC   AAR70323;
XX
DT   25-MAR-2003  (revised)
DT   28-SEP-1995  (first entry)
XX
DE   Hepatitis E virus ORF2 protein.
XX
KW   HEV; ORF2; antigen; vaccine; immunogen.
XX
OS   Hepatitis E virus.
XX
PN   WO9508632-A1.
XX
PD   30-MAR-1995.
XX
PF   23-SEP-1994;   94WO-AU000572.
XX
PR   24-SEP-1993;   93AU-00001423.
PR   15-DEC-1993;   93AU-00002964.
XX
PA   (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX
PI   Anderson DA,  Locarnini SA,  Torresi J,  Li F,  Hui Z;
XX
DR   WPI; 1995-139601/18.
DR   N-PSDB; AAQ86592.
XX
PT   Antigens of hepatitis E virus (HEV) - selectively immuno:reactive to
PT   convalescent and/or acute phase circulating antibodies to HEV.
XX
PS   Disclosure; Page 39-41; 78pp; English.
XX
CC   RNA from an HEV strain isolated in the Xinjiang region of China was
CC   subjected to RT-PCR to obtain fragments corresp. to ORF2 (given in
CC   AAQ86592) and ORF3 (AAQ86593) that encoded antigenic proteins (AAR70323-
CC   24, respectively). DNA fragments were manipulated into pGEX vectors for
CC   production of GST fusion proteins in E. coli. Applications include HEV
CC   infection diagnosis, therapy and vaccine development. (Updated on 25-MAR-
CC   2003 to correct PN field.)
XX
SQ   Sequence 660 AA;

  Query Match             95.5%;  Score 2579;  DB 2;  Length 660;
  Best Local Similarity   94.9%;  Pred. No. 8.1e-215;
  Matches  498;  Conservative   13;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||| |||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||:||||||||||||||||||||:||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| |||||||||| ||| ||||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQ 636


RESULT 12
AAW76369
ID   AAW76369 standard; protein; 660 AA.
XX
AC   AAW76369;
XX
DT   03-DEC-1998  (first entry)
XX
DE   Hepatitis E virus hollow particle protein #2.
XX
KW   Hollow particle protein; virus; antibody; detection; immunoassay;
KW   infection.
XX
OS   Hepatitis virus.
XX
PN   JP10234383-A.
XX
PD   08-SEP-1998.
XX
PF   28-FEB-1997;   97JP-00062445.
XX
PR   28-FEB-1997;   97JP-00062445.
XX
PA   (DENK-) DENKA SEIKEN KK.
PA   (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR   WPI; 1998-535037/46.
DR   N-PSDB; AAV61688.
XX
PT   Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids
PT   encoding it - useful for more accurate detection of HEV in samples, using
PT   immuno-assays and nucleic acid hybridisation.
XX
PS   Claim 13; Page 24-26; 29pp; Japanese.
XX
CC   This sequence represents a Hepatitis E viral hollow particle protein.
CC   This polypeptide can be used to raise antibodies to detect HEV infection
CC   in samples, e.g. by immuno-assay based techniques, and the nucleic acid
CC   can be used for the same in nucleic acid hybridisation assays. The
CC   polypeptides and nucleic acids allow more accurate detection of HEV than
CC   previously possible
XX
SQ   Sequence 660 AA;

  Query Match             95.5%;  Score 2579;  DB 2;  Length 660;
  Best Local Similarity   94.9%;  Pred. No. 8.1e-215;
  Matches  498;  Conservative   13;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||| |||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
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```
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:||||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:|||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||:|||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| |||||||||| ||| |||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 13
AAR91814
ID   AAR91814 standard; protein; 660 AA.
XX
AC   AAR91814;
XX
DT   26-NOV-1996  (first entry)
XX
DE   Hepatitis E virus strain SAR-55 ORF-2.
XX
KW   Hepatitis E virus; HEV; SAR-55 strain; enteric transmission;
KW   structural region; antigen; detection; antibody; vaccine; immunisation;
KW   infection.
XX
OS   Hepatitis E virus.
XX
PN   WO9610580-A2.
XX
PD   11-APR-1996.
XX
PF   03-OCT-1995;   95WO-US013102.
XX
PR   03-OCT-1994;   94US-00316765.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Tsarev SA,  Emerson SU,  Purcell RH;
XX
DR   WPI; 1996-209320/21.
DR   N-PSDB; AAT27394.
XX
PT   Isolated and purified hepatitis E virus strain SAR-55 DNA - encodes
PT   antigenic protein useful in diagnosis, prophylaxis and treatment of
PT   hepatitis E virus infection.
XX
PS   Claim 6; Page 13-15; 121pp; English.
XX
CC   The present sequence is the protein prod. of ORF-2 from the hepatitis E
CC   virus (HEV) strain SAR-55, which was implicated in an enterically
CC   transmitted non-A, non-B hepatitis in Pakistan. The protein encoded by
CC   the structural region of the virus (i.e. ORF-2), which is capable of
CC   forming HEV like particles, is useful for the detection of HEV antibodies
CC   (pref. IgG or IgM) in blood, plasma, sera, cerebrospinal fluid, tissue,
CC   urine or pleural fluid. The protein, and anti-HEV antibodies generated
CC   using the protein, can also be used in vaccines for immunising an animal
CC   against HEV infection. The protein is identified as a band of greater
CC   than 50 kD following SDS-PAGE of cell lysates of insect cells infected
CC   with a HEV ORF-2 contg. baculovirus, i.e. the claimed recombinant
CC   expression vectors pPIC9-1779, -1780 and -1781
XX

SQ   Sequence 660 AA;

  Query Match             95.3%;  Score 2575;  DB 2;  Length 660;
  Best Local Similarity   94.7%;  Pred. No. 1.8e-214;
  Matches  497;  Conservative   13;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| ||||||||||||||||||||||||||:|||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:||||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:|||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||:|||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| | ||||||| ||| |||||||||||| ||||
Db        592 PVSISAVAVLAPHSVLALLEDTMDYPARAHTFDDFCPECRPLGLQ 636


RESULT 14
AAW93386
ID   AAW93386 standard; protein; 660 AA.
XX
AC   AAW93386;
XX
DT   11-JUN-1999  (first entry)
XX
DE   Human HEV ORF 2 protein from strain Sar55.
XX
KW   Swine hepatitis E virus; HEV; cross-reaction; antibody; human; therapy;
KW   vaccine; immunise; infection; detection; diagnosis; prevention.
XX
OS   Hepatitis E virus.
XX
PN   WO9904029-A2.
XX
PD   28-JAN-1999.
XX
PF   17-JUL-1998;   98WO-US014665.
XX
PR   18-JUL-1997;   97US-0053069P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Meng X,  Emerson SU,  Purcell RH;
XX
DR   WPI; 1999-132270/11.
XX
PT   New isolated swine hepatitis E virus - used to develop products for the
```

```
PT   diagnosis, prevention and treatment of hepatitis E virus infection in
PT   mammals, particularly humans.
XX
PS   Example 1; Fig 3A; 70pp; English.
XX
CC   This invention describes a swine hepatitis E virus (HEV) and its natural
CC   mutants which are capable of cross-reacting with antibodies reactive with
CC   a human HEV strain or natural mutants. The HEV and the proteins can be
CC   used in vaccines for immunising against HEV infection. The swine HEV can
CC   be used in humans to prevent possible infection by human HEV. The swine
CC   HEV can also be used as a therapeutic treatment for infection by other
CC   strains of HEV. The swine HEV can also be used for the production of
CC   antibodies which can be used in therapy, detection and diagnosis. The
CC   products can also be used for determining the susceptibility of cells or
CC   organs to infection with swine HEV. The swine HEV is particularly useful
CC   for the development of agents for the prevention, treatment and detection
CC   of human HEV because it is not a human virus and thus can be handled both
CC   experimentally and clinically without fear of severe infection and/or
CC   contamination
XX
SQ   Sequence 660 AA;

  Query Match             95.3%;  Score 2575;  DB 2;  Length 660;
  Best Local Similarity   94.7%;  Pred. No. 1.8e-214;
  Matches  497;  Conservative   13;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:|||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||:|||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| | ||||||| ||| |||||||||||||| ||||
Db        592 PVSISAVAVLAPHSVLALLEDTMDYPARAHTFDDFCPECRPLGLQ 636


RESULT 15
AAW93388
ID   AAW93388 standard; protein; 660 AA.
XX
AC   AAW93388;
XX
DT   11-JUN-1999  (first entry)
XX
DE   Human HEV ORF 2 protein from strain KS2-87.
XX
KW   Swine hepatitis E virus; HEV; cross-reaction; antibody; human; therapy;
KW   vaccine; immunise; infection; detection; diagnosis; prevention.
XX
OS   Hepatitis E virus.
XX
PN   WO9904029-A2.
XX
PD   28-JAN-1999.
XX
PF   17-JUL-1998;   98WO-US014665.
XX
PR   18-JUL-1997;   97US-0053069P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Meng X,  Emerson SU,  Purcell RH;
XX
DR   WPI; 1999-132270/11.
XX
PT   New isolated swine hepatitis E virus - used to develop products for the
PT   diagnosis, prevention and treatment of hepatitis E virus infection in
PT   mammals, particularly humans.
XX
PS   Example 1; Fig 3A; 70pp; English.
XX
CC   This invention describes a swine hepatitis E virus (HEV) and its natural
CC   mutants which are capable of cross-reacting with antibodies reactive with
CC   a human HEV strain or natural mutants. The HEV and the proteins can be
CC   used in vaccines for immunising against HEV infection. The swine HEV can
CC   be used in humans to prevent possible infection by human HEV. The swine
CC   HEV can also be used as a therapeutic treatment for infection by other
CC   strains of HEV. The swine HEV can also be used for the production of
CC   antibodies which can be used in therapy, detection and diagnosis. The
CC   products can also be used for determining the susceptibility of cells or
CC   organs to infection with swine HEV. The swine HEV is particularly useful
CC   for the development of agents for the prevention, treatment and detection
CC   of human HEV because it is not a human virus and thus can be handled both
CC   experimentally and clinically without fear of severe infection and/or
CC   contamination
XX
SQ   Sequence 660 AA;

  Query Match             95.3%;  Score 2575;  DB 2;  Length 660;
  Best Local Similarity   94.7%;  Pred. No. 1.8e-214;
  Matches  497;  Conservative   13;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:|||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||:|||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531
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Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||| | ||||||||| ||| |||||||||||| ||||
Db        592 PVSISAVAVLTPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQ 636
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Search completed: July 14, 2005, 15:46:27
Job time : 44.4198 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 14, 2005, 01:31:43 ; Search time 38.3019 Seconds
(without alignments)
7019.016 Million cell updates/sec

Title: US-09-769-066-15_COPY_1_525
Perfect score: 2694
Sequence: 1 AVAPAHDTPPVPDVDSRGAI.....PARAHTFDDFCPECRPLGLQ 525

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2694	100.0	660	1	VST2_HEVBU	P29326 hepatitis e
2	2687	99.7	660	2	Q9E8G5	Q9e8g5 hepatitis e
3	2683	99.6	660	2	Q9W7W9	Q9w7w9 hepatitis e
4	2683	99.6	660	2	Q9WQA0	Q9wqa0 hepatitis e
5	2681	99.5	660	1	VST2_HEVPA	P33426 hepatitis e
6	2681	99.5	660	2	Q77EC8	Q77ec8 hepatitis e
7	2681	99.5	660	2	Q89468	Q89468 hepatitis e
8	2677	99.4	660	2	Q69419	Q69419 hepatitis e
9	2676	99.3	660	2	Q81871	Q81871 hepatitis e
10	2675	99.3	660	2	O91855	O91855 hepatitis e
11	2674	99.3	660	2	O91856	O91856 hepatitis e
12	2669	99.1	660	2	Q81878	Q81878 hepatitis e
13	2666	99.0	660	2	Q69411	Q69411 hepatitis e
14	2666	99.0	660	2	Q6XXV0	Q6xxv0 hepatitis e
15	2660	98.7	660	2	Q9WLL4	Q9wll4 hepatitis e
16	2656	98.6	660	2	Q68985	Q68985 hepatitis e
17	2655	98.6	659	2	Q8JT32	Q8jt32 hepatitis e
18	2653	98.5	660	1	VST2_HEVMY	Q04611 hepatitis e
19	2586	96.0	660	2	Q80IY5	Q80iy5 hepatitis e
20	2582	95.8	660	2	Q8JJM8	Q8jjm8 hepatitis e
21	2581	95.8	660	2	O36613	O36613 swine hepat
22	2581	95.8	660	2	Q6J8F7	Q6j8f7 hepatitis e
23	2580	95.8	660	2	Q8JJM4	Q8jjm4 hepatitis e
24	2578	95.7	660	2	Q8AZM3	Q8azm3 hepatitis e
25	2578	95.7	660	2	Q9YLQ9	Q9ylq9 hepatitis e
26	2575	95.6	660	2	Q6J8G3	Q6j8g3 hepatitis e
27	2575	95.6	660	2	Q80IR7	Q80ir7 hepatitis e
28	2574	95.5	660	2	Q8V729	Q8v729 swine hepat
29	2573	95.5	550	2	Q8JVV3	Q8jvv3 hepatitis e
30	2573	95.5	671	2	Q8JJM1	Q8jjm1 hepatitis e
31	2573	95.5	674	2	Q8JJN6	Q8jjn6 hepatitis e
32	2572	95.5	660	2	Q911I4	Q911i4 hepatitis e
33	2571	95.4	674	2	Q8JJN2	Q8jjn2 hepatitis e
34	2571	95.4	674	2	Q6BD83	Q6bd83 hepatitis e
35	2571	95.4	674	2	Q7TGF1	Q7tgf1 hepatitis e
36	2570	95.4	674	2	Q6BD78	Q6bd78 hepatitis e
37	2570	95.4	674	2	Q806D7	Q806d7 hepatitis e
38	2570	95.4	674	2	Q806E0	Q806e0 swine hepat
39	2570	95.4	674	2	Q80IR5	Q80ir5 hepatitis e
40	2568	95.3	660	2	Q9YLR2	Q9ylr2 hepatitis e
41	2567	95.3	660	2	Q8BB05	Q8bb05 swine hepat
42	2567	95.3	674	2	Q6PMR3	Q6pmr3 swine hepat
43	2543	94.4	672	2	Q9IVZ8	Q9ivz8 hepatitis e
44	2542.5	94.4	659	1	VST2_HEVME	Q03500 hepatitis e
45	2484	92.2	605	2	Q9YWL0	Q9ywl0 hepatitis e

ALIGNMENTS

RESULT 1
VST2_HEVBU
ID VST2_HEVBU STANDARD; PRT; 660 AA.
AC P29326;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Structural protein 2 precursor.
GN ORFNames=ORF2;
OS Hepatitis E virus (strain Burma) (HEV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=31767;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92024067; PubMed=1926770;
RA Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
RA Fry K.E., Reyes G.R.;
RT "Hepatitis E virus (HEV): molecular cloning and sequencing of the
RT full-length viral genome.";
RL Virology 185:120-131(1991).
CC -!- FUNCTION: Contains a high basic amino acid content suggesting that
CC it may be involved in the encapsidation of the genomic RNA by
CC effectively neutralizing the negatively charged RNA.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; M73218; AAA45736.1; -.
DR PIR; C40778; VHWWH2.
DR InterPro; IPR004261; SP2.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF03014; SP2; 1.
KW Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 660 Structural protein 2.
SQ SEQUENCE 660 AA; 70978 MW; 5832A013CCC4A61C CRC64;

Query Match 100.0%; Score 2694; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 1.5e-181;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231
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Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 2
Q9E8G5
ID Q9E8G5 PRELIMINARY; PRT; 660 AA.
AC Q9E8G5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Structural protein.
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Abb-2B;
RX MEDLINE=20271579; PubMed=10813471;
RA van Cuyck-Gandre H., Zhang H.Y., Tsarev S.A., Warren R.L.,
RA Caudill J.D., Snellings N.J., Begot L., Innis B.L., Longer C.F.;
RT "Phylogenetically distinct hepatitis E viruses in Pakistan.";
RL Am. J. Trop. Med. Hyg. 62:187-189(2000).
DR EMBL; AF185822; AAG16766.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70903 MW; 1F506BE3CFB3BACE CRC64;

Query Match 99.7%; Score 2687; DB 2; Length 660;
Best Local Similarity 99.8%; Pred. No. 4.7e-181;
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
```

RESULT 3
Q9W7W9
ID Q9W7W9 PRELIMINARY; PRT; 660 AA.
AC Q9W7W9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Structural protein 2 (Structural viral protein).
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HEV-Morocco;
RX MEDLINE=99107414; PubMed=9892396;
RX DOI=10.1002/(SICI)1096-9071(199902)57:2<126::AID-JMV7>3.3.CO;2-F;
RA Meng J., Cong M., Dai X., Pillot J., Purdy M.A., Fields H.A.,
RA Khudyakov Y.E.;
RT "Primary structure of open reading frame 2 and 3 of the hepatitis E
RT virus isolated from Morocco.";
RL J. Med. Virol. 57:126-133(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen G., Meng J.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF065061; AAD10627.1; -.
DR EMBL; AY230202; AAO72992.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70943 MW; 9719D30CCD932950 CRC64;

Query Match 99.6%; Score 2683; DB 2; Length 660;
Best Local Similarity 99.6%; Pred. No. 8.9e-181;
Matches 523; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291
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Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 4
Q9WQA0
ID   Q9WQA0      PRELIMINARY;      PRT;   660 AA.
AC   Q9WQA0;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   ORF-2.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99350000; PubMed=10423137;
RA   Arankalle V.A., Paranjape S., Emerson S.U., Purcell R.H.,
RA   Walimbe A.M.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from India (1976-
RT   1993).";
RL   J. Gen. Virol. 80:1691-1700(1999).
DR   EMBL; AF124407; AAD45493.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71040 MW;  03B72DDF0AB7B521 CRC64;

  Query Match             99.6%;  Score 2683;  DB 2;  Length 660;
  Best Local Similarity   99.6%;  Pred. No. 8.9e-181;
  Matches  523;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              ||||||||| |||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVFAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 5
VST2_HEVPA
ID   VST2_HEVPA     STANDARD;      PRT;   660 AA.
AC   P33426;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   Structural protein 2 precursor.
GN   ORFNames=ORF2;
OS   Hepatitis E virus (strain Pakistan) (HEV).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=33774;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92115700; PubMed=1731327;
RA   Tsarev S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J.,
RA   Malik I.A., Iqbal M., Purcell R.H.;
RT   "Characterization of a prototype strain of hepatitis E virus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).
CC   -!- FUNCTION: Contains a high basic amino acid content suggesting that
CC       it may be involved in the encapsidation of the genomic RNA by
CC       effectively neutralizing the negatively charged RNA.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M80581; AAA45727.1; -.
DR   InterPro; IPR004261; SP2.
DR   InterPro; IPR008975; Viral_cap_coat.
DR   Pfam; PF03014; SP2; 1.
KW   Signal.
FT   SIGNAL        1     22       By similarity.
FT   CHAIN        23    660       Structural protein 2.
SQ   SEQUENCE   660 AA;  70980 MW;  8085BC53CFB46FD3 CRC64;

  Query Match             99.5%;  Score 2681;  DB 1;  Length 660;
  Best Local Similarity   99.4%;  Pred. No. 1.2e-180;
  Matches  522;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
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Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525

Db        592 PVSISAVAVLAPHSVLALLEDTMDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 6
Q77EC8
ID Q77EC8 PRELIMINARY; PRT; 660 AA.
AC Q77EC8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Capsid protein.
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sar-55;
RX MEDLINE=21625046; PubMed=11742081; DOI=10.1073/pnas.251555098;
RA Emerson S.U., Zhang M., Meng X.-J., Nguyen H., St Claire M.,
RA Govindarajan S., Huang Y.K., Purcell R.H.;
RT "Recombinant hepatitis E virus genomes infectious for primates:
RT importance of capping and discovery of a cis-reactive element.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:15270-15275(2001).
DR EMBL; AF444003; AAL50059.1; -.
DR EMBL; AF444002; AAL50056.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70979 MW; 8085BC53CFB46FD3 CRC64;

Query Match 99.5%; Score 2681; DB 2; Length 660;
Best Local Similarity 99.4%; Pred. No. 1.2e-180;
Matches 522; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180

Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525

Db        592 PVSISAVAVLAPHSVLALLEDTMDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 7
Q89468
ID Q89468 PRELIMINARY; PRT; 660 AA.
AC Q89468;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Unnamed protein product (ORFs 1-3).
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RA Yin S.R., Purcell R.H., Emerson S.U.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K52-87;
RX MEDLINE=95176571; PubMed=7871758;
RA Yin S., Purcell R.H., Emerson S.U.;
RT "A new Chinese isolate of hepatitis E virus: comparison with strains
RT recovered from different geographical regions.";
RL Virus Genes 9:23-32(1994).
DR EMBL; L25547; AAA91080.1; -.
DR EMBL; L25595; AAA65490.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70979 MW; DC68116DCD639175 CRC64;

Query Match 99.5%; Score 2681; DB 2; Length 660;
Best Local Similarity 99.4%; Pred. No. 1.2e-180;
Matches 522; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180

Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
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Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||| |||||||||:|||||||||||||||||||||||
Db        592 PVSISAVAVLTPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQ 636


RESULT 8
Q69419
ID   Q69419      PRELIMINARY;      PRT;   660 AA.
AC   Q69419;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ORF1, ORF2 & ORF3.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   von Brunn A., Seebach J., Thyagarajan S.P., Mohanavalli B., Menon T.,
RA   Froesner G.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X99441; CAA67804.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70960 MW;  DAC3DF95F91689F8 CRC64;

  Query Match             99.4%;  Score 2677;  DB 2;  Length 660;
  Best Local Similarity   99.4%;  Pred. No. 2.4e-180;
  Matches  522;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              || ||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        412 LYRSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSALRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 9
Q81871
ID   Q81871      PRELIMINARY;      PRT;   660 AA.
AC   Q81871;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   ORF 2 precursor.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92024067; PubMed=1926770;
RA   Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
RA   Fry K.E., Reyes G.R.;
RT   "Hepatitis E virus (HEV): molecular cloning and sequencing of the
RT   full-length viral genome.";
RL   Virology 185:120-131(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92115700; PubMed=1731327;
RA   Tsarev S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J.,
RA   Malik I.A., Iqbal M., Purcell R.H.;
RT   "Characterization of a prototype strain of hepatitis E virus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92261377; PubMed=1584074;
RA   Uchida T., Suzuki K., Hayashi N., Iida F., Hara T., Oo S.S., Wang C.,
RA   Shikata T., Ichikawa M., Rikihisa T., Mizuno K., Win K.M.;
RT   "Hepatitis E virus: cDNA cloning and expression.";
RL   Microbiol. Immunol. 36:67-79(1992).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92335008; PubMed=1630924;
RA   Aye T.T., Uchida T., Ma M.Z., Iida F., Shikata T., Zhuang H.,
RA   Win K.M.;
RT   "Complete nucleotide sequence of a hepatitis E virus isolated from the
RT   Xinjiang epidemic (1986-1988) of China.";
RL   Nucleic Acids Res. 20:3512-3512(1992).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92271462; PubMed=1589964;
RA   Fry K.E., Tam A.W., Smith M.W., Kim J.P., Luk K.-C., Young L.M.,
RA   Piatak M., Feldman R.A., Yun K.Y., Purdy M.A., McCaustland K.A.,
RA   Bradley D.W., Reyes G.R.;
RT   "Hepatitis E virus (HEV): strain variation in the nonstructural gene
RT   region encoding consensus motifs for an RNA-dependent RNA polymerase
RT   and an ATP/GTP binding site.";
RL   Virus Genes 6:173-185(1992).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93348763; PubMed=8346669; DOI=10.1016/0168-1702(93)90024-H;
RA   Bi S-L., Purdy M.A., McCaustland K.A., Margolis H.S., Bradley D.W.;
RT   "The sequence of hepatitis E virus isolated directly from a single
RT   source during an outbreak in China.";
RL   Virus Res. 28:233-247(1993).
```

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DR   EMBL; L08816; AAA03191.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
KW   Signal.
FT   SIGNAL       1     19       Potential.
SQ   SEQUENCE   660 AA;  70979 MW;  B58F23955FDD6614 CRC64;
```

Query Match 99.3%; Score 2676; DB 2; Length 660;
Best Local Similarity 99.2%; Pred. No. 2.8e-180;
Matches 521; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASEHVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTTQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||:|||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 10
O91855
ID   O91855      PRELIMINARY;      PRT;   660 AA.
AC   O91855;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Structural protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=93-Egypt;
RX   MEDLINE=99105430; PubMed=9890424;
RX   DOI=10.1002/(SICI)1096-9071(199901)57:1<68::AID-JMV10>3.0.CO;2-E;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
RL   J. Med. Virol. 57:68-74(1999).
DR   EMBL; AF051351; AAC35761.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71039 MW;  044FF5EA7C492791 CRC64;
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Query Match 99.3%; Score 2675; DB 2; Length 660;
Best Local Similarity 99.0%; Pred. No. 3.3e-180;
Matches 520; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||:||||:|||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTSSDQLLIENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 11
O91856
ID   O91856      PRELIMINARY;      PRT;   660 AA.
AC   O91856;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Structural protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=94-Egypt;
RX   MEDLINE=99105430; PubMed=9890424;
RX   DOI=10.1002/(SICI)1096-9071(199901)57:1<68::AID-JMV10>3.0.CO;2-E;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
RL   J. Med. Virol. 57:68-74(1999).
DR   EMBL; AF051352; AAC35764.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71025 MW;  16C560FA16941F2A CRC64;
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Query Match 99.3%; Score 2674; DB 2; Length 660;
Best Local Similarity 99.0%; Pred. No. 3.9e-180;

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  Matches  520;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||:||| ||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLIENATGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 12
Q81878
ID   Q81878      PRELIMINARY;      PRT;   660 AA.
AC   Q81878;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Complete genome sequence.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Uchida T.;
RL   Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; D11093; BAA01867.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70937 MW;  5412313F1A2EF4A9 CRC64;

  Query Match             99.1%;  Score 2669;  DB 2;  Length 660;
  Best Local Similarity   98.9%;  Pred. No. 8.7e-180;
  Matches  519;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYGISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGTDGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YCKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||:|||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQ 636


RESULT 13
Q69411
ID   Q69411      PRELIMINARY;      PRT;   660 AA.
AC   Q69411;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Structural protein.
GN   Name=ORF2;
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Donati M.C., Fagan E.A., Harrison T.J.;
RT   "Sequence analysis of full length HEV clones derived directly from
RT   human liver in fulminant hepatitis E.";
RL   (In) Rizzetto M., Purcell R.H., Gerin J.L., Verme G (eds.);
RL   VIRAL HEPATITIS AND LIVER DISEASE, pp.313-316, Edizioni Minerva
RL   Medica, Torino (1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Harrison T.J.;
RL   Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X98292; CAA66937.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71024 MW;  F37E3FEFF7A4EAD1 CRC64;

  Query Match             99.0%;  Score 2666;  DB 2;  Length 660;
  Best Local Similarity   98.7%;  Pred. No. 1.4e-179;
  Matches  518;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSPVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGLPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
                |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALEFEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
                ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
                ||:||||||||||||||||:||||||||||||||||||||||||
Db        592 PVAISAVAVLAPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQ 636


RESULT 14
Q6XXV0
ID   Q6XXV0      PRELIMINARY;      PRT;   660 AA.
AC   Q6XXV0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Structural protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RX   MEDLINE=98071272; PubMed=9407381;
RX   DOI=10.1002/(SICI)1096-9071(199712)53:4<340::AID-JMV5>3.0.CO;2-7;
RA   van Cuyck-Gandre H., Zhang H.Y., Tsarev S.A., Clements N.J.,
RA   Cohen S.J., Caudill J.D., Buisson Y., Coursaget P., Warren R.L.,
RA   Longer C.F.;
RT   "Characterization of hepatitis E virus (HEV) from Algeria and Chad by
RT   partial genome sequence.";
RL   J. Med. Virol. 53:340-347(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RX   MEDLINE=99105430; PubMed=9890424;
RX   DOI=10.1002/(SICI)1096-9071(199901)57:1<68::AID-JMV10>3.0.CO;2-E;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
RL   J. Med. Virol. 57:68-74(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RX   MEDLINE=22987819; PubMed=14625096; DOI=10.1016/S0928-8244(03)00241-4;
RA   van Cuyck H., Juge F., Roques P.;
RT   "Phylogenetic analysis of the first complete hepatitis E virus (HEV)
RT   genome from Africa.";
RL   FEMS Immunol. Med. Microbiol. 39:133-139(2003).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RA   Van Cuyck-Gandre H., Zhang H.Y., Tsarev S.A., Clements N.J.,
RA   Cohen S.J., Caudill J.D., Buisson Y., Coursaget P., Warren R.L.,
RA   Longer C.F.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RA   van Cuyck H., Roberston D., Juge F., Roques P., Lemey P.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY204877; AAB61825.2; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70949 MW;  EA56732D458D0AB1 CRC64;

  Query Match             99.0%;  Score 2666;  DB 2;  Length 660;
  Best Local Similarity   98.9%;  Pred. No. 1.4e-179;
  Matches  519;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVSDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
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DT   01-NOV-1999 (TrEMBLrel. 12, Created)
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DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Capsid protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
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RP   SEQUENCE FROM N.A.
RC   STRAIN=TK15/92;
RX   MEDLINE=99049628; PubMed=9833882; DOI=10.1016/S0168-1702(98)00079-3;
RA   Gouvea V., Snellings N., Popek M.J., Longer C.F., Innis B.L.;
RT   "Hepatitis E virus: complete genome sequence and phylogenetic analysis
RT   of a Nepali isolate.";
RL   Virus Res. 57:21-26(1998).
DR   EMBL; AF051830; AAC97188.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
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SQ   SEQUENCE   660 AA;  70798 MW;  A04C0185ACC085DB CRC64;

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  Best Local Similarity   99.0%;  Pred. No. 3.8e-179;
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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
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Search completed: July 14, 2005, 15:50:27
Job time : 41.3019 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 14, 2005, 15:53:09 ; Search time 4650 Seconds
(without alignments)
5720.842 Million cell updates/sec

Title: US-09-769-066-16
Perfect score: 2819
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2792.5	99.1	1980	6	I73140	I73140 Sequence 2
3	2792.5	99.1	2055	6	AR002161	AR002161 Sequence
4	2792.5	99.1	2055	6	AR170405	AR170405 Sequence
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8	2792.5	99.1	7171	6	AR150916	AR150916 Sequence
9	2792.5	99.1	7171	6	AR207634	AR207634 Sequence
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11	2792.5	99.1	7180	14	HPENSSP	M74506 Hepatitis E
12	2694	95.6	1647	6	E17105	E17105 DNA encodin
13	2694	95.6	1686	6	AR278920	AR278920 Sequence
14	2694	95.6	1983	6	E17107	E17107 Hepatitis E
15	2694	95.6	1984	6	AR278906	AR278906 Sequence
16	2694	95.6	7143	14	AF185822	AF185822 Hepatitis
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ALIGNMENTS

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LOCUS AR170407 1644 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 4 from patent US 6291641.
ACCESSION AR170407
VERSION AR170407.1 GI:17908366
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1644)
AUTHORS Fuerst,T.R., McAtee,C.Patrick., Yarbough,P.O. and Zhang,Y.-F.
TITLE Hepatitis E virus antigens and uses therefor
JOURNAL Patent: US 6291641-A 4 18-SEP-2001;
FEATURES Location/Qualifiers
source 1. .1644
/organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity:	99.45%	Mismatches:	2
Query Match:	99.06%	Indels:	1
DB:	6	Gaps:	1

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US-09-769-066-16 (1-549) x AR170407 (1-1644)

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Db        241 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 300

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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ACCESSION   I73140
VERSION     I73140.1  GI:3009279
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1980)
  AUTHORS   Reyes,G.R., Tam,A.W. and Yarbough,P.O.
  TITLE     Hepatitis E virus peptides and methods
  JOURNAL   Patent: US 5686239-A 2 11-NOV-1997;
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Query Match:            99.06%          Indels:         1
DB:                     6               Gaps:           1

US-09-769-066-16 (1-549) x I73140 (1-1980)

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Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180

Db        814 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        874 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db        934 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 990

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db        991 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1050

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Db       1051 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1110

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Db       1111 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1170

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db       1171 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1230

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320

Db       1231 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1290

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db       1291 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1350

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1351 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1410

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1411 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1470

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Db       1471 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1530

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420

Db       1531 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1590

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1591 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1650

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Db       1711 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1770

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Db       1771 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1830

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1831 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1890

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1891 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1950

Qy        541 ValLysValGlyLysThrArgGluLeu 549

Db       1951 GTTAAGGTGGGTAAAACTCGGGAGTTG 1977
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RESULT 3
AR002161
LOCUS AR002161 2055 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 4 from patent US 5741490.
ACCESSION AR002161
VERSION AR002161.1 GI:3963715
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2055)
AUTHORS Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W., Krawczynski,K.Z. and Yarbough,P.D.
TITLE Hepatitis E virus vaccine and method
JOURNAL Patent: US 5741490-A 4 21-APR-1998;
FEATURES Location/Qualifiers
source 1. .2055
/organism="unknown"
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ORIGIN

Alignment Scores:

Pred. No.:	6.8e-189	Length:	2055
Score:	2792.50	Matches:	546
Percent Similarity:	99.45%	Conservative:	0
Best Local Similarity:	99.45%	Mismatches:	2
Query Match:	99.06%	Indels:	1
DB:	6	Gaps:	1

US-09-769-066-16 (1-549) x AR002161 (1-2055)

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Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20

Db        334 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
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Db        394 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60

Db        454 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

Db        514 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        574 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        634 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db        694 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db        754 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180

Db        814 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        874 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db        934 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 990

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db        991 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1050

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260

Db       1051 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1110

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db       1111 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1170

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db       1171 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1230

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320

Db       1231 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1290

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db       1291 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1350

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1351 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1410

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1411 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1470

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1471 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1530

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420

Db       1531 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1590

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1591 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1650

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460

Db       1651 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1710

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480

Db       1711 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1770

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuGluGlu 500

Db       1771 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1830

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1831 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1890

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1891 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1950

Qy        541 ValLysValGlyLysThrArgGluLeu 549

Db       1951 GTTAAGGTGGGTAAAACTCGGGAGTTG 1977
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RESULT 4
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LOCUS AR170405 2055 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 2 from patent US 6291641.
ACCESSION AR170405
VERSION AR170405.1 GI:17908364
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2055)
AUTHORS Fuerst,T.R., McAtee,C.Patrick., Yarbough,P.O. and Zhang,Y.-F.
TITLE Hepatitis E virus antigens and uses therefor
JOURNAL Patent: US 6291641-A 2 18-SEP-2001;
FEATURES Location/Qualifiers
source 1. .2055
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:

Pred. No.:	6.8e-189	Length:	2055
Score:	2792.50	Matches:	546
Percent Similarity:	99.45%	Conservative:	0
Best Local Similarity:	99.45%	Mismatches:	2
Query Match:	99.06%	Indels:	1
DB:	6	Gaps:	1

US-09-769-066-16 (1-549) x AR170405 (1-2055)

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Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20

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Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40

Db        394 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
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Db        454 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

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Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        634 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db        694 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db        754 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180

Db        814 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        874 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db        934 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 990

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db        991 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1050

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Db       1051 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1110

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Db       1231 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1290

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db       1291 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1350

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1351 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1410

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1411 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1470

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1471 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1530

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Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480

Db       1711 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1770

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500

Db       1771 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1830

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1831 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1890

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1891 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1950

Qy        541 ValLysValGlyLysThrArgGluLeu 549

Db       1951 GTTAAGGTGGGTAAAACTCGGGAGTTG 1977
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DEFINITION  Sequence 4 from patent US 6455492.
ACCESSION   AR232466
VERSION     AR232466.1  GI:27274535
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2055)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.O.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 6455492-A 4 24-SEP-2002;
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:                6.8e-189        Length:          2055
Score:                    2792.50         Matches:         546
Percent Similarity:       99.45%          Conservative:    0
Best Local Similarity:    99.45%          Mismatches:      2
Query Match:              99.06%          Indels:          1
DB:                       6               Gaps:            1

US-09-769-066-16 (1-549) x AR232466 (1-2055)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20

Db        334 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40

Db        394 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60

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Qy        81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db       574 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 633

Qy       101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       634 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 693

Qy       121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       694 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 753

Qy       141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       754 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 813

Qy       161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
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Db       814 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 873

Qy       181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Qy       201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Db       934 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 990

Qy       221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Db       991 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1050

Qy       241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
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Qy       281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Qy       301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1231 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1290

Qy       321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1291 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1350

Qy       341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1351 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1410

Qy       361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1411 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1470

Qy       381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1471 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1530

Qy       401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1531 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1590

Qy       421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1591 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1650

Qy       441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1651 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1710

Qy       461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1711 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1770

Qy       481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1771 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1830

Qy       501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1831 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1890

Qy       521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1891 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1950

Qy       541 ValLysValGlyLysThrArgGluLeu 549
             |||||||||||||||||||||||||||
Db      1951 GTTAAGGTGGGTAAAACTCGGGAGTTG 1977

RESULT 6
AR002159
LOCUS       AR002159               2100 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 2 from patent US 5741490.
ACCESSION   AR002159
VERSION     AR002159.1  GI:3963713
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2100)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.D.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 5741490-A 2 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .2100
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              7.01e-189       Length:         2100
Score:                  2792.50         Matches:        546
Percent Similarity:     99.45%          Conservative:   0
Best Local Similarity:  99.45%          Mismatches:     2
Query Match:            99.06%          Indels:         1
DB:                     6               Gaps:           1

US-09-769-066-16 (1-549) x AR002159 (1-2100)

Qy         1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       379 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 438

Qy        21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       439 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 498

Qy        41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       499 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 558

Qy        61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       559 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 618
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Qy        81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       619 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 678

Qy       101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       679 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 738

Qy       121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       739 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 798

Qy       141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Db       799 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 858

Qy       161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       859 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 918

Qy       181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       919 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 978

Qy       201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       979 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 1035

Qy       221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1036 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1095

Qy       241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
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Db      1096 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1155

Qy       261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1156 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1215

Qy       281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1216 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1275

Qy       301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1276 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1335

Qy       321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1336 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1395

Qy       341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1396 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1455

Qy       361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1456 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1515

Qy       381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1516 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1575

Qy       401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1576 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1635

Qy       421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1636 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1695

Qy       441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1696 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1755

Qy       461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1756 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1815

Qy       481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1816 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1875

Qy       501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1876 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1935

Qy       521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1936 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1995

Qy       541 ValLysValGlyLysThrArgGluLeu 549
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Db      1996 GTTAAGGTGGGTAAAACTCGGGAGTTG 2022
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RESULT 7
AR232464
LOCUS AR232464 2100 bp mRNA linear PAT 20-DEC-2002
DEFINITION Sequence 2 from patent US 6455492.
ACCESSION AR232464
VERSION AR232464.1 GI:27274533
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2100)
AUTHORS Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W., Krawczynski,K.Z. and Yarbough,P.O.
TITLE Hepatitis E virus vaccine and method
JOURNAL Patent: US 6455492-A 2 24-SEP-2002;
FEATURES Location/Qualifiers
source 1. .2100
/organism="unknown"
/mol_type="mRNA"
ORIGIN

Alignment Scores:

Pred. No.:	7.01e-189	Length:	2100
Score:	2792.50	Matches:	546
Percent Similarity:	99.45%	Conservative:	0
Best Local Similarity:	99.45%	Mismatches:	2
Query Match:	99.06%	Indels:	1
DB:	6	Gaps:	1

US-09-769-066-16 (1-549) x AR232464 (1-2100)

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Qy         1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       379 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 438

Qy        21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       439 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 498

Qy        41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       499 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 558

Qy        61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       559 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 618

Qy        81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        619 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 678

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 738

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 798

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 858

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 918

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Db        919 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 978

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 1035

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Db       1036 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1095

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1155

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1215

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1275

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1335

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1395

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1396 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1455

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1515

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1516 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1575

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1576 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1635

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1636 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1695

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1696 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1755

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1756 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1815

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1816 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1875

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1876 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1935

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1936 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1995

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1996 GTTAAGGTGGGTAAAACTCGGGAGTTG 2022

RESULT 8
AR150916
LOCUS       AR150916               7171 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 10 from patent US 6229005.
ACCESSION   AR150916
VERSION     AR150916.1  GI:15115507
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 7171)
  AUTHORS   Reyes,G.R., Yarbough,P.O., Bradley,D.W., Krawczynski,K.Z., Tam,A.W.
            and Fry,K.E.
  TITLE     DNA sequences of enterically transmitted non-A/non-B hepatitis
            viral agent
  JOURNAL   Patent: US 6229005-A 10 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .7171
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              3.91e-188       Length:         7171
Score:                  2792.50         Matches:        546
Percent Similarity:     99.45%          Conservative:   0
Best Local Similarity:  99.45%          Mismatches:     2
Query Match:            99.06%          Indels:         1
DB:                     6               Gaps:           1

US-09-769-066-16 (1-549) x AR150916 (1-7171)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5450 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 5509

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5510 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 5569

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5570 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 5629

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5630 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 5689

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5690 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 5749
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Qy       101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
Db      5750 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 5809

Qy       121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
Db      5810 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 5869

Qy       141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
Db      5870 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 5929

Qy       161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
Db      5930 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 5989

Qy       181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
Db      5990 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 6049

Qy       201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
Db      6050 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 6106

Qy       221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Qy       241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
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Qy       261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Qy       301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
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Qy       321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Qy       341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Qy       361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
Db      6527 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 6586

Qy       381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
Db      6587 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 6646

Qy       401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
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Qy       421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Qy       461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
Db      6827 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 6886

Qy       481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
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Qy       501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
Db      6947 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 7006

Qy       521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
Db      7007 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 7066

Qy       541 ValLysValGlyLysThrArgGluLeu 549
Db      7067 GTTAAGGTGGGTAAAACTCGGGAGTTG 7093
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RESULT 9
AR207634

LOCUS	AR207634	7171 bp DNA linear	PAT 20-JUN-2002
DEFINITION	Sequence 10 from patent US 6379891.		
ACCESSION	AR207634		
VERSION	AR207634.1 GI:21507439		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
	Unclassified.		
REFERENCE	1 (bases 1 to 7171)		
AUTHORS	Reyes,G.R., Yarbough,P.O., Bradley,D.W., Krawczynski,K.Z., Tam,A. and Fry,K.E.		
TITLE	Method of detecting HEV infection		
JOURNAL	Patent: US 6379891-A 10 30-APR-2002;		
FEATURES	Location/Qualifiers		
source	1. .7171		
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ORIGIN			

Alignment Scores:

Pred. No.:	3.91e-188	Length:	7171
Score:	2792.50	Matches:	546
Percent Similarity:	99.45%	Conservative:	0
Best Local Similarity:	99.45%	Mismatches:	2
Query Match:	99.06%	Indels:	1
DB:	6	Gaps:	1

US-09-769-066-16 (1-549) x AR207634 (1-7171)

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Qy        21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
Db      5510 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 5569

Qy        41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
Db      5570 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 5629

Qy        61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
Db      5630 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 5689

Qy        81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
Db      5690 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 5749

Qy       101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
Db      5750 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 5809
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Qy       121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
Db      5810 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 5869

Qy       141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
Db      5870 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 5929

Qy       161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
Db      5930 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 5989

Qy       181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
Db      5990 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 6049

Qy       201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
Db      6050 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 6106

Qy       221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
Db      6107 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 6166

Qy       241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
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Qy       261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
Db      6227 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 6286

Qy       281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Db      6347 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 6406

Qy       321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
Db      6407 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 6466

Qy       341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Qy       381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
Db      6587 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 6646

Qy       401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
Db      6647 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 6706

Qy       421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
Db      6707 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 6766

Qy       441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
Db      6767 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 6826

Qy       461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
Db      6827 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 6886

Qy       481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuGluGlu 500
Db      6887 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 6946

Qy       501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
Db      6947 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 7006

Qy       521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
Db      7007 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 7066

Qy       541 ValLysValGlyLysThrArgGluLeu 549
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RESULT 10
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LOCUS       BD189811               7180 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Polynucleotide probe and primer derived a hepatitis E virus strain
            from japanese, chip having them, kit having them, and methods of
            detecting a hepatitis E virus with them.
ACCESSION   BD189811
VERSION     BD189811.1  GI:32999550
KEYWORDS    WO 03000887-A/46.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 7180)
  AUTHORS   Takahashi,K., Mishiro,S., Ota,Y., Hashimoto,M. and Maekubo,H.
  TITLE     Polynucleotide probe and primer derived a hepatitis E virus strain
            from japanese, chip having them, kit having them, and methods of
            detecting a hepatitis E virus with them
  JOURNAL   Patent: WO 03000887-A 46 03-JAN-2003;
            TOSHIBA CORP,KAZUAKI TAKAHASHI,SHUNJI MISHIRO,YASUHIKO OTA, MICHIE
            HASHIMOTO,HIROSHI MAEKUBO
COMMENT     OS   Hepatitis E virus Mexico(M74506)
            PN   WO 03000887-A/46
            PD   03-JAN-2003
            PF   25-JUN-2002 WO 2002JP006365
            PR   25-JUN-2001 JP 01P   191837
            PI   KAZUAKI TAKAHASHI,SHUNJI MISHIRO,YASUHIKO
            OTA,MICHIE HASHIMOTO,
            PI   HIROSHI MAEKUBO
            PC   C12N15/09,C12Q1/68,G01N33/53
            CC   Polynucleotide probe and primer derived a hepatitis E virus
            CC           strain from
            CC   japanese, chip having them, kit having them, and methods of
            CC           detecting a
            CC   hepatitis E virus with them
            FH   Key             Location/Qualifiers
            FT   source          1. .7180
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FEATURES             Location/Qualifiers
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Alignment Scores:

Pred. No.:	3.91e-188	Length:	7180
Score:	2792.50	Matches:	546
Percent Similarity:	99.45%	Conservative:	0
Best Local Similarity:	99.45%	Mismatches:	2
Query Match:	99.06%	Indels:	1
DB:	6	Gaps:	1

US-09-769-066-16 (1-549) x BD189811 (1-7180)

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```

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Qy        21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
Db      5510 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 5569

Qy        41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
Db      5570 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 5629

Qy        61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
Db      5630 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 5689

Qy        81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Qy       101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
Db      5750 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 5809

Qy       121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
Db      5810 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 5869

Qy       141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
Db      5870 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 5929

Qy       161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
Db      5930 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 5989

Qy       181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
Db      5990 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 6049

Qy       201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
Db      6050 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 6106

Qy       221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Qy       241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
Db      6167 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 6226

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Db      6347 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 6406

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Qy       341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
Db      6467 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 6526

Qy       361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
Db      6527 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 6586

Qy       381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db      6947 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 7006

Qy       521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
Db      7007 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 7066

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RESULT 11
HPENSSP
LOCUS       HPENSSP                 7180 bp ss-RNA     linear   VRL 02-AUG-1993
DEFINITION  Hepatitis E virus (mexican strain) structural proteins and a
            nonstructural polyprotein genes, complete cds.
ACCESSION   M74506
VERSION     M74506.1  GI:330017
KEYWORDS    nonstructural protein; structural protein.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 7180)
  AUTHORS   Huang,C.C., Nguyen,D., Fernandez,J., Yun,K.Y., Fry,K.E.,
            Bradley,D.W., Tam,A.W. and Reyes,G.R.
  TITLE     Molecular cloning and sequencing of the Mexico isolate of hepatitis
            E virus (HEV)
  JOURNAL   Virology 191 (2), 550-558 (1992)
  MEDLINE   93079857
   PUBMED   1448913
COMMENT     Original source text: Hepatitis E virus cDNA to genomic RNA.
FEATURES             Location/Qualifiers
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                     NPPLPLQDGTNTHIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTT
                     PTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLV
                     MLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHSARGA
                     DGTAELTTTAATRFMKDLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGG
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                     PTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQA
                     VARSLDWSKVTLDGRPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASD
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ORIGIN

Alignment Scores:
Pred. No.:              3.91e-188       Length:         7180
Score:                  2792.50         Matches:        546
Percent Similarity:     99.45%          Conservative:   0
Best Local Similarity:  99.45%          Mismatches:     2
Query Match:            99.06%          Indels:         1
DB:                     14              Gaps:           1

US-09-769-066-16 (1-549) x HPENSSP (1-7180)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5450 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 5509

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5510 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 5569

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5570 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 5629

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5630 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 5689

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5690 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 5749

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5750 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 5809

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5810 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 5869

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5870 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 5929

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
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Db       5930 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 5989

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5990 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 6049

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6050 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 6106

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6107 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 6166

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6167 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 6226

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6227 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 6286

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6287 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 6346

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6347 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 6406

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6407 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 6466

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6467 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 6526

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6527 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 6586

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       6587 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 6646

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
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Db       6647 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 6706

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6707 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 6766

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6767 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 6826

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6827 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 6886

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
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Db       6887 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 6946

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6947 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 7006

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7007 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 7066

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       7067 GTTAAGGTGGGTAAAACTCGGGAGTTG 7093

RESULT 12
E17105
LOCUS       E17105                  1647 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  DNA encoding HEV hollow particle.
ACCESSION   E17105
VERSION     E17105.1  GI:5711788
KEYWORDS    JP 1998234383-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1647)
  AUTHORS   Takeda,N., Ri,T. and Miyamura,T.
  TITLE     HEPATITIS E VIRUS HOLLOW PARTICLE, GENE ENCODING THE SAME AND
            PREPARATION OF RECOMBINATION VECTOR CONTAINING THE GENE AND
            UTILIZATION OF THE RECOMBINATION VECTOR
  JOURNAL   Patent: JP 1998234383-A 1 08-SEP-1998;
            DENKA SEIKEN CO LTD, KOKURITSU KANSENSHIYOU KENKYUSHO
COMMENT     OS   Hepatitis E virus
            PN   JP 1998234383-A/1
            PD   08-SEP-1998
            PF   28-FEB-1997 JP 1997062445
            PI   TAKEDA NAOKAZU, RI TENSEI, MIYAMURA TATSUO
            PC   C12N15/09,C07K14/08,C12N5/10,C12P21/02;
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
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            FT                   /organism='Hepatitis E virus' FT   mat_peptide
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FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              4.98e-182       Length:         1647
Score:                  2694.00         Matches:        521
Percent Similarity:     97.45%          Conservative:   14
Best Local Similarity:  94.90%          Mismatches:     14

Query Match:            95.57%          Indels:         0
DB:                     6               Gaps:           0

US-09-769-066-16 (1-549) x E17105 (1-1647)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
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Db          1 GCGGTCGCTCCAGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCTCGCGGCGCCATC 60

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db         61 TTGCGCCGGCAGTATAATCTATCAACATCTCCCCTCACCTCTTCCGTGGCCACCGGCACT 120

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||:::|||  ||||||||||||||||||||||||
Db        121 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAAT 180

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 240

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTC 300

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 360

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 420

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 480

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAACACA 540

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 600

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 660

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAG 720

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||:::|||||||      ||||||||||||||:::||||||||||||||||||||
Db        721 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 780

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGTTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 840

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCGGCCAATGGCGAGCCGACTGTTAAG 900

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        901 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 960

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||:::||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGG 1020
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Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1080

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1140

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1200

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||:::|||||||||||||||||||||||||||||   |||||:::|||
Db       1201 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1260

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1320

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||:::
Db       1321 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1380

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||   |||||||||||
Db       1381 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1440

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||:::|||||||||   |||||||||||||||   |||||||||||||||||||||
Db       1441 CCCGTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1500

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              |||||||   |||||||||   ||||||||||||||||||||||||||||||||||||||||
Db       1501 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1560

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CCTCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1620

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              :::|||||||||||||||||||||||||
Db       1621 ATGAAGGTGGGTAAAACTCGGGAGTTA 1647
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RESULT 13
AR278920
LOCUS       AR278920                1686 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 19 from patent US 6514690.
ACCESSION   AR278920
VERSION     AR278920.1  GI:29713554
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1686)
  AUTHORS   Li,F., Hui,Z., Anderson,D.A., Logarnini,S.A. and Torresi,J.
  TITLE     Immunoreactive antigens of Hepatitis E Virus
  JOURNAL   Patent: US 6514690-A 19 04-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .1686
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ORIGIN

Alignment Scores:
Pred. No.:              5.15e-182       Length:         1686
Score:                  2694.00         Matches:        521
Percent Similarity:     97.45%          Conservative:   14
Best Local Similarity:  94.90%          Mismatches:     14
Query Match:            95.57%          Indels:         0
DB:                     6               Gaps:           0

US-09-769-066-16 (1-549) x AR278920 (1-1686)
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Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              |||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         38 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 97

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db         98 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 157

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
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Db        158 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 217

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 277

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db        278 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 337

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        338 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 397

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Db        398 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 457

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Db        458 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 517

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
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Db        518 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 577

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Db        578 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 637

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 697

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 CGTCGCGGTGCAGATGGGACTGCCGAGCTTACCACCACGGCTGCTACCCGCTTCATGAAG 757

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||:::|||||||       ||||||||||||||:::|||||||||||||||||||||
Db        758 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 817

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        818 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 877

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Db        878 GGTGGCCAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 937

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db        938 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 997

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Db        998 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1057

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Db       1058 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1117
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Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Db       1118 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1177

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       1178 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1237

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||:::|||||||||||||||||||||||||||||   |||::::::|||
Db       1238 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1297

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1298 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1357

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||:::
Db       1358 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1417

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
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Db       1418 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1477

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
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Db       1478 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCCGCGCTAGCATTGCTTGAG 1537

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||   |||||||||   ||||||||||||||||||||||||||||||||||||||||
Db       1538 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1597

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1598 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1657

Qy        541 ValLysValGlyLysThrArgGluLeu 549
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Db       1658 ATGAAGGTGGGTAAAACTCGGGAGTTA 1684
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RESULT 14
E17107
LOCUS E17107 1983 bp DNA linear PAT 28-JUL-1999
DEFINITION Hepatitis E virus ORF2.
ACCESSION E17107
VERSION E17107.1 GI:5711790
KEYWORDS JP 1998234383-A/3.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 1983)
AUTHORS Takeda,N., Ri,T. and Miyamura,T.
TITLE HEPATITIS E VIRUS HOLLOW PARTICLE, GENE ENCODING THE SAME AND PREPARATION OF RECOMBINATION VECTOR CONTAINING THE GENE AND UTILIZATION OF THE RECOMBINATION VECTOR
JOURNAL Patent: JP 1998234383-A 3 08-SEP-1998; DENKA SEIKEN CO LTD, KOKURITSU KANSENSHIYOU KENKYUSHO
COMMENT OS Hepatitis E virus
PN JP 1998234383-A/3
PD 08-SEP-1998
PF 28-FEB-1997 JP 1997062445
PI TAKEDA NAOKAZU, RI TENSEI, MIYAMURA TATSUO
PC C12N15/09,C07K14/08,C12N5/10,C12P21/02;
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FH
FT source 1. .1983
FT /organism='Hepatitis E virus' FT CDS
1. .1983
FT /product='structural protein'.
FEATURES Location/Qualifiers
source 1. .1983
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN

Alignment Scores:

Pred. No.:	6.46e-182	Length:	1983
Score:	2694.00	Matches:	521
Percent Similarity:	97.45%	Conservative:	14
Best Local Similarity:	94.90%	Mismatches:	14
Query Match:	95.57%	Indels:	0
DB:	6	Gaps:	0

US-09-769-066-16 (1-549) x E17107 (1-1983)

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Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        334 GCGGTCGCTCCAGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCTCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        394 TTGCGCCGGCAGTATAATCTATCAACATCTCCCCTCACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||:::|||   ||||||||||||||||||||||||||||
Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
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Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Db        754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
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Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAACACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Db        874 CCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Db        934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAG 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||:::||||||      ||||||||||||||:::|||||||||||||||||||||
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db       1114 CTGTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCGGCCAATGGCGAGCCGACTGTTAAG 1233

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Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||:::|||||||||||||||||||||||||||   |||:::::|||
Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||:::
Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
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Db       1774 CCCGTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||   |||||||||   ||||||||||||||||||||||||||||||||||||||
Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
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Db       1894 CCTCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 ValLysValGlyLysThrArgGluLeu 549
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RESULT 15
AR278906
LOCUS       AR278906                1984 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 1 from patent US 6514690.
ACCESSION   AR278906
VERSION     AR278906.1  GI:29713540
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1984)
  AUTHORS   Li,F., Hui,Z., Anderson,D.A., Logarnini,S.A. and Torresi,J.
  TITLE     Immunoreactive antigens of Hepatitis E Virus
  JOURNAL   Patent: US 6514690-A 1 04-FEB-2003;
FEATURES             Location/Qualifiers
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Alignment Scores:
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Score:                    2694.00        Matches:         521
Percent Similarity:       97.45%         Conservative:    14
Best Local Similarity:    94.90%         Mismatches:      14
Query Match:              95.57%         Indels:          0
DB:                       6              Gaps:            0

US-09-769-066-16 (1-549) x AR278906 (1-1984)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
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Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              |||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        394 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
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Db        454 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
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Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db        574 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Db        754 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
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Db        814 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Db        934 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 993

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Db        994 CGTCGCGGTGCAGATGGGACTGCCGAGCTTACCACCACGGCTGCTACCCGCTTCATGAAG 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
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Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db       1114 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Db       1174 GGTGGCCAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
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Db       1234 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db       1294 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1354 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1414 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1474 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420

Db       1534 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1594 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460

Db       1654 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480

Db       1714 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500

Db       1774 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCCGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1834 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1893

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1894 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 ValLysValGlyLysThrArgGluLeu 549

Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTA 1980
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Search completed: July 14, 2005, 19:31:33
Job time : 4706 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 14, 2005, 15:51:49 ; Search time 554 Seconds
(without alignments)
5866.314 Million cell updates/sec

Title: US-09-769-066-16
Perfect score: 2819
Sequence: 1 AVAPAHDTSPVPDVDSRGAI.....QSTVAELQRLKVKVGKTREL 549

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09769066/runat_13072005_133014_23047/app_query.fasta_1.1422
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09769066_@CGN_1_1_503_@runat_13072005_133014_23047 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2819	100.0	1647	2	AAT27110	Aat27110 Hepatitis
2	2819	100.0	2058	2	AAT27108	Aat27108 Hepatitis
3	2792.5	99.1	1980	2	AAT96960	Aat96960 Hepatitis
4	2792.5	99.1	2100	2	AAQ47130	Aaq47130 HEV third
5	2792.5	99.1	7171	2	AAQ14413	Aaq14413 Composite
6	2792.5	99.1	7171	2	AAV66322	Aav66322 ET-NANB (
7	2792.5	99.1	7171	2	AAV54730	Aav54730 Composite
8	2792.5	99.1	7171	3	AAA99260	Aaa99260 Hepatitis
9	2792.5	99.1	7171	4	AAF83496	Aaf83496 Mexican s
10	2792.5	99.1	7171	6	AAL50387	Aal50387 Hepatitis
11	2792.5	99.1	7171	10	ADD24378	Add24378 Hepatitis
12	2792.5	99.1	7180	10	ADE06698	Ade06698 Hepatitis
13	2789.5	99.0	2100	2	AAQ46814	Aaq46814 Mexico st
14	2694	95.6	1647	2	AAV61686	Aav61686 Hepatitis
15	2694	95.6	1983	2	AAV61688	Aav61688 Hepatitis
16	2694	95.6	1984	2	AAQ86592	Aaq86592 Hepatitis
17	2694	95.6	1990	6	ABL60053	Abl60053 Hepatitis
18	2694	95.6	1990	10	ADB97808	Adb97808 HEV ORF2
19	2694	95.6	2054	4	AAS01448	Aas01448 Hepatitis
20	2694	95.6	7194	2	AAV61690	Aav61690 Hepatitis
21	2690	95.4	7158	2	AAT27394	Aat27394 Hepatitis
22	2690	95.4	7168	2	AAQ45197	Aaq45197 HEV strai
23	2690	95.4	7168	2	AAV71604	Aav71604 Hepatitis
24	2690	95.4	7204	9	ADA50062	Ada50062 SK-HEV-3
25	2690	95.4	7204	9	ADA50065	Ada50065 Hepatitis
26	2690	95.4	7204	9	ADA50064	Ada50064 Hepatitis
27	2690	95.4	7204	9	ADA50063	Ada50063 SK-HEV-2
28	2684	95.2	1647	2	AAT27109	Aat27109 Hepatitis
29	2684	95.2	1983	2	AAT96959	Aat96959 Hepatitis
30	2684	95.2	2049	2	AAT27107	Aat27107 Hepatitis
31	2684	95.2	2094	2	AAQ47129	Aaq47129 HEV third
32	2684	95.2	2094	2	AAQ46813	Aaq46813 Burma str
33	2684	95.2	7195	2	AAV66321	Aav66321 ET-NANB (
34	2684	95.2	7195	2	AAV54729	Aav54729 DNA seque
35	2684	95.2	7195	3	AAA99259	Aaa99259 Hepatitis
36	2684	95.2	7195	4	AAF83495	Aaf83495 ET-NANB v
37	2684	95.2	7195	6	AAL50386	Aal50386 Hepatitis
38	2671	94.7	1989	6	ABL60054	Abl60054 Hepatitis
39	2671	94.7	1989	10	ADB97809	Adb97809 HEV relat
40	2669	94.7	7195	10	ADD24374	Add24374 Hepatitis
41	2666	94.6	7256	10	ADE06693	Ade06693 Hepatitis
42	2664	94.5	7233	10	ADE06694	Ade06694 Hepatitis
43	2663	94.5	1980	8	ABZ23919	Abz23919 Swine HEV
44	2663	94.5	7099	5	ADH13466	Adh13466 Hepatitis
45	2663	94.5	7194	5	ADH13469	Adh13469 Hepatitis

ALIGNMENTS

RESULT 1
AAT27110
ID AAT27110 standard; DNA; 1647 BP.
XX
AC AAT27110;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Mexico strain) 62K antigen DNA.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid; ds.
XX
OS Hepatitis E virus; Mexico strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;

XX
DR WPI; 1996-230608/23.
DR P-PSDB; AAR96092.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Disclosure; Page 73-74; 125pp; English.
XX
CC A DNA sequence (AAT27110) codes for 62K antigen (AAR96092) comprising the
CC C-terminal 549 amino acids of hepatitis E virus (HEV) Mexico strain
CC capsid protein (AAR96090). It is obtd. by PCR amplification of HEV Mexico
CC ORF-2 (AAT27108). The amplified fragment is inserted into vector pGEX for
CC prodn. 62K in E. coli cells. Expression of full-length ORF-2 in Sf9
CC insect cells using a baculovirus system also results in prodn. of 62K
CC antigen (see also AAR96101 and AAR96103). 62K represents an improved
CC antigen, in comparison to bacterial expressed proteins, for use in HEV
CC diagnostic assays, and also has excellent immunogenic properties.
CC (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 1647 BP; 327 A; 497 C; 400 G; 423 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5.59e-226	Length:	1647
Score:	2819.00	Matches:	549
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-09-769-066-16 (1-549) x AAT27110 (1-1647)

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Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 60

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 120

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 180

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 240

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 300

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 360

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 420

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 480

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 540

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 600

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACGGCCCGTCACCGGCTC 660

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 720

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 780

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 840

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 900

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 960

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1020

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1080

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1140

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1200

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1260

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1320

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1380

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1440

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1500

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1560

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1620

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1621 GTTAAGGTGGGTAAAACTCGGGAGTTG 1647
```

RESULT 2
AAT27108

ID AAT27108 standard; DNA; 2058 BP.
XX
AC AAT27108;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Mexico strain) ORF-2.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid; ds.
XX
OS Hepatitis E virus; Mexico strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
DR P-PSDB; AAR96090.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Disclosure; Page 71-72; 125pp; English.
XX
CC The hepatitis E virus (HEV) Mexico strain ORF-2 (AAT27108) codes for the
CC putative capsid protein (AAR96090). PCR amplification of ORF-2 allows
CC prodn. of capsid protein or of C-terminal regions of the capsid protein
CC (see also AAR96092, AAR96094 and AAR96096) and expression in Spodoptera
CC frugiperda Sf9 insect cells using a baculovirus vector provides
CC recombinant C-terminal regions (see also AAR96102 and AAR96104) useful as
CC diagnostic reagents and in vaccines. The HEV Burma strain ORF-2
CC (AAT27107) may similarly be used. (Updated on 16-OCT-2003 to standardise
CC OS field)
XX
SQ Sequence 2058 BP; 372 A; 649 C; 507 G; 530 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.48e-226	Length:	2058
Score:	2819.00	Matches:	549
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-09-769-066-16 (1-549) x AAT27108 (1-2058)

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Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACGGCCCGTCACCGGCTC 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1653
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Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1774 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1833

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1893

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1953

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1954 GTTAAGGTGGGTAAAACTCGGGAGTTG 1980
```

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RESULT 3
AAT96960
ID   AAT96960 standard; DNA; 1980 BP.
XX
AC   AAT96960;
XX
DT   17-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   26-FEB-1998  (first entry)
XX
DE   Hepatitis E virus Mexico strain ORF2.
XX
KW   Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
KW   diagnosis; HEV; ds.
XX
OS   Hepatitis E virus; - Mexico strain.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1980
FT                   /*tag=  a
FT                   /product= "ORF2_protein"
XX
PN   US5686239-A.
XX
PD   11-NOV-1997.
XX
PF   09-MAY-1994;   94US-00240049.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   17-JAN-1992;   92US-00822335.
PR   20-APR-1992;   92US-00870985.
PR   01-MAY-1992;   92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Tam AW,  Reyes GR,  Yarbough PO;
XX
DR   WPI; 1997-558132/51.
DR   P-PSDB; AAW35827.
XX
PT   Diagnosis of hepatitis E virus Burma and Mexico strain infection - by
PT   immunoassay with hepatitis E virus peptide antigens.
XX
PS   Disclosure; Col 25-28; 36pp; English.
XX
CC   A method has been developed for detecting hepatitis E virus (HEV)
CC   antibodies (Ab). The method comprises: (a) reacting a serum sample with a
CC   HEV peptide antigen; and (b) examining the peptide for the presence of
CC   bound Ab, where the presence of bound Ab indicates the presence of HEV
CC   Ab. The present sequence encodes the protein from the open reading frame,
CC   ORF2, from HEV Mexico strain. The method can be used to diagnose
CC   infection with the enterically transmitted non-A/non-B viral hepatitis
CC   agent HEV, specifically the HEV Burma and Mexico strains. (Updated on 25-
CC   MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to standardise OS
CC   field)
XX
SQ   Sequence 1980 BP; 364 A; 624 C; 493 G; 499 T; 0 U; 0 Other;
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Alignment Scores:
Pred. No.:              1.17e-223      Length:          1980
Score:                  2792.50        Matches:         546
Percent Similarity:     99.45%         Conservative:    0
Best Local Similarity:  99.45%         Mismatches:      2
Query Match:            99.06%         Indels:          1
DB:                     2              Gaps:            1

US-09-769-066-16 (1-549) x AAT96960 (1-1980)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 990

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1050

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1110

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1170

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1230

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1290

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1291 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1350

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1410

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1411 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1470

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1471 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1530

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1531 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1590

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1591 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1650

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1651 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1710

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1711 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1770

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1771 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1830

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1831 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1890

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1891 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1950

Qy        541 ValLysValGlyLysThrArgGluLeu 549
                ||||||||||||||||||||||||||
Db       1951 GTTAAGGTGGGTAAAACTCGGGAGTTG 1977

RESULT 4
AAQ47130
ID   AAQ47130 standard; DNA; 2100 BP.
XX
AC   AAQ47130;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   11-JAN-1994  (first entry)
XX
DE   HEV third and second ORFs.
XX
KW   Enterically transmitted non-A non-B hepatitis; ET-NANB; vaccine; ss.
XX
OS   Hepatitis E virus; Mexico strain.
XX
FH   Key             Location/Qualifiers
FT   CDS             5. .376
FT                   /*tag=  a
FT                   /label= ORF3
FT   CDS             46. .2100
FT                   /*tag=  b
FT                   /label= ORF2
FT   misc_RNA        275. .376
FT                   /*tag=  c
FT                   /label= 406.4-2
FT   misc_RNA        718. .2026
FT                   /*tag=  d
FT                   /label= C2
FT   misc_RNA        1045. .2026
FT                   /*tag=  e
FT                   /label= SG3
FT   misc_RNA        1882. .2026
FT                   /*tag=  f
FT                   /label= 406.3-2
XX
PN   WO9314116-A1.
XX
PD   22-JUL-1993.
XX
PF   15-JAN-1993;   93WO-US000459.
XX
PR   17-JAN-1992;   92US-00822335.
PR   01-MAY-1992;   92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
PA   (USSH ) US SEC DEPT HEALTH.
XX
PI   Reyes GR,  Bradley DW,  Tam AW,  Carl M;
XX
DR   WPI; 1993-243144/30.
DR   P-PSDB; AAR38786, AAR38787.
XX
PT   New immunogenic hepatitis E virus (HEV) peptide(s) - are from the ORF1,
PT   ORF2 and ORF3 regions of HEV, useful as a vaccine against HEV infection.
XX
PS   Disclosure; Fig 7; 48pp; English.
XX
CC   Immunogenic hepatitis E virus (HEV) peptides are selected from the ORF1,
CC   ORF2 and ORF3 regions of HEV. The peptides can be used in vaccines to
CC   prevent infection by HEV. The antibodies can neutralise and block HEV
CC   infection and can be used to prevent or treat HEV infection. The peptides
CC   and antibodies can also be used as diagnostic reagents. (Updated on 25-
CC   MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS
CC   field)
XX
SQ   Sequence 2100 BP; 381 A; 659 C; 516 G; 544 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.26e-223       Length:         2100
Score:                  2792.50         Matches:        546
Percent Similarity:     99.45%          Conservative:   0
Best Local Similarity:  99.45%          Mismatches:     2
Query Match:            99.06%          Indels:         1
DB:                     2               Gaps:           1

US-09-769-066-16 (1-549) x AAQ47130 (1-2100)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 438

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
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Db        439 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 498

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60

Db        499 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 558

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

Db        559 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 618

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        619 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 678

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        679 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 738

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db        739 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 798

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db        799 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 858

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180

Db        859 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 918

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        919 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 978

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db        979 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 1035

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db       1036 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1095

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260

Db       1096 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1155

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db       1156 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1215

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db       1216 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1275

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320

Db       1276 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1335

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db       1336 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1395

Qy        341 ProThrProSerProAlaProSerArgProProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1396 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1455

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1456 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1515

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1516 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1575

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420

Db       1576 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1635

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1636 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1695

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460

Db       1696 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1755

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480

Db       1756 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1815

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500

Db       1816 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1875

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1876 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1935

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1936 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1995

Qy        541 ValLysValGlyLysThrArgGluLeu 549

Db       1996 GTTAAGGTGGGTAAAACTCGGGAGTTG 2022
```

RESULT 5
AAQ14413
ID AAQ14413 standard; DNA; 7171 BP.
XX
AC AAQ14413;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-JAN-1992 (first entry)
XX
DE Composite sequence from Mexican isolate of ET-NANB virus.
XX
KW enterically transmitted non-A, non-B hepatitis virus; hepatitis C; HCV;
KW E.coli strain BB4; ATCC deposit number 67717; Mexico; ss.
XX
OS Non-A.
OS non-B hepatitis virus.
XX
PN WO9115603-A.
XX
PD 17-OCT-1991.
XX
PF 05-APR-1990; 90US-00505888.
XX
PR 05-APR-1990; 90US-00505888.
XX
PA (GENE-) GENELABS INC.
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
PA (USSH) US DEPT OF HEALTH.
XX
PI Reyes GR, Yarbough PO, Bradley DW, Krawxzynsk KZ, Tam A, Fry KE;
XX
DR WPI; 1991-325242/44.
XX
PT New viral proteins from non A-non-B hepatitis agent - used to treat and
PT prevent enterically-transmitted non-A non-B hepatitis virus.
XX
PS Claim 13; Page 102; 117pp; English.
XX

```
CC   The sequence from a Mexican strain of ET-NANB virus is about 75 per cent
CC   identical to the ET1.1 sequence (see AAQ14410). The Mexican sequence was
CC   identified in a cDNA library made directly from a semi-purified human
CC   stool specimen collected from an outbreak of ET-NANB in Telixtac.
CC   Screening was with a serum considered to have high titer anti-ET-NANB
CC   antibodies. Two clones were identified from a total of 60,000 screened.
CC   The sequence of these clones was subsequently localised to the 3' half of
CC   the viral genome by homology comparison to the Burma strain sequence (see
CC   AAQ14412). (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
CC   MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS
CC   field.)
XX
SQ   Sequence 7171 BP; 1285 A; 2145 C; 1908 G; 1833 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.28e-223      Length:          7171
Score:                    2792.50        Matches:         546
Percent Similarity:       99.45%         Conservative:    0
Best Local Similarity:    99.45%         Mismatches:      2
Query Match:              99.06%         Indels:          1
DB:                       2              Gaps:            1

US-09-769-066-16 (1-549) x AAQ14413 (1-7171)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5450 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 5509

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5510 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 5569

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5570 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 5629

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5630 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 5689

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5690 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 5749

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5750 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 5809

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5810 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 5869

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5870 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 5929

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5930 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 5989

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5990 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 6049

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6050 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 6106

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6107 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 6166

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6167 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 6226

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6227 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 6286

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6287 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 6346

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6347 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 6406

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6407 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 6466

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6467 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 6526

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6527 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 6586

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6587 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 6646

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6647 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 6706

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6707 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 6766

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6767 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 6826

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6827 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 6886

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6887 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 6946

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6947 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 7006

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7007 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 7066

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       7067 GTTAAGGTGGGTAAAACTCGGGAGTTG 7093

RESULT 6
AAV66322
ID   AAV66322 standard; cDNA; 7171 BP.
XX
AC   AAV66322;
XX
DT   27-AUG-2003  (revised)
DT   25-MAR-2003  (revised)
DT   23-DEC-1998  (first entry)
XX
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DE   ET-NANB (HEV) composite Mexico strain cDNA sequence.
XX
KW   Enterically transmitted non A non B hepatitis virus; ET-NANB;
KW   Hepatitis E virus; HEV; Burma HEV isolate; vaccine; mexico strain;
KW   diagnostic probe; ds.
XX
OS   Non-A.
OS   non-B hepatitis virus.
XX
PN   US5824649-A.
XX
PD   20-OCT-1998.
XX
PF   07-JUN-1995;   95US-00475807.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   25-JUL-1994;   94US-00279823.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Bradley DW,  Reyes GR,  Krawczynski KZ,  Tam A,  Fry KE,  Yarbough PO;
XX
DR   WPI; 1998-582599/49.
XX
PT   Hepatitis E virus proteins - useful for diagnosis or vaccine production
PT   the virus.
XX
PS   Claim 4; Col 69-76; 47pp; English.
XX
CC   The present sequence represents the composite Mexico strain sequence of
CC   enterically transmitted non A non B hepatitis virus (ET-NANB) (hepatitis
CC   E virus (HEV)). The specification describes an isolated protein which is
CC   specifically immunoreactive with antibodies present in individuals
CC   infected with HEV and encoded by a sequence contained in an open reading
CC   frame (ORF) of an HEV genome. The genome has a sequence that is more than
CC   70% identical to the ORF1 sequence from Burma HEV isolate (AAV66321). The
CC   protein is used as a vaccine and a diagnostic probe for ET-NANB. (Updated
CC   on 25-MAR-2003 to correct PR field.) (Updated on 27-AUG-2003 to correct
CC   OS field.)
XX
SQ   Sequence 7171 BP; 1285 A; 2147 C; 1907 G; 1832 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.28e-223      Length:          7171
Score:                    2792.50        Matches:         546
Percent Similarity:       99.45%         Conservative:    0
Best Local Similarity:    99.45%         Mismatches:      2
Query Match:              99.06%         Indels:          1
DB:                       2              Gaps:            1

US-09-769-066-16 (1-549) x AAV66322 (1-7171)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5450 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 5509

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5510 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 5569

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5570 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 5629

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5630 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 5689

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5690 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 5749

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5750 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 5809

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5810 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 5869

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5870 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 5929

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5930 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 5989

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5990 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 6049

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6050 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 6106

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6107 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 6166

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6167 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 6226

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6227 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 6286

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6287 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 6346

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6347 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 6406

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6407 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 6466

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6467 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 6526

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6527 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 6586

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6587 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 6646

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6647 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 6706

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6707 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 6766

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       6767 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 6826

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6827 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 6886

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6887 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 6946

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6947 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 7006

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7007 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 7066

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       7067 GTTAAGGTGGGTAAAACTCGGGAGTTG 7093
```

RESULT 7
AAV54730
ID AAV54730 standard; cDNA; 7171 BP.
XX
AC AAV54730;
XX
DT 25-MAR-2003 (revised)
DT 30-OCT-1998 (first entry)
XX
DE Composite cDNA sequence of the Mexico strain of ET-NANB.
XX
KW Enterically transmitted nonA/nonB hepatitis virus; identification; HEV;
KW ET-NANB; detection; vaccine; ds.
XX
OS Hepatitis virus.
XX
PN US5789559-A.
XX
PD 04-AUG-1998.
XX
PF 25-JUL-1994; 94US-00279823.
XX
PR 17-JUN-1988; 88US-00208997.
PR 11-APR-1989; 89US-00336672.
PR 19-JUN-1989; 89US-00367486.
PR 13-OCT-1989; 89US-00420921.
PR 05-APR-1990; 90US-00505888.
PR 05-APR-1991; 91US-00681078.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Bradley DW, Reyes GR, Krawczynski KZ, Tam A, Fry KE, Yarbough PO;
XX
DR WPI; 1998-446186/38.
XX
PT Hepatitis E virus DNA - useful for e.g. virus detection and viral protein
PT production.
XX
PS Disclosure; Col 67-74; 45pp; English.
XX
CC The present sequence represents the composite sequence of the Mexico
CC strain of an enterically transmitted nonA/nonB viral hepatitis agent (ET-
CC NANB). The nucleic acid sequence may be used for identifying and
CC sequencing the entire viral agent (also referred to as HEV), detecting ET
CC -NANB in infected samples, e.g. by specific amplification of virus-
CC derived DNA sequences and for producing recombinant viral proteins for
CC use in vaccines. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 7171 BP; 1285 A; 2147 C; 1907 G; 1832 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.28e-223	Length:	7171
Score:	2792.50	Matches:	546
Percent Similarity:	99.45%	Conservative:	0
Best Local Similarity:	99.45%	Mismatches:	2
Query Match:	99.06%	Indels:	1
DB:	2	Gaps:	1

US-09-769-066-16 (1-549) x AAV54730 (1-7171)

```
Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5450 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 5509

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5510 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 5569

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5570 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 5629

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5630 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 5689

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5690 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 5749

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5750 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 5809

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5810 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 5869

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5870 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 5929

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5930 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 5989

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5990 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 6049

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6050 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 6106

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6107 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 6166

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6167 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 6226

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6227 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 6286

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6287 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 6346

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6347 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 6406
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Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6407 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 6466

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6467 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 6526

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6527 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 6586

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6587 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 6646

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6647 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 6706

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6707 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 6766

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6767 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 6826

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6827 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 6886

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6887 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 6946

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6947 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 7006

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7007 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 7066

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       7067 GTTAAGGTGGGTAAAACTCGGGAGTTG 7093

RESULT 8
AAA99260
ID   AAA99260 standard; DNA; 7171 BP.
XX
AC   AAA99260;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Hepatitis E virus Mexican strain nucleotide sequence SEQ ID NO:10.
XX
KW   Hepatitis E virus; HEV; non-A/non-B viral hepatitis; viral protein;
KW   immunological; diagnosis; hepatitis; infection; identification;
KW   detection; immunoreactive; hepatotropic; antiinflammatory; virucide;
KW   vaccine; antiviral; antigenic; antibody; antigen; ds.
XX
OS   Hepatitis E virus.
XX
PN   US6120988-A.
XX
PD   19-SEP-2000.
XX
PF   07-JUN-1995;   95US-00478507.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   25-JUL-1994;   94US-00279823.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
PA   (USGO ) US GOVERNMENT.
XX
PI   Yarbough PO,  Krawczynski KZ,  Fry KE,  Bradley DW,  Tam A,  Reyes GR;
XX
DR   WPI; 2000-593712/56.
XX
PT   Identifying recombinant antigen immunoreactive with antibody induced by
PT   hepatitis E virus (HEV), for detecting HEV infection, comprises
PT   immunoreacting a polypeptide from an HEV genome with an HEV-positive
PT   antiserum.
XX
PS   Claim 5; Col 69-76; 46pp; English.
XX
CC   The present invention describes a method for identifying a recombinant
CC   antigen immunoreactive with a hepatitis E virus (HEV)-induced antibody.
CC   The method comprises producing a polypeptide derived from an HEV genome,
CC   immunoreacting the polypeptide with an HEV-positive antiserum and
CC   selecting the polypeptide as a recombinant antigen if the polypeptide
CC   reacts with the HEV-positive antiserum. The method is useful for
CC   identifying recombinant antigen immunoreactive with antibody induced by
CC   HEV. The enterically transmitted non-A/non-B hepatitis (ET-NANB (also
CC   known as HEV))-specific fragments are useful for identifying ET-NANB-
CC   derived cDNAs, which contain additional sequence information, as primers
CC   for detecting ET-NANB viral genomic material in a patient sample, for the
CC   synthesis of polypeptides for use in immunoassays, and for identifying
CC   similar antigenic regions encoded by related viral strains, e.g. Burmese
CC   strain. The antigens are especially useful in the preparation of vaccine
CC   against ET-NANB infection. These antigens may further be used to prepare
CC   antibodies to ET-NANB virus particles for use directly as antiviral
CC   agents, and to produce antiserum designed for pre- or post-exposure
CC   prophylaxis. The present sequence represents a specifically claimed HEV
CC   composite Mexican strain gene sequence for use in the present invention
XX
SQ   Sequence 7171 BP; 1285 A; 2147 C; 1907 G; 1832 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.28e-223       Length:         7171
Score:                  2792.50         Matches:        546
Percent Similarity:     99.45%          Conservative:   0
Best Local Similarity:  99.45%          Mismatches:     2
Query Match:            99.06%          Indels:         1
DB:                     3               Gaps:           1

US-09-769-066-16 (1-549) x AAA99260 (1-7171)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5450 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 5509

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5510 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 5569

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5570 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 5629

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5630 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 5689

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5690 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 5749

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db       5750 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 5809

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db       5810 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 5869

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db       5870 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 5929

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180

Db       5930 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 5989

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db       5990 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 6049

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db       6050 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 6106

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db       6107 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 6166

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260

Db       6167 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 6226

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db       6227 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 6286

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db       6287 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 6346

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320

Db       6347 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 6406

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db       6407 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 6466

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       6467 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 6526

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       6527 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 6586

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       6587 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 6646

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420

Db       6647 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 6706

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       6707 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 6766

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460

Db       6767 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 6826

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480

Db       6827 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 6886

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500

Db       6887 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 6946

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       6947 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 7006

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       7007 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 7066

Qy        541 ValLysValGlyLysThrArgGluLeu 549

Db       7067 GTTAAGGTGGGTAAAACTCGGGAGTTG 7093
```

RESULT 9
AAF83496
ID AAF83496 standard; cDNA; 7171 BP.
XX
AC AAF83496;
XX
DT 23-JUL-2001 (first entry)
XX
DE Mexican strain ET-NANB viral ET1.1 composite cDNA sequence.
XX
KW HEV; enterically transmitted nonA/nonB viral hepatitis agent; viral;
KW ET-NANB; infection; vaccine; ss.
XX
OS Hepatitis E virus.
XX
PN US6229005-B1.
XX
PD 08-MAY-2001.
XX
PF 03-AUG-1998; 98US-00128275.
XX
PR 17-JUN-1988; 88US-00208997.
PR 11-APR-1989; 89US-00336672.
PR 16-JUN-1989; 89US-00367486.
PR 13-OCT-1989; 89US-00420921.
PR 05-APR-1990; 90US-00505888.
PR 05-APR-1991; 91US-00681078.
PR 25-JUL-1994; 94US-00279823.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Reyes GR, Yarbough PO, Bradley DW, Krawczynski KZ, Tam AW;
PI Fry KE;
XX
DR WPI; 2001-342705/36.
XX
PT New DNA sequences of enterically transmitted non-A/non-B (ET-NANB)
PT hepatitis viral agent, useful in diagnosing infection by an enterically
PT transmitted agent (e.g. ET-NANB virus), as well as in vaccine production.
XX
PS Disclosure; Col 69-76; 45pp; English.
XX
CC The invention relates to an isolated DNA comprising the genome of an
CC enterically transmitted nonA/nonB (ET-NANB) viral hepatitis agent (also
CC referred as HEV). The DNA sequences or their fragments are useful in
CC preparing ET-NANB viral proteins and as probes for virus detection. These
CC are particularly useful in diagnosing infection by an enterically
CC transmitted agent (e.g. ET-NANB virus), as well as in vaccine production.
CC The present sequence represents a Mexican strain composite ET-NANB viral
CC cDNA sequence
XX
SQ Sequence 7171 BP; 1285 A; 2147 C; 1907 G; 1832 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.28e-223	Length:	7171
Score:	2792.50	Matches:	546
Percent Similarity:	99.45%	Conservative:	0
Best Local Similarity:	99.45%	Mismatches:	2
Query Match:	99.06%	Indels:	1
DB:	4	Gaps:	1

US-09-769-066-16 (1-549) x AAF83496 (1-7171)

```
Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5450 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 5509

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5510 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 5569

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5570 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 5629

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5630 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 5689

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5690 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 5749

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5750 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 5809

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5810 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 5869

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5870 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 5929

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5930 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 5989

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5990 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 6049

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6050 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 6106

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6107 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 6166

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6167 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 6226

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6227 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 6286

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6287 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 6346

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6347 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 6406

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6407 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 6466

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6467 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 6526

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6527 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 6586

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6587 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 6646

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6647 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 6706

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6707 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 6766

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6767 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 6826

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6827 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 6886

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6887 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 6946

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6947 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 7006

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7007 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 7066

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       7067 GTTAAGGTGGGTAAAACTCGGGAGTTG 7093
```

RESULT 10
AAL50387
ID AAL50387 standard; DNA; 7171 BP.
XX
AC AAL50387;
XX
DT 08-NOV-2002 (first entry)
XX
DE Hepatitis E virus (Mexican strain) DNA sequence 1.
XX
KW HEV; enterically transmitted nonA/nonB hepatitis viral agent;
KW Mexican strain; bile; ds.
XX
OS Hepatitis E virus.
XX
PN US6379891-B1.
XX
PD 30-APR-2002.
XX
PF 19-APR-2000; 2000US-00553427.
XX
PR 17-JUN-1988; 88US-00208997.
PR 11-APR-1989; 89US-00336672.
PR 16-JUN-1989; 89US-00367486.
PR 13-OCT-1989; 89US-00420921.

PR 05-APR-1990; 90US-00505888.
PR 15-APR-1991; 91US-00681078.
PR 25-JUL-1994; 94US-00279823.
PR 07-JUN-1995; 95US-00478507.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Reyes GR, Yarbough PO, Bradley DW, Krawczynski KZ, Tam A, Fry KE;
XX
DR WPI; 2002-517277/55.
XX
PT Detecting the presence of enterically transmitted nonA/nonB hepatitis
PT viral (HEV) agents in bile samples from infected humans and monkeys using
PT polymerase chain reaction.
XX
PS Disclosure; Col 25-32; 61pp; English.
XX
CC The invention comprises a method for detecting the presence of
CC enterically transmitted nonA/nonB hepatitis viral (HEV) agents in a
CC sample and isolating HEV agents or nucleic acid fragments produced by the
CC agent. The method utilises PCR - using bile from a human or cynomolgus
CC monkey actively infected with HEV as a source of the agent. The method of
CC the invention is used for detecting the presence of a viral agent in a
CC sample of cultured cells infected with the agent and isolating
CC enterically transmitted nonA/nonB HEV agents or nucleic acid fragments
CC produced by the agent. The present DNA sequence was isolated from a
CC Mexican strain of the Hepatitis E virus
XX
SQ Sequence 7171 BP; 1285 A; 2147 C; 1907 G; 1832 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.28e-223	Length:	7171
Score:	2792.50	Matches:	546
Percent Similarity:	99.45%	Conservative:	0
Best Local Similarity:	99.45%	Mismatches:	2
Query Match:	99.06%	Indels:	1
DB:	6	Gaps:	1

US-09-769-066-16 (1-549) x AAL50387 (1-7171)

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Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5450 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 5509

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5510 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 5569

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5570 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 5629

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5630 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 5689

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5690 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 5749

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5750 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 5809

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5810 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 5869

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5870 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 5929

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5930 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 5989

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5990 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 6049

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6050 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 6106

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6107 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 6166

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6167 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 6226

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6227 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 6286

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6287 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 6346

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6347 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 6406

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6407 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 6466

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6467 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 6526

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6527 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 6586

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6587 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 6646

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6647 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 6706

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6707 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 6766

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6767 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 6826

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6827 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 6886

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6887 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 6946

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6947 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 7006

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7007 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 7066

Qy        541 ValLysValGlyLysThrArgGluLeu 549
                ||||||||||||||||||||||||||
Db       7067 GTTAAGGTGGGTAAAACTCGGGAGTTG 7093

RESULT 11
ADD24378
ID   ADD24378 standard; cDNA; 7171 BP.
XX
AC   ADD24378;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Hepatitis E virus strain Mexico composite cDNA #1.
XX
KW   ss; gene; non-A/non-B viral hepatitis; ET-NANB; HEV; vaccine.
XX
OS   Hepatitis E virus; strain Mexico.
XX
PN   US2003124510-A1.
XX
PD   03-JUL-2003.
XX
PF   07-MAY-2001; 2001US-00851410.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   25-JUL-1994;   94US-00279823.
PR   03-AUG-1998;   98US-00128275.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Reyes GR,  Yarbough PO,  Bradley DW,  Krawczynski KZ,  Tam AW;
PI   Fry KE;
XX
DR   WPI; 2003-810978/76.
XX
PT   New proteins derived from an enterically transmitted non-A/non-B (ET-
PT   NANB) viral hepatitis agent, useful for diagnosing ET-NANB infection and
PT   producing vaccines for immunizing an individual against ET-NANB hepatitis
PT   viral agent.
XX
PS   Claim 3; SEQ ID NO 10; 81pp; English.
XX
CC   The invention relates to a protein derived from an enterically
CC   transmitted non-A/non-B viral hepatitis agent. The viral proteins are
CC   useful for detecting infection by the enterically transmitted non-A/non-B
CC   (ET-NANB/HEV) hepatitis viral agent. The proteins are also useful for
CC   producing vaccines for immunising an individual against HEV hepatitis
CC   viral agent. The DNA fragments are useful for identifying and sequencing
CC   the entire viral agent and for assaying the viral agent in an infected
CC   sample. The present sequence is used in the exemplification of the
CC   invention.
XX
SQ   Sequence 7171 BP; 1285 A; 2147 C; 1907 G; 1832 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.28e-223       Length:          7171
Score:                    2792.50         Matches:         546
Percent Similarity:       99.45%          Conservative:    0
Best Local Similarity:    99.45%          Mismatches:      2
Query Match:              99.06%          Indels:          1
DB:                       10              Gaps:            1

US-09-769-066-16 (1-549) x ADD24378 (1-7171)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5450 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 5509

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5510 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 5569

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5570 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 5629

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5630 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 5689

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5690 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 5749

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5750 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 5809

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5810 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 5869

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5870 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 5929

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5930 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 5989

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5990 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 6049

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6050 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 6106

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6107 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 6166

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6167 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 6226

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6227 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 6286

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6287 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 6346

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6347 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 6406

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6407 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 6466

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6467 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 6526

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       6527 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 6586

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       6587 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 6646

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420

Db       6647 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 6706

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       6707 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 6766

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460

Db       6767 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 6826

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480

Db       6827 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 6886

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500

Db       6887 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 6946

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       6947 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 7006

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       7007 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 7066

Qy        541 ValLysValGlyLysThrArgGluLeu 549

Db       7067 GTTAAGGTGGGTAAAACTCGGGAGTTG 7093
```

RESULT 12
ADE06698
ID ADE06698 standard; DNA; 7180 BP.
XX
AC ADE06698;
XX
DT 29-JAN-2004 (first entry)
XX
DE Hepatitis E virus strain Mexico genomic sequence.
XX
KW hepatitis E virus; chips; kit; detection; ds.
XX
OS Hepatitis E virus; strain Mexico.
XX
PN WO2003000887-A1.
XX
PD 03-JAN-2003.
XX
PF 25-JUN-2002; 2002WO-JP006365.
XX
PR 25-JUN-2001; 2001JP-00191837.
XX
PA (TOKE) TOSHIBA KK.
XX
PI Takahashi K, Mishiro S, Oota Y, Hashimoto M, Maekubo H;
XX
DR WPI; 2003-239144/23.
XX
PT Polynucleotide probes and primers originating in Japanese hepatitis E
PT virus, applicable in chips and kits for detecting hepatitis E virus and
PT its infection.
XX
PS Disclosure; SEQ ID NO 49; 238pp; Japanese.
XX
CC The invention relates to novel polynucleotide probes for detecting
CC hepatitis E virus polynucleotides which contain a sequence of at least 8
CC consecutive nucleotides of the hepatitis E virus genome. The hepatitis E
CC virus genomic sequences are derived from various strains of the Japanese
CC Hepatitis E virus. The probes and primers are applicable in chips and
CC kits for detecting hepatitis E virus and its infection. This sequence
CC represents the genomic sequence from the Hepatitis E virus strain Mexico.
XX
SQ Sequence 7180 BP; 1294 A; 2147 C; 1907 G; 1832 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.29e-223	Length:	7180
Score:	2792.50	Matches:	546
Percent Similarity:	99.45%	Conservative:	0
Best Local Similarity:	99.45%	Mismatches:	2
Query Match:	99.06%	Indels:	1
DB:	10	Gaps:	1

US-09-769-066-16 (1-549) x ADE06698 (1-7180)

```
Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20

Db       5450 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 5509

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40

Db       5510 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 5569

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60

Db       5570 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 5629

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

Db       5630 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 5689

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db       5690 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 5749

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db       5750 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 5809

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db       5810 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 5869

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db       5870 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 5929

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180

Db       5930 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 5989

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db       5990 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 6049

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db       6050 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 6106

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db       6107 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 6166

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260

Db       6167 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 6226

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
```

```
Db       6227 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 6286

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6287 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 6346

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6347 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 6406

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6407 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 6466

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6467 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 6526

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6527 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 6586

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6587 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 6646

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6647 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 6706

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6707 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 6766

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6767 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 6826

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6827 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 6886

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6887 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 6946

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6947 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 7006

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7007 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 7066

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       7067 GTTAAGGTGGGTAAAACTCGGGAGTTG 7093
```

```
RESULT 13
AAQ46814
ID   AAQ46814 standard; DNA; 2100 BP.
XX
AC   AAQ46814;
XX
DT   25-MAR-2003  (revised)
DT   14-FEB-1994  (first entry)
XX
DE   Mexico strain HEV ORF2 and ORF3.
XX
KW   Hepatitis E virus; vaccine; neutralising antibodies; infection; block;
KW   open reading frame; antibodies; ss.
XX
OS   Hepatitis E virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             5. .311
FT                   /*tag=  a
FT                   /note= "ORF2"
FT   CDS             46. .2100
FT                   /*tag=  b
FT                   /note= "ORF3"
XX
PN   WO9314208-A2.
XX
PD   22-JUL-1993.
XX
PF   19-JAN-1993;   93WO-US000475.
XX
PR   17-JAN-1992;   92US-00822335.
PR   20-APR-1992;   92US-00870985.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Reyes GR,  Bradley DW,  Twu J,  Purdy MA,  Tam AW,  Krawczynski KZ;
XX
DR   WPI; 1993-243223/30.
DR   P-PSDB; AAR39307, AAR39308.
XX
PT   Antigen and antibody vaccines against hepatitis E virus infection -
PT   contain peptide(s) derived from capsid protein C-terminal or antibodies
PT   against protein.
XX
PS   Disclosure; Fig 7; 43pp; English.
XX
CC   The sequence is that encoding Mexico strain hepatitis E virus (HEV) open
CC   reading frames ORF2 and ORF3. ORF2 encodes the putative capsid protein of
CC   the virus, this protein or peptide fragments of it may be used in a
CC   vaccine composition for immunising an individual against HEV. Antibodies
CC   raised against these peptides can also be used in such vaccines. (Updated
CC   on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 2100 BP; 381 A; 660 C; 515 G; 544 T; 0 U; 0 Other;
```

Alignment Scores:			
Pred. No.:	2.25e-223	Length:	2100
Score:	2789.50	Matches:	545
Percent Similarity:	99.45%	Conservative:	1
Best Local Similarity:	99.27%	Mismatches:	2
Query Match:	98.95%	Indels:	1
DB:	2	Gaps:	1

US-09-769-066-16 (1-549) x AAQ46814 (1-2100)

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Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 438

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 498

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 558

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 618

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 678

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        679 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 738

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 798

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 858

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 918

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 978

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTCC--- 1035

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1036 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1095

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1155

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1215

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1275

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1335

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1395

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1396 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1455

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1515

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1516 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1575

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db       1576 CGATCGCTTGACTGGTCCAAACTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1635

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1636 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1695

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1696 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1755

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1756 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1815

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1816 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1875

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1876 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1935

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1936 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1995

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1996 GTTAAGGTGGGTAAAACTCGGGAGTTG 2022
```

RESULT 14
AAV61686
ID AAV61686 standard; DNA; 1647 BP.
XX
AC AAV61686;
XX
DT 03-DEC-1998 (first entry)
XX
DE Hepatitis E virus hollow particle protein ORF2 DNA.
XX
KW Hollow particle protein; virus; antibody; detection; immunoassay;
KW infection; ss.
XX
OS Hepatitis virus.
XX
FH Key   Location/Qualifiers
FT CDS   1. .1647
FT   /*tag= a
FT   /product= "hollow particle protein"
FT   /note= "No start codon given for ORF2"
XX
PN JP10234383-A.
XX
PD 08-SEP-1998.
XX
PF 28-FEB-1997; 97JP-00062445.
XX
PR 28-FEB-1997; 97JP-00062445.
XX
PA (DENK-) DENKA SEIKEN KK.
PA (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR WPI; 1998-535037/46.
DR P-PSDB; AAW76367.
XX
PT Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids
PT encoding it - useful for more accurate detection of HEV in samples, using
PT immuno-assays and nucleic acid hybridisation.
XX
PS Claim 1; Page 15-17; 29pp; Japanese.
XX
CC This sequence encodes a Hepatitis E viral hollow particle protein
CC described as ORF2. This polypeptide can be used to raise antibodies to
CC detect HEV infection in samples, e.g. by immuno-assay based techniques,
CC and the nucleic acid can be used for the same in nucleic acid
CC hybridisation assays. The polypeptide and nucleic acid allow more
CC accurate detection of HEV than previously possible
XX
SQ Sequence 1647 BP; 303 A; 535 C; 390 G; 419 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.59e-215	Length:	1647
Score:	2694.00	Matches:	521
Percent Similarity:	97.45%	Conservative:	14
Best Local Similarity:	94.90%	Mismatches:	14
Query Match:	95.57%	Indels:	0

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DB:                 2          Gaps:          0

US-09-769-066-16 (1-549) x AAV61686 (1-1647)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              |||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db          1 GCGGTCGCTCCAGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCTCGCGGCGCCATC 60

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db         61 TTGCGCCGGCAGTATAATCTATCAACATCTCCCCTCACCTCTTCCGTGGCCACCGGCACT 120

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||:::|||   ||||||||||||||||||||||||
Db        121 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAAT 180

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 240

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTC 300

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 360

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 420

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 480

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAACACA 540

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 600

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 660

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAG 720

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||:::||||||      |||||||||||||:::||||||||||||||||||||||
Db        721 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 780

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGTTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 840

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Db        841 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCGGCCAATGGCGAGCCGACTGTTAAG 900

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
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Db        901 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 960

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Db        961 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGG 1020

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1080

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1140

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1200

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||:::|||||||||||||||||||||||||||   |||::::::|||
Db       1201 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1260

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1320

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||:::
Db       1321 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1380

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db       1381 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1440

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuGluGlu 500
              ||||||:::|||||||||   |||||||||||||||||||   ||||||||||||||||||
Db       1441 CCCGTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1500

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||   |||||||||   ||||||||||||||||||||||||||||||||||||||
Db       1501 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1560

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CCTCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1620

Qy        541 ValLysValGlyLysThrArgGluLeu 549
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Db       1621 ATGAAGGTGGGTAAAACTCGGGAGTTA 1647

RESULT 15
AAV61688
ID   AAV61688 standard; DNA; 1983 BP.
XX
AC   AAV61688;
XX
DT   03-DEC-1998  (first entry)
XX
DE   Hepatitis E virus hollow particle protein DNA #2.
XX
KW   Hollow particle protein; virus; antibody; detection; immunoassay;
KW   infection; ss.
XX
OS   Hepatitis virus.
XX
PN   JP10234383-A.
XX
PD   08-SEP-1998.
XX
PF   28-FEB-1997;   97JP-00062445.
XX
PR   28-FEB-1997;   97JP-00062445.
XX
PA   (DENK-) DENKA SEIKEN KK.
PA   (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR   WPI; 1998-535037/46.
DR   P-PSDB; AAW76369.
XX
PT   Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids
```

PT encoding it - useful for more accurate detection of HEV in samples, using
PT immuno-assays and nucleic acid hybridisation.
XX
PS Claim 13; Page 24-26; 29pp; Japanese.
XX
CC This sequence encodes a Hepatitis E viral hollow particle protein. This
CC polypeptide can be used to raise antibodies to detect HEV infection in
CC samples, e.g. by immuno-assay based techniques, and the nucleic acid can
CC be used for the same in nucleic acid hybridisation assays. The
CC polypeptides and nucleic acids allow more accurate detection of HEV than
CC previously possible
XX
SQ Sequence 1983 BP; 342 A; 665 C; 485 G; 491 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.03e-215	Length:	1983
Score:	2694.00	Matches:	521
Percent Similarity:	97.45%	Conservative:	14
Best Local Similarity:	94.90%	Mismatches:	14
Query Match:	95.57%	Indels:	0
DB:	2	Gaps:	0

US-09-769-066-16 (1-549) x AAV61688 (1-1983)

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Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        334 GCGGTCGCTCCAGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCTCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        394 TTGCGCCGGCAGTATAATCTATCAACATCTCCCCTCACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||:::|||   ||||||||||||||||||||||||
Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAACACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Db        994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAG 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||:::||||||     ||||||||||||||:::|||||||||||||||||||||
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CTGTTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCGGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
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Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              |||||||||:::||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
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Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
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Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
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Db       1774 CCCGTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||   |||||||||   ||||||||||||||||||||||||||||||||||||||||
Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 CCTCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              :::|||||||||||||||||||||||||
Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTA 1980
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Search completed: July 14, 2005, 16:57:00
Job time : 634 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 14, 2005, 01:31:43 ; Search time 38.3019 Seconds
(without alignments)
7019.016 Million cell updates/sec

Title: US-09-769-066-16_COPY_1_525
Perfect score: 2701
Sequence: 1 AVAPAHDTSPVPDVDSRGAI.....PGRAHTFDDFCPECRALGLQ 525

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2674.5	99.0	659	1	VST2_HEVME	Q03500 hepatitis e
2	2579	95.5	660	2	Q9E8G5	Q9e8g5 hepatitis e
3	2575	95.3	660	1	VST2_HEVPA	P33426 hepatitis e
4	2575	95.3	660	2	Q77EC8	Q77ec8 hepatitis e
5	2575	95.3	660	2	Q89468	Q89468 hepatitis e
6	2575	95.3	660	2	Q9W7W9	Q9w7w9 hepatitis e
7	2575	95.3	660	2	Q9WQA0	Q9wqa0 hepatitis e
8	2569	95.1	660	1	VST2_HEVBU	P29326 hepatitis e
9	2569	95.1	660	2	O91855	O91855 hepatitis e
10	2569	95.1	660	2	Q69419	Q69419 hepatitis e
11	2568	95.1	660	2	O91856	O91856 hepatitis e
12	2568	95.1	660	2	Q69411	Q69411 hepatitis e
13	2563	94.9	660	2	Q81878	Q81878 hepatitis e
14	2560	94.8	660	2	Q6XXV0	Q6xxv0 hepatitis e
15	2559	94.7	660	2	Q80IY5	Q80iy5 hepatitis e
16	2556	94.6	660	2	Q8JJM8	Q8jjm8 hepatitis e
17	2555	94.6	660	2	Q81871	Q81871 hepatitis e
18	2554	94.6	660	2	Q8JJM4	Q8jjm4 hepatitis e
19	2553	94.5	660	2	O36613	O36613 swine hepat
20	2553	94.5	660	2	Q6J8F7	Q6j8f7 hepatitis e
21	2552	94.5	660	2	Q8V729	Q8v729 swine hepat
22	2552	94.5	660	2	Q8AZM3	Q8azm3 hepatitis e
23	2552	94.5	660	2	Q9WLL4	Q9wll4 hepatitis e
24	2552	94.5	660	2	Q9YLQ9	Q9ylq9 hepatitis e
25	2550	94.4	660	2	Q80IR7	Q80ir7 hepatitis e
26	2548	94.3	660	2	Q68985	Q68985 hepatitis e
27	2547	94.3	659	2	Q8JT32	Q8jt32 hepatitis e
28	2547	94.3	660	2	Q911I4	Q911i4 hepatitis e
29	2547	94.3	660	2	Q6J8G3	Q6j8g3 hepatitis e
30	2545	94.2	660	1	VST2_HEVMY	Q04611 hepatitis e
31	2543	94.2	660	2	Q8BB05	Q8bb05 swine hepat
32	2542	94.1	660	2	Q9YLR2	Q9ylr2 hepatitis e
33	2532	93.7	674	2	Q8JJN2	Q8jjn2 hepatitis e
34	2532	93.7	674	2	Q7TGF1	Q7tgf1 hepatitis e
35	2531	93.7	674	2	Q6BD78	Q6bd78 hepatitis e
36	2529	93.6	550	2	Q8JVV3	Q8jvv3 hepatitis e
37	2529	93.6	671	2	Q8JJM1	Q8jjm1 hepatitis e
38	2529	93.6	674	2	Q8JJN6	Q8jjn6 hepatitis e
39	2528	93.6	674	2	Q6BD83	Q6bd83 hepatitis e
40	2526	93.5	674	2	Q806D7	Q806d7 hepatitis e
41	2526	93.5	674	2	Q806E0	Q806e0 swine hepat
42	2526	93.5	674	2	Q80IR5	Q80ir5 hepatitis e
43	2525	93.5	674	2	Q6PMR3	Q6pmr3 swine hepat
44	2506	92.8	672	2	Q9IVZ8	Q9ivz8 hepatitis e
45	2395	88.7	605	2	Q9YWL0	Q9yw10 hepatitis e

ALIGNMENTS

RESULT 1
VST2_HEVME
ID VST2_HEVME STANDARD; PRT; 659 AA.
AC Q03500;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Structural protein 2 precursor.
GN ORFNames=ORF2;
OS Hepatitis E virus (strain Mexico) (HEV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=31768;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93079857; PubMed=1448913;
RA Huang C.C., Nguyen D., Fernandez J., Yun K.Y., Fry K.E., Bradley D.W.,
RA Tam A.W., Reyes G.R.;
RT "Molecular cloning and sequencing of the Mexico isolate of hepatitis E
RT virus (HEV).";
RL Virology 191:550-558(1992).
CC -!- FUNCTION: Contains a high basic amino acid content suggesting that
CC it may be involved in the encapsidation of the genomic RNA by
CC effectively neutralizing the negatively charged RNA.
CC ---
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; M74506; AAA45732.1; -.
DR PIR; B44212; B44212.
DR InterPro; IPR004261; SP2.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF03014; SP2; 1.
KW Signal.
FT SIGNAL 1 22 By similarity.
FT CHAIN 23 659 Structural protein 2.
SQ SEQUENCE 659 AA; 70640 MW; CF75E75EFD8FBE2C CRC64;

Query Match 99.0%; Score 2674.5; DB 1; Length 659;
Best Local Similarity 99.4%; Pred. No. 6.1e-178;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231
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Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 635
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RESULT 2
Q9E8G5
ID Q9E8G5 PRELIMINARY; PRT; 660 AA.
AC Q9E8G5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Structural protein.
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Abb-2B;
RX MEDLINE=20271579; PubMed=10813471;
RA van Cuyck-Gandre H., Zhang H.Y., Tsarev S.A., Warren R.L.,
RA Caudill J.D., Snellings N.J., Begot L., Innis B.L., Longer C.F.;
RT "Phylogenetically distinct hepatitis E viruses in Pakistan.";
RL Am. J. Trop. Med. Hyg. 62:187-189(2000).
DR EMBL; AF185822; AAG16766.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70903 MW; 1F506BE3CFB3BACE CRC64;

Query Match 95.5%; Score 2579; DB 2; Length 660;
Best Local Similarity 94.9%; Pred. No. 2.8e-171;
Matches 498; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||:|||||||||:|||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||||:|||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||:|:|||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| |||| |||||||| ||| ||||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 3
VST2_HEVPA
ID VST2_HEVPA STANDARD; PRT; 660 AA.
AC P33426;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Structural protein 2 precursor.
GN ORFNames=ORF2;
OS Hepatitis E virus (strain Pakistan) (HEV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=33774;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92115700; PubMed=1731327;
RA Tsarev S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J.,
RA Malik I.A., Iqbal M., Purcell R.H.;
RT "Characterization of a prototype strain of hepatitis E virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).
CC -!- FUNCTION: Contains a high basic amino acid content suggesting that
CC it may be involved in the encapsidation of the genomic RNA by
CC effectively neutralizing the negatively charged RNA.
CC ---
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CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; M80581; AAA45727.1; -.
DR InterPro; IPR004261; SP2.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF03014; SP2; 1.
KW Signal.
FT SIGNAL 1 22 By similarity.
FT CHAIN 23 660 Structural protein 2.
SQ SEQUENCE 660 AA; 70980 MW; 8085BC53CFB46FD3 CRC64;

Query Match 95.3%; Score 2575; DB 1; Length 660;
Best Local Similarity 94.7%; Pred. No. 5.3e-171;
Matches 497; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||:|||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171
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Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:||||||| ||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||:|||||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| | ||||||| ||| ||||||||||||| ||||
Db        592 PVSISAVAVLAPHSVLALLEDTMDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 4
Q77EC8
ID Q77EC8 PRELIMINARY; PRT; 660 AA.
AC Q77EC8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Capsid protein.
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sar-55;
RX MEDLINE=21625046; PubMed=11742081; DOI=10.1073/pnas.251555098;
RA Emerson S.U., Zhang M., Meng X.-J., Nguyen H., St Claire M.,
RA Govindarajan S., Huang Y.K., Purcell R.H.;
RT "Recombinant hepatitis E virus genomes infectious for primates:
RT importance of capping and discovery of a cis-reactive element.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:15270-15275(2001).
DR EMBL; AF444003; AAL50059.1; -.
DR EMBL; AF444002; AAL50056.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70979 MW; 8085BC53CFB46FD3 CRC64;

Query Match 95.3%; Score 2575; DB 2; Length 660;
Best Local Similarity 94.7%; Pred. No. 5.3e-171;
Matches 497; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:||||||| ||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||:|||||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| | ||||||| ||| ||||||||||||| ||||
Db        592 PVSISAVAVLAPHSVLALLEDTMDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 5
Q89468
ID Q89468 PRELIMINARY; PRT; 660 AA.
AC Q89468;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Unnamed protein product (ORFs 1-3).
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RA Yin S.R., Purcell R.H., Emerson S.U.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K52-87;
RX MEDLINE=95176571; PubMed=7871758;
RA Yin S., Purcell R.H., Emerson S.U.;
RT "A new Chinese isolate of hepatitis E virus: comparison with strains
RT recovered from different geographical regions.";
RL Virus Genes 9:23-32(1994).
DR EMBL; L25547; AAA91080.1; -.
DR EMBL; L25595; AAA65490.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70979 MW; DC68116DCD639175 CRC64;

Query Match 95.3%; Score 2575; DB 2; Length 660;
Best Local Similarity 94.7%; Pred. No. 5.3e-171;
Matches 497; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

```
Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
                 ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
                 ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
                 |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
                 ||||||||||||||||||||||:|||||||||||||||||||||:|||||||||  |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
                 ||||||||||||||||||||||||||||||||||||:|:|||||||||||||||  ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
                 ||:||| ||| | ||||||||| ||| ||||||||||||| ||||
Db        592 PVSISAVAVLTPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQ 636


RESULT 6
Q9W7W9
ID   Q9W7W9      PRELIMINARY;      PRT;   660 AA.
AC   Q9W7W9;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Structural protein 2 (Structural viral protein).
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HEV-Morocco;
RX   MEDLINE=99107414; PubMed=9892396;
RX   DOI=10.1002/(SICI)1096-9071(199902)57:2<126::AID-JMV7>3.3.CO;2-F;
RA   Meng J., Cong M., Dai X., Pillot J., Purdy M.A., Fields H.A.,
RA   Khudyakov Y.E.;
RT   "Primary structure of open reading frame 2 and 3 of the hepatitis E
RT   virus isolated from Morocco.";
RL   J. Med. Virol. 57:126-133(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Chen G., Meng J.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF065061; AAD10627.1; -.
DR   EMBL; AY230202; AAO72992.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70943 MW;  9719D30CCD932950 CRC64;

  Query Match             95.3%;  Score 2575;  DB 2;  Length 660;
  Best Local Similarity   94.7%;  Pred. No. 5.3e-171;
  Matches  497;  Conservative   14;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
                ||||||||  ||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
                ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
                ||:|:  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
                |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
                ||||||||||||||||||||:|||||||||||||||||||||:|||||||||  |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
                ||||||||||||||||||||||||||||||||||||:|:|||||||||||||||  ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
                ||:||| ||||| ||||||||| ||| ||||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 7
Q9WQA0
ID   Q9WQA0      PRELIMINARY;      PRT;   660 AA.
AC   Q9WQA0;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   ORF-2.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99350000; PubMed=10423137;
RA   Arankalle V.A., Paranjape S., Emerson S.U., Purcell R.H.,
RA   Walimbe A.M.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from India (1976-
RT   1993).";
RL   J. Gen. Virol. 80:1691-1700(1999).
DR   EMBL; AF124407; AAD45493.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71040 MW;  03B72DDF0AB7B521 CRC64;

  Query Match             95.3%;  Score 2575;  DB 2;  Length 660;
  Best Local Similarity   94.7%;  Pred. No. 5.3e-171;
  Matches  497;  Conservative   13;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
                ||||||||  ||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
                ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
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Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||:|||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| || || ||||||||| ||| ||||||||||||| ||||
Db        592 PVSISAVAVFAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 8
VST2_HEVBU
ID   VST2_HEVBU     STANDARD;      PRT;   660 AA.
AC   P29326;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   Structural protein 2 precursor.
GN   ORFNames=ORF2;
OS   Hepatitis E virus (strain Burma) (HEV).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=31767;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92024067; PubMed=1926770;
RA   Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
RA   Fry K.E., Reyes G.R.;
RT   "Hepatitis E virus (HEV): molecular cloning and sequencing of the
RT   full-length viral genome.";
RL   Virology 185:120-131(1991).
CC   -!- FUNCTION: Contains a high basic amino acid content suggesting that
CC       it may be involved in the encapsidation of the genomic RNA by
CC       effectively neutralizing the negatively charged RNA.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M73218; AAA45736.1; -.
DR   PIR; C40778; VHWWH2.
DR   InterPro; IPR004261; SP2.
DR   InterPro; IPR008975; Viral_cap_coat.
DR   Pfam; PF03014; SP2; 1.
KW   Signal.
FT   SIGNAL       1     19       Potential.
FT   CHAIN       20    660       Structural protein 2.
SQ   SEQUENCE   660 AA;  70978 MW;  5832A013CCC4A61C CRC64;

  Query Match             95.1%;  Score 2569;  DB 1;  Length 660;
  Best Local Similarity   94.7%;  Pred. No. 1.4e-170;
  Matches  497;  Conservative   13;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||:|||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| ||||||||| ||| |||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 9
O91855
ID   O91855      PRELIMINARY;      PRT;   660 AA.
AC   O91855;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Structural protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=93-Egypt;
RX   MEDLINE=99105430; PubMed=9890424;
RX   DOI=10.1002/(SICI)1096-9071(199901)57:1<68::AID-JMV10>3.0.CO;2-E;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
RL   J. Med. Virol. 57:68-74(1999).
DR   EMBL; AF051351; AAC35761.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71039 MW;  044FF5EA7C492791 CRC64;

  Query Match             95.1%;  Score 2569;  DB 2;  Length 660;
  Best Local Similarity   94.5%;  Pred. No. 1.4e-170;
  Matches  496;  Conservative   14;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231
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Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:|:  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||:||||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||:|||:|||||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTSSDQLLIENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| |||||||| ||| ||||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 10
Q69419
ID Q69419 PRELIMINARY; PRT; 660 AA.
AC Q69419;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ORF1, ORF2 & ORF3.
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RA von Brunn A., Seebach J., Thyagarajan S.P., Mohanavalli B., Menon T.,
RA Froesner G.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; X99441; CAA67804.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70960 MW; DAC3DF95F91689F8 CRC64;

Query Match 95.1%; Score 2569; DB 2; Length 660;
Best Local Similarity 94.5%; Pred. No. 1.4e-170;
Matches 496; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| ||||||||||||||||||||||||||:|||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:|:  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYRSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSALRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||:||||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||:|:|||||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| |||||||| ||| ||||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 11
O91856
ID O91856 PRELIMINARY; PRT; 660 AA.
AC O91856;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Structural protein.
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=94-Egypt;
RX MEDLINE=99105430; PubMed=9890424;
RX DOI=10.1002/(SICI)1096-9071(199901)57:1<68::AID-JMV10>3.0.CO;2-E;
RA Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RT "Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
RL J. Med. Virol. 57:68-74(1999).
DR EMBL; AF051352; AAC35764.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 71025 MW; 16C560FA16941F2A CRC64;

Query Match 95.1%; Score 2568; DB 2; Length 660;
Best Local Similarity 94.5%; Pred. No. 1.6e-170;
Matches 496; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| ||||||||||||||||||||||||||:|||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:|:  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
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Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||||:|||||||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              |||||||||||||||||||||||||||||||||||||:||||| |||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLIENATGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| ||||||||| ||| |||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 12
Q69411
ID   Q69411      PRELIMINARY;      PRT;   660 AA.
AC   Q69411;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Structural protein.
GN   Name=ORF2;
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Donati M.C., Fagan E.A., Harrison T.J.;
RT   "Sequence analysis of full length HEV clones derived directly from
RT   human liver in fulminant hepatitis E.";
RL   (In) Rizzetto M., Purcell R.H., Gerin J.L., Verme G (eds.);
RL   VIRAL HEPATITIS AND LIVER DISEASE, pp.313-316, Edizioni Minerva
RL   Medica, Torino (1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Harrison T.J.;
RL   Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X98292; CAA66937.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71024 MW;  F37E3FEFF7A4EAD1 CRC64;

  Query Match           95.1%;  Score 2568;  DB 2;  Length 660;
  Best Local Similarity   94.7%;  Pred. No. 1.6e-170;
  Matches  497;  Conservative   11;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||| ||:|||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSPVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGLPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||| ||||||  ||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALEFEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||||:|||||||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              |||||||||||||||||||||||||||||||||||||:||||| |||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||| ||||| ||||||||| ||| |||||||||||| ||||
Db        592 PVAISAVAVLAPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQ 636


RESULT 13
Q81878
ID   Q81878      PRELIMINARY;      PRT;   660 AA.
AC   Q81878;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Complete genome sequence.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Uchida T.;
RL   Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; D11093; BAA01867.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70937 MW;  5412313F1A2EF4A9 CRC64;

  Query Match           94.9%;  Score 2563;  DB 2;  Length 660;
  Best Local Similarity   94.1%;  Pred. No. 3.7e-170;
  Matches  494;  Conservative   14;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||||:|||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYGISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||:|||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGVLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGTDGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||||:|||||||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              | ||||||||||||||||||||||||||||||||||:|:||||||||||||||| ||||
Db        532 YCKTPFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
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              ||:||| ||||| ||||||||| ||| |||||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQ 636


RESULT 14
Q6XXV0
ID   Q6XXV0      PRELIMINARY;      PRT;   660 AA.
AC   Q6XXV0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Structural protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RX   MEDLINE=98071272; PubMed=9407381;
RX   DOI=10.1002/(SICI)1096-9071(199712)53:4<340::AID-JMV5>3.0.CO;2-7;
RA   van Cuyck-Gandre H., Zhang H.Y., Tsarev S.A., Clements N.J.,
RA   Cohen S.J., Caudill J.D., Buisson Y., Coursaget P., Warren R.L.,
RA   Longer C.F.;
RT   "Characterization of hepatitis E virus (HEV) from Algeria and Chad by
RT   partial genome sequence.";
RL   J. Med. Virol. 53:340-347(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RX   MEDLINE=99105430; PubMed=9890424;
RX   DOI=10.1002/(SICI)1096-9071(199901)57:1<68::AID-JMV10>3.0.CO;2-E;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
RL   J. Med. Virol. 57:68-74(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RX   MEDLINE=22987819; PubMed=14625096; DOI=10.1016/S0928-8244(03)00241-4;
RA   van Cuyck H., Juge F., Roques P.;
RT   "Phylogenetic analysis of the first complete hepatitis E virus (HEV)
RT   genome from Africa.";
RL   FEMS Immunol. Med. Microbiol. 39:133-139(2003).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RA   Van Cuyck-Gandre H., Zhang H.Y., Tsarev S.A., Clements N.J.,
RA   Cohen S.J., Caudill J.D., Buisson Y., Coursaget P., Warren R.L.,
RA   Longer C.F.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RA   van Cuyck H., Roberston D., Juge F., Roques P., Lemey P.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY204877; AAB61825.2; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70949 MW;  EA56732D458D0AB1 CRC64;

  Query Match             94.8%;  Score 2560;  DB 2;  Length 660;
  Best Local Similarity   94.3%;  Pred. No. 5.9e-170;
  Matches  495;  Conservative   13;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
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Db        112 AVAPAHDTPPVSDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:|:  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||:||||||||||||||||||||:||||||||  |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||:|||| ||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLIENVAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| ||||||||| ||| |||||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 15
Q80IY5
ID   Q80IY5      PRELIMINARY;      PRT;   660 AA.
AC   Q80IY5;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Structural protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Osh 205;
RA   Robertson B.H., Lu L., Drobeniuc J., Favorov M., Usmanov R.,
RA   Kobylnilkov N., Balayan M.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF455784; AAO67359.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70881 MW;  AB83CAC3F181164E CRC64;

  Query Match             94.7%;  Score 2559;  DB 2;  Length 660;
  Best Local Similarity   94.1%;  Pred. No. 6.9e-170;
  Matches  494;  Conservative   13;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||:|| ||:|||||||||||||||||||||||||||||||||||||||| ||||||||
Db        112 AVSPAPDTAPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
                ||||||||||||||||||||  |||||||||:|||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
                ||||||  ||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        352 DLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
                |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
                ||||||||||:|||||| |:|:||:|| |||||||||||||||||||||||| |::|
Db        472 WLSLTAAEYDQTTYGSSTNPMYVSDTVTFVNVATGAQAVARSLDWSKVTLDGRPLTTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
                |||||:|||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        532 YSKTFYVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
                ||::||  |||| |||| |||| ||| ||||||||||||| ||||
Db        592 PVSVSAVGVLAPHSALAALEDTIDYPARAHTFDDFCPECRNLGLQ 636


Search completed: July 14, 2005, 15:50:28
Job time : 39.3019 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 14, 2005, 00:29:03 ; Search time 44.6604 Seconds
(without alignments)
4676.418 Million cell updates/sec

Title: US-09-769-066-25
Perfect score: 2769
Sequence: 1 AVAPAHDTPPVPDVDSRGAI.....PLGLQGCAFQSTVAELQRLK 540

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2769	100.0	540	2	AAR96101	Aar96101 Hepatitis
2	2769	100.0	549	2	AAR96091	Aar96091 Hepatitis
3	2769	100.0	660	2	AAR38785	Aar38785 HEV ORF2
4	2769	100.0	660	2	AAR39306	Aar39306 Burma str
5	2769	100.0	660	2	AAR96089	Aar96089 Hepatitis
6	2769	100.0	660	2	AAW35826	Aaw35826 Hepatitis
7	2769	100.0	660	2	AAW80197	Aaw80197 Protein e
8	2769	100.0	660	2	AAW93389	Aaw93389 Human HEV
9	2769	100.0	660	3	AAB24120	Aab24120 Hepatitis
10	2769	100.0	660	4	AAB62523	Aab62523 HEV-Burma
11	2769	100.0	660	5	AAO15699	Aao15699 Hepatitis
12	2769	100.0	660	7	ADD24376	Add24376 Hepatitis
13	2762	99.7	549	2	AAW76367	Aaw76367 Hepatitis
14	2762	99.7	660	2	AAW76369	Aaw76369 Hepatitis
15	2762	99.7	660	2	AAW71210	Aaw71210 Protein e
16	2760	99.7	660	2	AAR70323	Aar70323 Hepatitis
17	2760	99.7	660	4	AAE12980	Aae12980 Hepatitis
18	2756	99.5	660	2	AAR91814	Aar91814 Hepatitis
19	2756	99.5	660	2	AAW93386	Aaw93386 Human HEV
20	2756	99.5	660	2	AAW93388	Aaw93388 Human HEV
21	2756	99.5	660	5	ABB81670	Abb81670 Hepatitis
22	2756	99.5	660	6	ADA50060	Ada50060 Hepatitis
23	2756	99.5	660	7	ADB97807	Adb97807 HEV ORF2
24	2754	99.5	660	5	ABJ04803	Abj04803 Hepatitis
25	2752	99.4	660	2	AAW93390	Aaw93390 Human HEV
26	2751	99.3	660	2	AAW93395	Aaw93395 Human HEV
27	2747	99.2	660	2	AAR51265	Aar51265 HEV strai
28	2747	99.2	660	2	AAW81520	Aaw81520 Hepatitis
29	2745	99.1	660	5	ABJ04811	Abj04811 Hepatitis
30	2744	99.1	660	2	AAW93391	Aaw93391 Human HEV
31	2743	99.1	660	5	ABJ04820	Abj04820 Hepatitis
32	2743	99.1	660	5	ABJ04819	Abj04819 Hepatitis
33	2741	99.0	660	2	AAW93392	Aaw93392 Human HEV
34	2741	99.0	660	5	ABJ04807	Abj04807 Hepatitis
35	2741	99.0	660	5	ABJ04809	Abj04809 Hepatitis
36	2738	98.9	660	5	ABJ04822	Abj04822 Hepatitis
37	2737	98.8	660	5	ABJ04818	Abj04818 Hepatitis
38	2737	98.8	660	5	ABJ04805	Abj04805 Hepatitis
39	2736	98.8	660	5	ABJ04806	Abj04806 Hepatitis
40	2734	98.7	660	2	AAR14619	Aar14619 Protein e
41	2734	98.7	660	5	ABJ04821	Abj04821 Hepatitis
42	2733	98.7	660	2	AAW93394	Aaw93394 Human HEV
43	2731	98.6	660	2	AAW93393	Aaw93393 Human HEV
44	2731	98.6	660	4	ADH13471	Adh13471 Hepatitis
45	2729	98.6	660	5	ABJ04810	Abj04810 Hepatitis

ALIGNMENTS

RESULT 1
AAR96101
ID AAR96101 standard; protein; 540 AA.
XX
AC AAR96101;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Burma strain) recombinant 62K antigen.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid.
XX
OS Hepatitis E virus; Burma strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Claim 5; Page 92-93; 125pp; English.
XX
CC DNA (AAT27109) coding for the 62K antigen (AAR96091) of hepatitis E virus
CC (HEV) Burma strain capsid protein was cloned into baculovirus expression
CC vector pBluBacIII and recombinant 62K was expressed in Sf9 insect cells.
CC High levels of expression were obtd. and the recombinant 62K was obtd. in
CC over 95% purity. However, C-terminal processing resulted in the deletion
CC of 9 or 23 amino acids from 62K, giving 2 related polypeptide species
CC (AAR96101 and AAR96103). Similar results were obtd. with HEV Mexico 62K
CC antigen (see also AAR96102 and AAR96104). Recombinant 62K represents an
CC improved antigen, in comparison to bacterial expressed proteins, for use
CC in HEV diagnostic assays, and also has excellent immunogenic properties.
CC (Updated on 16-OCT-2003 to standardise OS field)

```
XX
SQ   Sequence 540 AA;

  Query Match            100.0%;  Score 2769;  DB 2;  Length 540;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-224;
  Matches  540;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540


RESULT 2
AAR96091
ID   AAR96091 standard; protein; 549 AA.
XX
AC   AAR96091;
XX
DT   16-OCT-2003  (revised)
DT   06-AUG-1996  (first entry)
XX
DE   Hepatitis E virus (Burma strain) 62K antigen.
XX
KW   HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW   diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW   capsid.
XX
OS   Hepatitis E virus; Burma strain.
XX
PN   WO9612807-A2.
XX
PD   02-MAY-1996.
XX
PF   23-OCT-1995;   95WO-US013703.
XX
PR   24-OCT-1994;   94US-00327952.
PR   13-OCT-1995;   95US-00542634.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fuerst TR,  Mcatee CP,  Yarbough PO,  Zhang Y;
XX
DR   WPI; 1996-230608/23.
DR   N-PSDB; AAT27109.
XX
PT   Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT   diagnostic reagents for determining HEV infection and in vaccines.
XX
PS   Claim 3; Page 83-84; 125pp; English.
XX
CC   62K antigen (AAR96091) comprises the C-terminal 549 amino acids of
CC   hepatitis E virus (HEV) Burma strain capsid protein (see also AAR96089).
CC   It is obtd. by PCR amplification of HEV Burma ORF-2 (AAT27107), insertion
CC   of amplified DNA (AAT27109) into vector pGEX and expression in E. coli
CC   cells. Expression of full-length ORF-2 in Sf9 insect cells using a
CC   baculovirus system also results in prodn. of 62K antigen (see also
CC   AAR96101 and AAR96103). 62K represents an improved antigen, in comparison
CC   to bacterial expressed proteins, for use in HEV diagnostic assays, and
CC   also has excellent immunogenic properties. (Updated on 16-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 549 AA;

  Query Match            100.0%;  Score 2769;  DB 2;  Length 549;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-224;
  Matches  540;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540


RESULT 3
AAR38785
ID   AAR38785 standard; protein; 660 AA.
XX
AC   AAR38785;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   11-JAN-1994  (first entry)
XX
```

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DE   HEV ORF2 protein.
XX
KW   Enterically transmitted non-A non-B hepatitis; ET-NANB; vaccine.
XX
OS   Hepatitis E virus; Burma strain.
XX
FH   Key             Location/Qualifiers
FT   Peptide         225. .660
FT                   /label= C2
FT   Peptide         334. .660
FT                   /label= SG3
FT   Peptide         613. .660
FT                   /label= 406.3-2
XX
PN   WO9314116-A1.
XX
PD   22-JUL-1993.
XX
PF   15-JAN-1993;   93WO-US000459.
XX
PR   17-JAN-1992;   92US-00822335.
PR   01-MAY-1992;   92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
PA   (USSH ) US SEC DEPT HEALTH.
XX
PI   Reyes GR,  Bradley DW,  Tam AW,  Carl M;
XX
DR   WPI; 1993-243144/30.
DR   N-PSDB; AAQ47129.
XX
PT   New immunogenic hepatitis E virus (HEV) peptide(s) - are from the ORF1,
PT   ORF2 and ORF3 regions of HEV, useful as a vaccine against HEV infection.
XX
PS   Disclosure; Fig 8; 48pp; English.
XX
CC   Immunogenic hepatitis E virus (HEV) peptides are selected from the ORF1,
CC   ORF2 and ORF3 regions of HEV. The peptides can be used in vaccines to
CC   prevent infection by HEV. The antibodies can neutralise and block HEV
CC   infection and can be used to prevent or treat HEV infection. The peptides
CC   and antibodies can also be used as diagnostic reagents. (Updated on 25-
CC   MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS
CC   field)
XX
SQ   Sequence 660 AA;

  Query Match             100.0%;  Score 2769;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-224;
  Matches  540;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 4
AAR39306
ID   AAR39306 standard; protein; 660 AA.
XX
AC   AAR39306;
XX
DT   25-MAR-2003  (revised)
DT   14-FEB-1994  (first entry)
XX
DE   Burma strain HEV ORF2 puative virus capsid protein.
XX
KW   Hepatitis E virus; vaccine; neutralising antibodies; infection; block;
KW   open reading frame; antibodies.
XX
OS   Hepatitis E virus.
XX
PN   WO9314208-A2.
XX
PD   22-JUL-1993.
XX
PF   19-JAN-1993;   93WO-US000475.
XX
PR   17-JAN-1992;   92US-00822335.
PR   20-APR-1992;   92US-00870985.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Reyes GR,  Bradley DW,  Twu J,  Purdy MA,  Tam AW,  Krawczynski KZ;
XX
DR   WPI; 1993-243223/30.
DR   N-PSDB; AAQ46813.
XX
PT   Antigen and antibody vaccines against hepatitis E virus infection -
PT   contain peptide(s) derived from capsid protein C-terminal or antibodies
PT   against protein.
XX
PS   Disclosure; Fig 7; 43pp; English.
XX
CC   The sequence is that of the putative virus capsid protein encoded by
CC   Burma strain hepatitis E virus (HEV) open reading frame ORF2. This
CC   protein or peptide fragments of it may be used in a vaccine composition
CC   for immunising an individual against HEV. Antibodies raised against these
CC   peptides can also be used in such vaccines. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 660 AA;

  Query Match             100.0%;  Score 2769;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-224;
  Matches  540;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231
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Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651
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RESULT 5
AAR96089
ID AAR96089 standard; protein; 660 AA.
XX
AC AAR96089;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Burma strain) capsid protein.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid.
XX
OS Hepatitis E virus; Burma strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
DR N-PSDB; AAT27107.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Disclosure; Page 78-80; 125pp; English.
XX
CC The putative capsid protein (AAR96089) of hepatitis E virus (HEV) Burma
CC strain is encoded by ORF-2 (AAT27107) of the virus. PCR amplification of
CC ORF-2 allows prodn. of capsid protein or of C-terminal regions of the
CC capsid protein (see also AAR96091, AAR96093 and AAR96095) and expression
CC in Spodoptera frugiperda Sf9 insect cells using a baculovirus vector
CC provides recombinant C-terminal regions (see also AAR96101 and AAR96103)
CC useful as diagnostic reagents and in vaccines. The HEV Mexico strain
CC capsid protein (AAR96090) may similarly be used. (Updated on 16-OCT-2003
CC to standardise OS field)
XX
SQ Sequence 660 AA;

```
  Query Match             100.0%;  Score 2769;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-224;
  Matches  540;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651
```

RESULT 6
AAW35826
ID AAW35826 standard; protein; 660 AA.
XX
AC AAW35826;
XX
DT 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 26-FEB-1998 (first entry)
XX
DE Hepatitis E virus Burma strain protein from ORF2.
XX
KW Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
KW diagnosis; HEV.
XX
OS Hepatitis E virus; - Burma strain.
XX
PN US5686239-A.
XX
PD 11-NOV-1997.
XX
PF 09-MAY-1994; 94US-00240049.
XX
PR 17-JUN-1988; 88US-00208997.
PR 11-APR-1989; 89US-00336672.

```
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   17-JAN-1992;   92US-00822335.
PR   20-APR-1992;   92US-00870985.
PR   01-MAY-1992;   92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Tam AW,  Reyes GR,  Yarbough PO;
XX
DR   WPI; 1997-558132/51.
DR   N-PSDB; AAT96959.
XX
PT   Diagnosis of hepatitis E virus Burma and Mexico strain infection - by
PT   immunoassay with hepatitis E virus peptide antigens.
XX
PS   Disclosure; Col 39-42; 36pp; English.
XX
CC   A method has been developed for detecting hepatitis E virus (HEV)
CC   antibodies (Ab). The method comprises: (a) reacting a serum sample with a
CC   HEV peptide antigen; and (b) examining the peptide for the presence of
CC   bound Ab, where the presence of bound Ab indicates the presence of HEV
CC   Ab. The present sequence represents the protein from the open reading
CC   frame, ORF2, from HEV Burma strain. The method can be used to diagnose
CC   infection with the enterically transmitted non-A/non-B viral hepatitis
CC   agent HEV, specifically the HEV Burma and Mexico strains. (Updated on 25-
CC   MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to standardise OS
CC   field)
XX
SQ   Sequence 660 AA;

  Query Match             100.0%;  Score 2769;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-224;
  Matches  540;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651
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RESULT 7
AAW80197
ID   AAW80197 standard; protein; 660 AA.
XX
AC   AAW80197;
XX
DT   27-AUG-2003  (revised)
DT   25-MAR-2003  (revised)
DT   23-DEC-1998  (first entry)
XX
DE   Protein encoded by ORF2 of ET-NANB (HEV) Burma strain DNA sequence.
XX
KW   Enterically transmitted non A non B hepatitis virus; ET-NANB;
KW   Hepatitis E virus; HEV; Burma HEV isolate; vaccine; diagnostic probe.
XX
OS   Non-A.
OS   non-B hepatitis virus.
XX
PN   US5824649-A.
XX
PD   20-OCT-1998.
XX
PF   07-JUN-1995;   95US-00475807.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   25-JUL-1994;   94US-00279823.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Bradley DW,  Reyes GR,  Krawczynski KZ,  Tam A,  Fry KE,  Yarbough PO;
XX
DR   WPI; 1998-582599/49.
DR   N-PSDB; AAV66321.
XX
PT   Hepatitis E virus proteins - useful for diagnosis or vaccine production
PT   the virus.
XX
PS   Claim 6; Col 65-70; 47pp; English.
XX
CC   AAW80196-98 are encoded by the genome of the Burma strain of enterically
CC   transmitted non A non B hepatitis virus (ET-NANB) (hepatitis E virus
CC   (HEV)). The specification describes an isolated protein which is
CC   specifically immunoreactive with antibodies present in individuals
CC   infected with HEV and encoded by a sequence contained in an open reading
CC   frame (ORF) of an HEV genome. The genome has a sequence that is more than
CC   70% identical to the ORF1 sequence from Burma HEV isolate. The protein is
CC   used as a vaccine and a diagnostic probe for ET-NANB. (Updated on 25-MAR-
CC   2003 to correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 660 AA;

  Query Match             100.0%;  Score 2769;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-224;
  Matches  540;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651
```

RESULT 8
AAW93389
ID AAW93389 standard; protein; 660 AA.
XX
AC AAW93389;
XX
DT 11-JUN-1999 (first entry)
XX
DE Human HEV ORF 2 protein from strain Burma.
XX
KW Swine hepatitis E virus; HEV; cross-reaction; antibody; human; therapy;
KW vaccine; immunise; infection; detection; diagnosis; prevention.
XX
OS Hepatitis E virus.
XX
PN WO9904029-A2.
XX
PD 28-JAN-1999.
XX
PF 17-JUL-1998; 98WO-US014665.
XX
PR 18-JUL-1997; 97US-0053069P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Meng X, Emerson SU, Purcell RH;
XX
DR WPI; 1999-132270/11.
XX
PT New isolated swine hepatitis E virus - used to develop products for the
PT diagnosis, prevention and treatment of hepatitis E virus infection in
PT mammals, particularly humans.
XX
PS Example 1; Fig 3A; 70pp; English.
XX
CC This invention describes a swine hepatitis E virus (HEV) and its natural
CC mutants which are capable of cross-reacting with antibodies reactive with
CC a human HEV strain or natural mutants. The HEV and the proteins can be
CC used in vaccines for immunising against HEV infection. The swine HEV can
CC be used in humans to prevent possible infection by human HEV. The swine
CC HEV can also be used as a therapeutic treatment for infection by other
CC strains of HEV. The swine HEV can also be used for the production of
CC antibodies which can be used in therapy, detection and diagnosis. The
CC products can also be used for determining the susceptibility of cells or
CC organs to infection with swine HEV. The swine HEV is particularly useful
CC for the development of agents for the prevention, treatment and detection
CC of human HEV because it is not a human virus and thus can be handled both
CC experimentally and clinically without fear of severe infection and/or
CC contamination
XX
SQ Sequence 660 AA;

Query Match 100.0%; Score 2769; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.3e-224;
Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651
```

RESULT 9
AAB24120
ID AAB24120 standard; protein; 660 AA.
XX
AC AAB24120;
XX
DT 29-JAN-2001 (first entry)
XX
DE Hepatitis E virus Burma strain ORF2 protein sequence SEQ ID NO:8.
XX
KW Hepatitis E virus; HEV; non-A/non-B viral hepatitis; viral protein;
KW immunological; diagnosis; hepatitis; infection; identification;
KW detection; immunoreactive; hepatotropic; antiinflammatory; virucide;
KW vaccine; antiviral; antigenic; antibody; antigen.
XX
OS Hepatitis E virus.
XX
PN US6120988-A.
XX
PD 19-SEP-2000.
XX
PF 07-JUN-1995; 95US-00478507.
XX
PR 17-JUN-1988; 88US-00208997.
PR 11-APR-1989; 89US-00336672.
PR 16-JUN-1989; 89US-00367486.
PR 13-OCT-1989; 89US-00420921.
PR 05-APR-1990; 90US-00505888.
PR 05-APR-1991; 91US-00681078.

```
PR   25-JUL-1994;   94US-00279823.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
PA   (USGO ) US GOVERNMENT.
XX
PI   Yarbough PO,  Krawczynski KZ,  Fry KE,  Bradley DW,  Tam A,  Reyes GR;
XX
DR   WPI; 2000-593712/56.
DR   N-PSDB; AAA99259.
XX
PT   Identifying recombinant antigen immunoreactive with antibody induced by
PT   hepatitis E virus (HEV), for detecting HEV infection, comprises
PT   immunoreacting a polypeptide from an HEV genome with an HEV-positive
PT   antiserum.
XX
PS   Claim 6; Col 63-68; 46pp; English.
XX
CC   The present invention describes a method for identifying a recombinant
CC   antigen immunoreactive with a hepatitis E virus (HEV)-induced antibody.
CC   The method comprises producing a polypeptide derived from an HEV genome,
CC   immunoreacting the polypeptide with an HEV-positive antiserum and
CC   selecting the polypeptide as a recombinant antigen if the polypeptide
CC   reacts with the HEV-positive antiserum. The method is useful for
CC   identifying recombinant antigen immunoreactive with antibody induced by
CC   HEV. The enterically transmitted non-A/non-B hepatitis (ET-NANB (also
CC   known as HEV))-specific fragments are useful for identifying ET-NANB-
CC   derived cDNAs, which contain additional sequence information, as primers
CC   for detecting ET-NANB viral genomic material in a patient sample, for the
CC   synthesis of polypeptides for use in immunoassays, and for identifying
CC   similar antigenic regions encoded by related viral strains, e.g. Burmese
CC   strain. The antigens are especially useful in the preparation of vaccine
CC   against ET-NANB infection. These antigens may further be used to prepare
CC   antibodies to ET-NANB virus particles for use directly as antiviral
CC   agents, and to produce antiserum designed for pre- or post-exposure
CC   prophylaxis. The present sequence represents a specifically claimed HEV
CC   Burma strain protein sequence for use in the present invention
XX
SQ   Sequence 660 AA;

  Query Match            100.0%;  Score 2769;  DB 3;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-224;
  Matches  540;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 10
AAB62523
ID   AAB62523 standard; protein; 660 AA.
XX
AC   AAB62523;
XX
DT   23-JUL-2001  (first entry)
XX
DE   HEV-Burma strain viral protein ORF2.
XX
KW   HEV; enterically transmitted nonA/nonB viral hepatitis agent; viral;
KW   ET-NANB; infection; vaccine.
XX
OS   Hepatitis E virus.
XX
PN   US6229005-B1.
XX
PD   08-MAY-2001.
XX
PF   03-AUG-1998;   98US-00128275.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   25-JUL-1994;   94US-00279823.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Reyes GR,  Yarbough PO,  Bradley DW,  Krawczynski KZ,  Tam AW;
PI   Fry KE;
XX
DR   WPI; 2001-342705/36.
DR   N-PSDB; AAF83495.
XX
PT   New DNA sequences of enterically transmitted non-A/non-B (ET-NANB)
PT   hepatitis viral agent, useful in diagnosing infection by an enterically
PT   transmitted agent (e.g. ET-NANB virus), as well as in vaccine production.
XX
PS   Disclosure; Col 63-68; 45pp; English.
XX
CC   The invention relates to an isolated DNA comprising the genome of an
CC   enterically transmitted nonA/nonB (ET-NANB) viral hepatitis agent (also
CC   referred as HEV). The DNA sequences or their fragments are useful in
CC   preparing ET-NANB viral proteins and as probes for virus detection. These
CC   are particularly useful in diagnosing infection by an enterically
CC   transmitted agent (e.g. ET-NANB virus), as well as in vaccine production.
CC   The present sequence represents a ORF2 protein encoded by a ET-NANB viral
CC   DNA sequence from HEV-Burma strain
XX
SQ   Sequence 660 AA;

  Query Match            100.0%;  Score 2769;  DB 4;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-224;
  Matches  540;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231
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Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651
```

RESULT 11
AAO15699
ID AAO15699 standard; protein; 660 AA.
XX
AC AAO15699;
XX
DT 08-NOV-2002 (first entry)
XX
DE Hepatitis E virus (Burma strain) ORF2 protein.
XX
KW HEV; enterically transmitted nonA/nonB hepatitis viral agent;
KW Burma strain; bile; ORF2.
XX
OS Hepatitis E virus.
XX
PN US6379891-B1.
XX
PD 30-APR-2002.
XX
PF 19-APR-2000; 2000US-00553427.
XX
PR 17-JUN-1988; 88US-00208997.
PR 11-APR-1989; 89US-00336672.
PR 16-JUN-1989; 89US-00367486.
PR 13-OCT-1989; 89US-00420921.
PR 05-APR-1990; 90US-00505888.
PR 15-APR-1991; 91US-00681078.
PR 25-JUL-1994; 94US-00279823.
PR 07-JUN-1995; 95US-00478507.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Reyes GR, Yarbough PO, Bradley DW, Krawczynski KZ, Tam A, Fry KE;
XX
DR WPI; 2002-517277/55.
DR N-PSDB; AAL50386.
XX
PT Detecting the presence of enterically transmitted nonA/nonB hepatitis
PT viral (HEV) agents in bile samples from infected humans and monkeys using
PT polymerase chain reaction.
XX
PS Disclosure; Col 19-24; 61pp; English.
XX
CC The invention comprises a method for detecting the presence of
CC enterically transmitted nonA/nonB hepatitis viral (HEV) agents in a
CC sample and isolating HEV agents or nucleic acid fragments produced by the
CC agent. The method utilises PCR - using bile from a human or cynomolgus
CC monkey actively infected with HEV as a source of the agent. The method of
CC the invention is used for detecting the presence of a viral agent in a
CC sample of cultured cells infected with the agent and isolating
CC enterically transmitted nonA/nonB HEV agents or nucleic acid fragments
CC produced by the agent. The present amino acid sequence represents the
CC protein encoded by open reading frame 2 (ORF2) of a DNA sequence isolated
CC from a Burmese strain of the Hepatitis E virus
XX
SQ Sequence 660 AA;

```
  Query Match             100.0%;  Score 2769;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-224;
  Matches  540;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651
```

RESULT 12
ADD24376
ID ADD24376 standard; protein; 660 AA.
XX
AC ADD24376;
XX
DT 15-JAN-2004 (first entry)
XX
DE Hepatitis E virus strain Burma ORF 2.
XX
KW non-A/non-B viral hepatitis; ET-NANB; HEV; vaccine.
XX
OS Hepatitis E virus; strain Burma.
XX
PN US2003124510-A1.
XX
PD 03-JUL-2003.

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XX
PF   07-MAY-2001; 2001US-00851410.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   25-JUL-1994;   94US-00279823.
PR   03-AUG-1998;   98US-00128275.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Reyes GR,  Yarbough PO,  Bradley DW,  Krawczynski KZ,  Tam AW;
PI   Fry KE;
XX
DR   WPI; 2003-810978/76.
DR   N-PSDB; ADD24374.
XX
PT   New proteins derived from an enterically transmitted non-A/non-B (ET-
PT   NANB) viral hepatitis agent, useful for diagnosing ET-NANB infection and
PT   producing vaccines for immunizing an individual against ET-NANB hepatitis
PT   viral agent.
XX
PS   Disclosure; SEQ ID NO 8; 81pp; English.
XX
CC   The invention relates to a protein derived from an enterically
CC   transmitted non-A/non-B viral hepatitis agent. The viral proteins are
CC   useful for detecting infection by the enterically transmitted non-A/non-B
CC   (ET-NANB/HEV) hepatitis viral agent. The proteins are also useful for
CC   producing vaccines for immunising an individual against HEV hepatitis
CC   viral agent. The DNA fragments are useful for identifying and sequencing
CC   the entire viral agent and for assaying the viral agent in an infected
CC   sample. The present sequence is used in the exemplification of the
CC   invention.
XX
SQ   Sequence 660 AA;

  Query Match             100.0%;  Score 2769;  DB 7;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-224;
  Matches  540;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTPFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTPFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 13
AAW76367
ID   AAW76367 standard; protein; 549 AA.
XX
AC   AAW76367;
XX
DT   03-DEC-1998  (first entry)
XX
DE   Hepatitis E virus hollow particle protein ORF2.
XX
KW   Hollow particle protein; virus; antibody; detection; immunoassay;
KW   infection.
XX
OS   Hepatitis virus.
XX
FH   Key             Location/Qualifiers
FT   Protein         1. .549
FT                   /label= ORF2
FT                   /note= "partial sequence"
XX
PN   JP10234383-A.
XX
PD   08-SEP-1998.
XX
PF   28-FEB-1997;   97JP-00062445.
XX
PR   28-FEB-1997;   97JP-00062445.
XX
PA   (DENK-) DENKA SEIKEN KK.
PA   (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR   WPI; 1998-535037/46.
DR   N-PSDB; AAV61686.
XX
PT   Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids
PT   encoding it - useful for more accurate detection of HEV in samples, using
PT   immuno-assays and nucleic acid hybridisation.
XX
PS   Claim 1; Page 15-17; 29pp; Japanese.
XX
CC   This sequence represents a Hepatitis E viral hollow particle protein
CC   described as ORF2. This polypeptide can be used to raise antibodies to
CC   detect HEV infection in samples, e.g. by immuno-assay based techniques,
CC   and the nucleic acid can be used for the same in nucleic acid
CC   hybridisation assays. The polypeptide and nucleic acid allow more
CC   accurate detection of HEV than previously possible
XX
SQ   Sequence 549 AA;

  Query Match             99.7%;  Score 2762;  DB 2;  Length 549;
  Best Local Similarity   99.8%;  Pred. No. 7e-224;
  Matches  539;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540


RESULT 14
AAW76369
ID   AAW76369 standard; protein; 660 AA.
XX
AC   AAW76369;
XX
DT   03-DEC-1998  (first entry)
XX
DE   Hepatitis E virus hollow particle protein #2.
XX
KW   Hollow particle protein; virus; antibody; detection; immunoassay;
KW   infection.
XX
OS   Hepatitis virus.
XX
PN   JP10234383-A.
XX
PD   08-SEP-1998.
XX
PF   28-FEB-1997;   97JP-00062445.
XX
PR   28-FEB-1997;   97JP-00062445.
XX
PA   (DENK-) DENKA SEIKEN KK.
PA   (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR   WPI; 1998-535037/46.
DR   N-PSDB; AAV61688.
XX
PT   Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids
PT   encoding it - useful for more accurate detection of HEV in samples, using
PT   immuno-assays and nucleic acid hybridisation.
XX
PS   Claim 13; Page 24-26; 29pp; Japanese.
XX
CC   This sequence represents a Hepatitis E viral hollow particle protein.
CC   This polypeptide can be used to raise antibodies to detect HEV infection
CC   in samples, e.g. by immuno-assay based techniques, and the nucleic acid
CC   can be used for the same in nucleic acid hybridisation assays. The
CC   polypeptides and nucleic acids allow more accurate detection of HEV than
CC   previously possible
XX
SQ   Sequence 660 AA;

  Query Match           99.7%;  Score 2762;  DB 2;  Length 660;
  Best Local Similarity   99.8%;  Pred. No. 9.1e-224;
  Matches  539;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
                |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 15
AAW71210
ID   AAW71210 standard; protein; 660 AA.
XX
AC   AAW71210;
XX
DT   25-MAR-2003  (revised)
DT   30-OCT-1998  (first entry)
XX
DE   Protein encoded by ORF 2 of the Burmese isolate of ET-NANB.
XX
KW   Enterically transmitted nonA/nonB hepatitis virus; identification; HEV;
KW   ET-NANB; detection; vaccine.
XX
OS   Hepatitis virus.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 496
FT                   /note= "not specified"
XX
PN   US5789559-A.
XX
PD   04-AUG-1998.
XX
PF   25-JUL-1994;   94US-00279823.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   19-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Bradley DW,  Reyes GR,  Krawczynski KZ,  Tam A,  Fry KE,  Yarbough PO;
XX
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DR   WPI; 1998-446186/38.
XX
PT   Hepatitis E virus DNA - useful for e.g. virus detection and viral protein
PT   production.
XX
PS   Disclosure; Col 63-68; 45pp; English.
XX
CC   AAW71209-11 represent the proteins encoded by the open reading frames
CC   (ORFs) of the DNA sequence of the Burmese isolate of an enterically
CC   transmitted nonA/nonB viral hepatitis agent (ET-NANB). The nucleic acid
CC   sequence may be used for identifying and sequencing the entire viral
CC   agent (also referred to as HEV), detecting ET-NANB in infected samples,
CC   e.g. by specific amplification of virus-derived DNA sequences and for
CC   producing recombinant viral proteins for use in vaccines. (Updated on 25-
CC   MAR-2003 to correct PF field.)
XX
SQ   Sequence 660 AA;

  Query Match             99.7%;  Score 2762;  DB 2;  Length 660;
  Best Local Similarity   99.8%;  Pred. No. 9.1e-224;
  Matches  539;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
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Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSXSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


Search completed: July 14, 2005, 15:46:29
Job time : 46.6604 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 14, 2005, 02:26:53 ; Search time 9.33962 Seconds
(without alignments)
5563.078 Million cell updates/sec

Title: US-09-769-066-25
Perfect score: 2769
Sequence: 1 AVAPAHDTPPVPDVDSRGAI.....PLGLQGCAFQSTVAELQRLK 540

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2769	100.0	660	1	VHWWH2	structural protein
2	2617.5	94.5	659	1	B44212	structural protein
3	135.5	4.9	1041	2	S55862	probable membrane
4	129.5	4.7	2130	2	AB0821	probable exported
5	127	4.6	583	2	S67571	hypothetical prote
6	125.5	4.5	1306	2	S25370	MSB2 protein - yea
7	125.5	4.5	1879	2	S74915	extracellular nucl
8	125	4.5	3282	2	E82750	hemagglutinin-like
9	125	4.5	3442	2	E82589	hemagglutinin-like
10	125	4.5	3455	2	B82519	hemagglutinin-like
11	124.5	4.5	3570	2	T45025	mucin MUC5B, trach
12	122	4.4	1180	2	E86719	hypothetical prote
13	122	4.4	5188	2	B85547	probable RTX famil
14	122	4.4	5291	2	P90696	hypothetical prote
15	121.5	4.4	766	1	A47001	transcription fact
16	120.5	4.4	687	2	T09994	arginine-tRNA liga
17	120.5	4.4	1483	2	C97012	probably celluloso
18	120	4.3	636	2	S63131	probable membrane
19	120	4.3	1131	2	T41144	hypothetical serin
20	119.5	4.3	948	2	T11678	hypothetical prote
21	118	4.3	725	2	A41258	a-agglutinin core
22	117	4.2	1802	2	S69703	HKR1 protein precu
23	117	4.2	3972	2	S75251	hypothetical prote
24	116.5	4.2	796	2	T21460	hypothetical prote
25	116.5	4.2	918	2	T02759	hypothetical prote
26	116.5	4.2	1161	2	S57180	probable membrane
27	116	4.2	1367	1	S48478	glucan 1,4-alpha-g
28	115.5	4.2	1077	2	H96007	probable acriflavi
29	115.5	4.2	3507	2	T34513	hypothetical prote
30	115	4.2	1213	2	T51032	hypothetical prote
31	115	4.2	3083	2	AH2493	hypothetical prote
32	114.5	4.1	739	2	I56187	transcription fact
33	114	4.1	1350	2	AF2005	RNA polymerase bet
34	114	4.1	2054	2	T46612	multi PDZ domain p
35	113.5	4.1	1419	2	T30531	agglutinin-like ad
36	113.5	4.1	4199	2	S76412	hypothetical prote
37	113	4.1	1975	2	B81192	hemagglutinin/hemo
38	113	4.1	1995	2	G81044	hemagglutinin/hemo
39	113	4.1	2383	2	D64962	probable membrane
40	113	4.1	3013	2	AB0480	probable invasin Y
41	112.5	4.1	547	2	T41213	probable zinc fing
42	112.5	4.1	1014	1	NMCLSS	exo-alpha-sialidas
43	112.5	4.1	1324	2	S52863	DNA-binding protei
44	112	4.0	4753	1	A47437	LDL-receptor-relat
45	111.5	4.0	1104	2	S59310	probable membrane

ALIGNMENTS

RESULT 1
VHWWH2
structural protein 2 precursor - hepatitis E virus (strain Burma)
C;Species: hepatitis E virus
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: C40778
R;Tam, A.W.; Smith, M.M.; Guerra, M.E.; Huang, C.C.; Bradley, D.W.; Fry, K.E.; Reyes, G.P
Virology 185, 120-131, 1991
A;Title: Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length vir
A;Reference number: A40778; MUID:92024067; PMID:1926770
A;Accession: C40778
A;Molecule type: genomic RNA
A;Residues: 1-660 <TAM>
A;Cross-references: UNIPROT:P29326; GB:M73218; NID:g330023; PIDN:AAA45736.1; PID:g330026
A;Note: the authors translated the codon CGC for residue 2 as Ala
C;Superfamily: hepatitis E virus structural protein 2
C;Keywords: structural protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-660/Product: structural protein 2 #status predicted <SP2>

Query Match 100.0%; Score 2769; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 9.4e-185;
Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
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Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531
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Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 2
B44212
structural protein 2 precursor - hepatitis E virus (strain Mexico)
C;Species: hepatitis E virus
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: B44212
R;Huang, C.C.; Nguyen, D.; Fernandez, J.; Yun, K.Y.; Fry, K.E.; Bradley, D.W.; Tam, A.W.
Virology 191, 550-558, 1992
A;Title: Molecular cloning and sequencing of the Mexico isolate of hepatitis E virus (HE
A;Reference number: A44212; MUID:93079857; PMID:1448913
A;Accession: B44212
A;Molecule type: genomic RNA
A;Residues: 1-659 <HUA>
A;Cross-references: UNIPROT:Q03500; GB:M74506; NID:g330017; PIDN:AAA45732.1; PID:g330020
C;Superfamily: hepatitis E virus structural protein 2
C;Keywords: structural protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-659/Product: structural protein 2 #status predicted <SP2>

  Query Match             94.5%;  Score 2617.5;  DB 1;  Length 659;
  Best Local Similarity   94.3%;  Pred. No. 3.2e-174;
  Matches  509;  Conservative   13;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:||||||||:| |||||||| |||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||  |||||||||||||||  ||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:|||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              |||||||||||||||||||:|||||||||||||||||||||:|||||||||| |::|
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||:||| ||||| ||||||||| ||| |||||||||||| ||||||||||||||||||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 650


RESULT 3
S55862
probable membrane protein YNL327w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N0320
C;Species: Saccharomyces cerevisiae
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55862; S63308; S51288
R;Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin, C.
Yeast 11, 567-572, 1995
A;Title: Sequencing analysis of a 15.4 kb fragment of yeast chromosome XIV identifies the
A;Reference number: S55859; MUID:95373280; PMID:7645347
A;Accession: S55862
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1041 <MAF>
A;Cross-references: UNIPROT:P42835; EMBL:Z46259; NID:g633655; PIDN:CAA86371.1; PID:g63365
R;Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin, C.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63287
A;Accession: S63308
A;Molecule type: DNA
A;Residues: 1-1041 <MAW>
A;Cross-references: EMBL:Z71603; NID:g1302444; PID:e239572; PID:g1302445; MIPS:YNL327w
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:EGT2
A;Cross-references: SGD:S0005271; MIPS:YNL327w
A;Map position: 14L
C;Keywords: transmembrane protein
F;4-20/Domain: transmembrane #status predicted <TM1>
F;1025-1041/Domain: transmembrane #status predicted <TM2>

  Query Match              4.9%;  Score 135.5;  DB 2;  Length 1041;
  Best Local Similarity   20.6%;  Pred. No. 0.29;
  Matches  125;  Conservative   82;  Mismatches  211;  Indels  189;  Gaps   27;

Qy         29 TSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEASNYAQYRVAR---ATIRYRP 85
              |:| :|  || |  :: :| :|          :|    |::::      |    :|: |
Db        405 TTPSSSLSATETYSIISSASISVTQASYIDNSTTTAVTQSTSTIAVSSAEKLSSTLSY-- 462

Qy         86 LVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQ 145
                    ||:|    | ||||: |  || | :   :|
Db        463 -----TSNVTISVSSATQHTTTPSYVS-NSTTLSSSSVL---------------------- 495

Qy        146 GWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPY---------TGALGLLDFALELE 196
                || :|          ||          |  :  || ||          |    :  ||: :
Db        496 --ESVISSPYLANTTVSG-------ASSASQSTNPPYVSNSTTSSATQLATIAPFAINIT 546

Qy        197 FRNLTPGNTNTRVSRYSSTARHRLRRG--------ADGTAELTTTAATRFMKDL------ 242
                :::   |||  |  |||     |  |          | |:  ||||  :  : ::
Db        547 GTSISSSITNT--SSVSSTT-SSLSSGPFVSNTAVASGSYILTTTTESAQLTEIGSLIPI 603

Qy        243 ----YFTSTNGVGEIGRG-------IALTLFNLADTLLGGLPTELISSA----------- 280
                  |:|:|  : |           || :: | :   :  : |   ::|
Db        604 STITTSTTTSGTDKTGSNKVASSTEIAQSIVNNSSLSVSTINTNAATAAANARNATFTHA 663

Qy        281 --GGQL---FYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQ 335
                | |   ::|  ::|:  :   |: |:  :  :|   ::      | :| |   |
Db        664 THSGSLQPSYHSSSLLSSTID--TKVTTATTSTSRDGSSSLAFTTGLNQSVVTGTD---- 717

Qy        336 HEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQ----STY------GSSTGPVYVSD 385
                      | :||: : :    |    |||     ||        |:|    :
Db        718 -----------KSDTYSVISSTE----SAQVTEYDSLLPISTLKPTVVTGTSRNSTFSMV 762

Qy        386 SVTLVNVATG-----AQAVARSLDWTKVTLDGR--PLSTIQ------------------ 419
              | | :  ||      | :|  |    :||  |   |:||::
Db        763 SSTKLTEATATDKGDAYSVISSTQSAQVTEYGSMLPISTLETPTVIMSTDESGYFTLTTC 822

Qy        420 -------QYSKTFFVLPLRGKLSFWEAG--------TTKAGYPYNYNTTASDQLLVENAA 464
                    :|     :  | | : :   |         ||      |  :|:    : |
Db        823 TESGQATEYGSLIPISTLDGSVIYTFTGESVVVGYSTTVGAAQYAQHTSL---VPVSTIK 879

Qy        465 GHRVAIST-------YTTSLGAG---------PVSI---SAVAVLAPHSALALLEDTLDY 505
              | : ::||       |:|::||          |||    |  ::    | :|    |:|
Db        880 GSKTSLSTEESVVAGYSTTVGAAQYAQHTSLVPVSTIKGSKTSLSTEESVVAGYSTTVDS 939

Qy        506 PARA-HT 511
```

```
Db        940 AQYAEHT 946


RESULT 4
AB0821
probable exported protein STY2760 [imported] - Salmonella enterica subsp. enterica serov
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB0821
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0821
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2130 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02718.1; PID:g16503731; GSPDB:GN00176
C;Genetics:
A;Gene: STY2760

  Query Match             4.7%;  Score 129.5;  DB 2;  Length 2130;
  Best Local Similarity   21.4%;  Pred. No. 2.1;
  Matches  108;  Conservative   59;  Mismatches  217;  Indels  121;  Gaps   21;

Qy         28 STSPLTSSVATGTNLVLYAAPLSPLLPLQ--DGTNTHIMATEASNYAQYRVARATIRYRP 85
Db        985 NTSVYTSCLAS-DNPVPAAITIEPVDPSQWYDGSGVHALKVKKGDTLQLKVTVKDASGKP 1043

Qy         86 LVPNAV------GGYAISISFWP-------QTTTTPTSVDMNSITSTDVRILVQPGIASE 132
Db       1044 -VPEAPFVLTRGDGYDRKGEKYTAQDGSDLQNIVTPVVIDGESLAWTTTKMGSQTGPDGT 1102

Qy        133 LVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFA 192
Db       1103 RIISVTRPD--THGTRTAITATLYENVAVSASI------DTIFTVVTSP--------DVS 1146

Qy        193 LELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAE--------------LTTTAATR 237
Db       1147 VARMWGHMTPSLTAADSAVYKRPLLYDELASKTGAAEYPEDNERWVVFYGPNTTKTVSPE 1206

Qy        238 FMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEP 297
Db       1207 ACSKGYFPSVEQL--------------DSLYSKYPNGAIK------------TAQGWP 1238

Qy        298 TVKLYTSVENAQQDKGIAIPHD---IDLGES--RVV--IQDYDNQHEQDRPTPSPAPSRP 350
Db       1239 IIRSYWSGTNAGTITPGAPPYDYYTVDLNDDAHRKVPNISDSDRQYQICAATPQPLAGR- 1297

Qy        351 FSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTL 410
Db       1298 --------ITLTSTLATDSDIQAVKAKN-----SDSIPL--VITTTDAAGNPVPYTPFSL 1342

Qy        411 DGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYN------TTASDQLLVENAA 464
Db       1343 I-RDAGTARNTSYTF-----TGSTNMMLAPPTGSAQQFYYNGYTIYGATGAD-------- 1388

Qy        465 GHRVAISTYTTSLGAGPVSISAVAV 489
Db       1389 --GTAVLTLTQAAGPGVKNVITAAL 1411


RESULT 5
S67571
hypothetical protein YDL038c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein D2726
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C;Accession: S67571
R;Paulin, L.; Saren, A.M.; Laamanen, P.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67560
A;Accession: S67571
A;Molecule type: DNA
A;Residues: 1-583 <PAU>
A;Cross-references: UNIPROT:Q99175; EMBL:Z74087; NID:g1431021; PID:e252991; PID:g1431023;
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YDL038c
A;Cross-references: SGD:S0002196
A;Map position: 4L
C;Superfamily: pig submaxillary mucin

  Query Match             4.6%;  Score 127;  DB 2;  Length 583;
  Best Local Similarity   20.6%;  Pred. No. 0.49;
  Matches  106;  Conservative   82;  Mismatches  241;  Indels   86;  Gaps   17;

Qy         28 STSPLTSS-VATGTNLVLYAAPLSPLLPLQD---GTNTHIMATEASNYAQYRVARATIRY 83
Db         79 SIDPTSSSDVITSTVQTTSIEPTTSLVSSNDITTSTSLNISVVISTSTDSTSLIESTTTV 138

Qy         84 RPLVPNAVGG-YAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIAS---ELVIPSER 139
Db        139 GPHASSSVAGMYRTRSSDEVTTSTDPTS-------SSDVATSADPTSSSAVTTLVDPTTS 191

Qy        140 LHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFALELEFRN 199
Db        192 V---------VISTSVDQTSSSDVATSVDPTTSVISSTSADPTTSA------------DS 230

Qy        200 LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIAL 259
Db        231 TTSTVQTTSVDPTSSVVSSAPVDPASSVVSLTSSYPTSSSTVTISANSNGSATLA----- 285

Qy        260 TLFNLADTLLGGLPTELISSAGGQLFYSRP--------VVSANGEPTVKLYTSVE-NAQQ 310
Db        286 -----AQTTSIDPVSSIVSSSGATTIISSASIDPASSVVSSTSSEPTSFIVSSTSVYSTR 340

Qy        311 DKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYD 370
Db        341 PSGPTTSTDLATFSDTIILRVSTTSTSQDTQTVSSSLTDMVSSTGSADLSVSSIQRSQVD 400

Qy        371 QSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTK------------VTLDGRPLSTI 418
Db        401 PSTFAVSNSPVYPTASTG--STSTGIPIASESLSLSRQQGISATSSSSIVTLTPVDSASS 458

Qy        419 QQYSKTFFVLP----------LRGKLSFWEA-GTTKAGYP----YNYNTTASDQLLV-EN 462
Db        459 SRSSATSIIKPNMPVSSNDSKTQSSVSVVDAFQSTKSSYPSITSADPTTLASENGLVGSS 518

Qy        463 AAGHRVAIS-TYTTSLGAGPVSISAVAVLAPHSAL 496
Db        519 SSAHPITLDRTYASAHASVTDIVSRVTDSTRHTTL 553


RESULT 6
S25370
MSB2 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein G4017; protein YGR014w
C;Species: Saccharomyces cerevisiae
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S25370; S64305
R;Bender, A.; Pringle, J.R.
Yeast 8, 315-323, 1992
A;Title: A Ser/Thr-rich multicopy suppressor of a cdc24 bud emergence defect.
A;Reference number: S25370; MUID:92383951; PMID:1514328
A;Accession: S25370
A;Molecule type: DNA
A;Residues: 1-1306 <BEN>
A;Cross-references: UNIPROT:P32334; GB:M77354; NID:g171993; PIDN:AAA34798.1; PID:g171994
R;Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996
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A;Reference number: S64071
A;Accession: S64305
A;Molecule type: DNA
A;Residues: 1-1306 <RIE>
A;Cross-references: EMBL:Z72799; NID:g1322977; PID:g1322978; MIPS:YGR014w
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:MSB2
A;Cross-references: SGD:S0003246; MIPS:YGR014w
A;Map position: 7R
C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase
C;Keywords: transmembrane protein
F;3-19/Domain: transmembrane #status predicted <TM1>
F;1189-1205/Domain: transmembrane #status predicted <TM2>

  Query Match             4.5%;  Score 125.5;  DB 2;  Length 1306;
  Best Local Similarity   19.9%;  Pred. No. 2;
  Matches  110;  Conservative   91;  Mismatches  212;  Indels  141;  Gaps   24;

Qy         27 LSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEASNYAQYRVARATIRYRP- 85
Db        441 LDSSSLASSSASSSDLTDYGVSSTASIPLLSASE------QASTSSSFSVVSPSVSFVPS 494

Qy         86 ---------LVPNAV-----------GG-----------YAISISFWPQTTTTPTSVDM 113
Db        495 QSSSDVASTSAPSVVSSSFSYTSLQAGGSSMTNPSSSTIVYSSSTGSSEESAASTASATL 554

Qy        114 NSITSTDV--RILVQPGIASELVIPSERLH--------------YRNQGW--------- 147
Db        555 SGSSSTYMAGNLQSQPPSTSSLLSESQATSTSAVLASSSVSTTSPYTTAGGASTEASSLI 614

Qy        148 --RSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTG-----ALGLLDFALELEFRNL 200
Db        615 SSTSAETSQVSYSQSTTALQTSSFASSSTTEGSETSSQGFSTSSVLVQMPSSISSEF--- 671

Qy        201 TPGNTNTRVSRYSSTARHR------LRRGADGTAELTTTAAT-RFMKDL---YFTSTNGV 250
Db        672 SPSQTTTQMNSASSSSQYTISSTGILSQVSDTSVSYTTSSSSVSQVSDTPVSYTTSSSSV 731

Qy        251 GEIG-RGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQ 309
Db        732 SQVSDTPVSYTTSSSSVSQVSDTPVSYTTSSSS--------VSQVSDTPVSYTTSSSSVS 783

Qy        310 QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAE- 368
Db        784 QVSDTSVPST----SSRSSV-------SQVSDTPVPSTSSRSSVSQTSSSLQPTTTSSQR 832

Qy        369 YDQSTYGSSTGPVYVSDSVTLVNVATGAQAVA-RSLDWTKVTLDGRPLSTIQQYSKTFFV 427
Db        833 FTISTHGALSESSSVSQQASEITSSINATASEYHSIQTTAAT----------QSTT--- 878

Qy        428 LPLRGKLSFWEAGTTKAGYPYNYNTT-------ASDQLLVENAAG-HRVAIST-YTTSLG 478
Db        879 ------LSFTDANSSSASAPLEVATSTPTPSSKASSLLLTPSTSSLSQVATNTNVQTSL- 931

Qy        479 AGPVSISAVAVLAP 492
Db        932 ----TTESTTVLEP 941


RESULT 7
S74915
extracellular nuclease - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein sll0656
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74915
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.

A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74915
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1879 <KAN>
A;Cross-references: UNIPROT:P72938; EMBL:D90902; GB:AB001339; NID:g1652027; PIDN:BAA1695
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: nucH
A;Start codon: GTG

  Query Match             4.5%;  Score 125.5;  DB 2;  Length 1879;
  Best Local Similarity   20.6%;  Pred. No. 3.4;
  Matches  118;  Conservative   72;  Mismatches  196;  Indels  187;  Gaps   26;

Qy         28 STSPLTSSVATGTNLVLYAAPLSPLLPLQD--------GTNT-HIMATEASNYAQYRVAR 78
Db        466 NAAPVTVSVANGVNNLLENANTTSAIKLGNIIIGDDSLGTNTLSLSGADASNF------- 518

Qy         79 ATIRYRPLVPNAV-------------GGYAISISFWPQTT-TTPTSVDMNSITSTDVRIL 124
Db        519 ------EIVGNGLFLKAGTVLDFSTQSSYEVTIAVDDATLGNTP-----DAITTFTLDIT 567

Qy        125 VQPGIASELVIPSERLHYRNQGWRSVETSGVAE--EEATSGLVMLCIHGSLVN----SYT 178
Db        568 NTAGI-SDLIISEV------APWSSGNSSVGADWFEVTNTGANAIDITGWKVDDDSASFA 620

Qy        179 NTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRF 238
Db        621 NASALAGV-----------TNIAPGQSVVFV---------------DGDAN-TITA---- 649

Qy        239 MKDLYFTSTNGVG-EIGR---------GIALTLFNLADTLLGGLPTELISSAGGQLFYSR 288
Db        650 FIDLWFGGTAPAGLAIGTYGGPGLGTGGDAINLFDATGSLITG---------------- 692

Qy        289 PVVSANGEPTVKLYTSVENAQQDKGIAIPHD---------IDLGE--------------- 324
Db        693 --VTFGSSPSTSPFSTFDNALGNPSVANLSTVGSNGAFSVIDAGEGVILNGSPGAIAGSV 750

Qy        325 ---SRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYG-SSTGP 380
Db        751 SSNTTVGIAATGATGSENGPTPG-----EFTILRTGD----TSTALDVTYSISGDAANGT 801

Qy        381 VYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAG 440
Db        802 DYAAIDPTTVTIPAGQSQVKISIN---------PIDDVIIESTESIVITLTDTANYDVAT 852

Qy        441 TTKAG--------YPYNYNTTASDQLLVENAAGHRVAISTYTTS-------------LGA 479
Db        853 SASSATVNIEDNDTPITVSRLQITEFMYSGADGEFIEFTNIDTSSVDMTGWSFSDSGRVA 912

Qy        480 GPVSISAVAVLAPHSALALLEDTLDYPARAHTF 512
Db        913 GSVDLSAFGVVQPGESVILTE------ADAETF 939


RESULT 8
E82750
hemagglutinin-like secreted protein XF0889 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82750
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82750
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3282 <SIM>
A;Cross-references: UNIPROT:Q9PEY9; GB:AE003928; GB:AE003849; NID:g9105798; PIDN:AAF8369
A;Experimental source: strain 9a5c
```

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0889

Query Match 4.5%; Score 125; DB 2; Length 3282;
Best Local Similarity 21.6%; Pred. No. 8.2;
Matches 130; Conservative 63; Mismatches 212; Indels 196; Gaps 26;

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Qy          1 AVAPAHDTP------PVP-----------------DVDSRGAILRRQYNLSTSPLTSSV 36
              :| || |||      |:|                   |:|:||  :     :     |
Db        439 SVPPATDTPPSTGTMPIPSHPQTAPVLAAGRLTLENDIDNRGGHITAGGAIDAILTTLDN 498

Qy         37 ATGTNLVLYAAPLSPL-LPLQDGTNTH---IMATEA-------SNYAQYRVARATIRYRP 85
                ||      | |: | |  |   | |    :||||       :| | |          |:
Db        499 RDGT------AALNRLTLQGQRLDNQHGILTLATEATIHTHTLNNAAGQLHVNGTLDLTA 552

Qy         86 LVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQ 145
                |   |: ::    ||: |  |  |:   ||  :         |  | : :  |
Db        553 QHLNNASGHLLTTG--PQSATL-TIADLLDNTSGTL------ASAGSLTLTAATL----- 598

Qy        146 GWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFALELEFRNLTPGNT 205
                          : | | |         ::: | | : | |   |          ||   |
Db        599 ------------DTTDGTVQSGQGPLHMDAATLTAHRGTLTSQD--------TLTLTGT 637

Qy        206 NTRVSRYSSTAR--------------------HRLRRGA------------DGTAELT 231
              :| :|  ::||:                   | |:  |            :|| :|
Db        638 HTDLSHATTTAQQITLHTGDLTTAGGHLTAYGTHTLQLEARTRLDNTGGTIATNGTLDLH 697

Qy        232 TTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELI----SSAGGQLFYS 287
              | |        |: |:|   |      |  || | |  ||   || |      :: || |  :
Db        698 TAALDNTGGTLHSTAT---GPNRLDITDTLTNTAGHLLLNGPTTLTTGTWTNTGGHLQIT 754

Qy        288 RPVV-------------SANGEPTVKLYTSVENAQQDKGIAIPHD-IDLGESRVVIQDY 332
              |               :| |   :::  :: |  || |:    | : |  : ::
Db        755 GPATLHATTLDNRGGILHTATGPLDLRITGTLNN--QDNGLLTTTDALTLTAASLL---- 808

Qy        333 DNQH-EQDRPTPSPAP-----SRPFSVLRANDVLWL----------SLTAAEYDQSTYGS 376
               |||    |   |:          :|:    |||          :|||::    | |
Db        809 -NQHGTLDAAGPAHLTLTGLLDNTAGLLQTAHTLWLTSAGLTNRSGTLTASQLTLDTQGH 867

Qy        377 S-----------------TGPV-------------YVSDSVTLVNVATGAQAVARSLD 404
              :                 :||:                 : : || |   ||   | :||
Db        868 TLDNTRGRLGTTTGNLTLHSGPLDNTAGLLQTAAALTIDTGAATLTNRDGGALLAATALD 927

Qy        405 WTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAA 464
              |  |||  |   ||   : |          |       | ||:  :  |   |   : |
Db        928 LTTATLDNRG-GTIDSQTAT--------HLHTTTLDNTTAGHISSSGTLQIDGTTLTNTG 978

Qy        465 G 465
              |
Db        979 G 979
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RESULT 9
E82589
hemagglutinin-like secreted protein XF2196 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82589
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82589
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3442 <SIM>
A;Cross-references: UNIPROT:Q9PBE8; GB:AE004032; GB:AE003849; NID:g9107324; PIDN:AAF8499
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2196

Query Match 4.5%; Score 125; DB 2; Length 3442;
Best Local Similarity 21.6%; Pred. No. 8.8;
Matches 130; Conservative 63; Mismatches 212; Indels 196; Gaps 26;

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Qy          1 AVAPAHDTP------PVP-----------------DVDSRGAILRRQYNLSTSPLTSSV 36
              :| || |||      |:|                   |:|:||  :     :     |
Db        439 SVPPATDTPPSTGTMPIPSHPQTAPVLAAGRLTLENDIDNRGGHITAGGAIDAILTTLDN 498

Qy         37 ATGTNLVLYAAPLSPL-LPLQDGTNTH---IMATEA-------SNYAQYRVARATIRYRP 85
                ||      | |: | |  |   | |    :||||       :| | |          |:
Db        499 RDGT------AALNRLTLQGQRLDNQHGILTLATEATIHTHTLNNAAGQLHVNGTLDLTA 552

Qy         86 LVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQ 145
                |   |: ::    ||: |  |  |:   ||  :         |  | : :  |
Db        553 QHLNNASGHLLTTG--PQSATL-TIADLLDNTSGTL------ASAGSLTLTAATL----- 598

Qy        146 GWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFALELEFRNLTPGNT 205
                          : | | |         ::: | | : | |   |          ||   |
Db        599 ------------DTTDGTVQSGQGPLHMDAATLTAHRGTLTSQD--------TLTLTGT 637

Qy        206 NTRVSRYSSTAR--------------------HRLRRGA------------DGTAELT 231
              :| :|  ::||:                   | |:  |            :|| :|
Db        638 HTDLSHATTTAQQITLHTGDLTTAGGHLTAYGTHTLQLEARTRLDNTGGTIATNGTLDLH 697

Qy        232 TTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELI----SSAGGQLFYS 287
              | |        |: |:|   |      |  || | |  ||   || |      :: || |  :
Db        698 TAALDNTGGTLHSTAT---GPNRLDITDTLTNTAGHLLLNGPTTLTTGTWTNTGGHLQIT 754

Qy        288 RPVV-------------SANGEPTVKLYTSVENAQQDKGIAIPHD-IDLGESRVVIQDY 332
              |               :| |   :::  :: |  || |:    | : |  : ::
Db        755 GPATLHATTLDNRGGILHTATGPLDLRITGTLNN--QDNGLLTTTDALTLTAASLL---- 808

Qy        333 DNQH-EQDRPTPSPAP-----SRPFSVLRANDVLWL----------SLTAAEYDQSTYGS 376
               |||    |   |:          :|:    |||          :|||::    | |
Db        809 -NQHGTLDAAGPAHLTLTGLLDNTAGLLQTAHTLWLTSAGLTNRSGTLTASQLTLDTQGH 867

Qy        377 S-----------------TGPV-------------YVSDSVTLVNVATGAQAVARSLD 404
              :                 :||:                 : : || |   ||   | :||
Db        868 TLDNTRGRLGTTTGNLTLHSGPLDNTAGLLQTAAALTIDTGAATLTNRDGGALLAATALD 927

Qy        405 WTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAA 464
              |  |||  |   ||   : |          |       | ||:  :  |   |   : |
Db        928 LTTATLDNRG-GTIDSQTAT--------HLHTTTLDNTTAGHISSSGTLQIDGTTLTNTG 978

Qy        465 G 465
              |
```

```
Db        979 G 979


RESULT 10
B82519
hemagglutinin-like secreted protein XF2775 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82519
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: B82519
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3455 <SIM>
A;Cross-references: UNIPROT:Q9P9U6; GB:AE004082; GB:AE003849; NID:g9108003; PIDN:AAF8556
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2775

  Query Match             4.5%;  Score 125;  DB 2;  Length 3455;
  Best Local Similarity   21.6%;  Pred. No. 8.9;
  Matches  130;  Conservative   63;  Mismatches  212;  Indels  196;  Gaps   26;

Qy          1 AVAPAHDTP------PVP-----------------DVDSRGAILRRQYNLSTSPLTSSV 36
              :| || |||      |:|                 |:|:||  :     :     |
Db        439 SVPPATDTPPSTGTMPIPSHPQTAPVLAAGRLTLENDIDNRGGHITAGGAIDAILTTLDN 498

Qy         37 ATGTNLVLYAAPLSPL-LPLQDGTNTH---IMATEA-------SNYAQYRVARATIRYRP 85
                ||      | |: | | |   | |    :||||       :| |       |:
Db        499 RDGT------AALNRLTLQGQRLDNQHGILTLATEATIHTHTLNNAAGQLHVNGTLDLTA 552

Qy         86 LVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQ 145
                 |   |: ::    ||: |  |  |:   ||  :        |  | : :  |
Db        553 QHLNNASGHLLTTG--PQSATL-TIADLLDNTSGTL------ASAGSLTLTAATL----- 598

Qy        146 GWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFALELEFRNLTPGNT 205
                        : | | |        ::: | | : | |   |          ||   |
Db        599 ------------DTTDGTVQSGQGPLHMDAATLTAHRGTLTSQD--------TLTLTGT 637

Qy        206 NTRVSRYSSTAR--------------------HRLRRGA------------DGTAELT 231
              :| :|  ::||:                    | |:  |             :|| :|
Db        638 HTDLSHATTTAQQITLHTGDLTTAGGHLTAYGTHTLQLEARTRLDNTGGTIATNGTLDLH 697

Qy        232 TTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELI----SSAGGQLFYS 287
              | |       |: |:|    |     |  || | |  ||   || |     :: || |  :
Db        698 TAALDNTGGTLHSTAT---GPNRLDITDTLTNTAGHLLLNGPTTLTTGTWTNTGGHLQIT 754

Qy        288 RPVV-------------SANGEPTVKLYTSVENAQQDKGIAIPHD-IDLGESRVVIQDY 332
                |             :| |   :::  :: |  || |:    | : |  : ::
Db        755 GPATLHATTLDNRGGILHTATGPLDLRITGTLNN--QDNGLLTTTDALTLTAASLL---- 808

Qy        333 DNQH-EQDRPTPSPAP-----SRPFSVLRANDVLWL----------SLTAAEYDQSTYGS 376
               |||    |   |:             :|:    |||          :|||::    | |
Db        809 -NQHGTLDAAGPAHLTLTGLLDNTAGLLQTAHTLWLTSAGLTNRSGTLTASQLTLDTQGH 867
```

```
Qy        377 S------------------TGPV-------------YVSDSVTLVNVATGAQAVARSLD 404
              :                 :||:               : : || |   ||   | :||
Db        868 TLDNTRGRLGTTTGNLTLHSGPLDNTAGLLQTAAALTIDTGAATLTNRDGGALLAATALD 927

Qy        405 WTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAA 464
               |  ||| |   ||   : |        |       | ||:  :  |   |   : |
Db        928 LTTATLDNRG-GTIDSQTAT--------HLHTTTLDNTTAGHISSSGTLQIDGTTLTNTG 978

Qy        465 G 465
               |
Db        979 G 979


RESULT 11
T45025
mucin MUC5B, tracheobronchial [imported] - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45025
R;Desseyn, J.L.; Guyonnet-Duperat, V.; Porchet, N.; Aubert, J.P.; Laine, A.
J. Biol. Chem. 272, 3168-3178, 1997
A;Title: Human mucin gene MUC5B, the 10.7 kb large central exon encodes various alternate
A;Reference number: Z22899; MUID:97166151; PMID:9013550
A;Accession: T45025
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3570 <DES>
A;Cross-references: EMBL:Z72496; NID:g1834502; PIDN:CAA96577.1; PID:g1834503
A;Experimental source: placenta
C;Genetics:
A;Gene: MUC5B

  Query Match             4.5%;  Score 124.5;  DB 2;  Length 3570;
  Best Local Similarity   19.8%;  Pred. No. 10;
  Matches  112;  Conservative   56;  Mismatches  252;  Indels  147;  Gaps   19;

Qy          8 TPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAP-LSPLLPLQDGTNTHIMAT 66
              | | | |              |||  |:  || :     ::|  :  ||:   | |   ||
Db       2892 TAPPPKV------------LTSPATTPTATSSKATSSSSPRTATTLPVLTSTATKSTAT 2938

Qy         67 EASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSI---------- 116
                :                |:  : :|    :     |: |||| :   |::|
Db       2939 SVT--------------PIPSSTLG----TTGTLPEQTTTPVAT-MSTIHPSSTPETTH 2978

Qy        117 TSTDVRILVQPGIASELVIPSERLHYRNQGWRSVE----------TSGVAEEEATSGLVM 166
              ||| :              |    ||          |   |           |   |   :| |
Db       2979 TSTVLTTKATTRATSSTSTPSST---PGTTWILTELTTAATTTAGTGPTATPSSTPGTTW 3035

Qy        167 LCIHGSLVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADG 226
              :     | : | |  ||:   |        :     |  | |  :   |||     :  |
Db       3036 ILT--ELTTTATTTASTGSTATLSSTPGTTWILTEPSTTATVTAPPGSTATASSTQATAG 3093

Qy        227 TAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFY 286
              |  ::||| |  :     ||:        | |  |  | |       |   :     |
Db       3094 TPHVSTTATTPTV-----TSSKATPSSSPGTATALPALRSTATTPTATSFTAIPSSSLGT 3148

Qy        287 SRPVVSANGEPTVKLYTSVENAQQDK-----------------GIAIPHDIDLGESRVV 328
              :   :|     ||  : |:  ::  :                 :| |
Db       3149 TWTRLSQTTTPTATMSTATPSSTPETVHTSTVLTTTATTTGATGSVATPSSTP------- 3201

Qy        329 IQDYDNQHEQDRP---------TPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTG 379
                    |     |         |||  :|    :        :|:| |       |  ::|
Db       3202 ----GTAHTTKVPTTTTTGFTATPSSSPGTALT-----PPVWISTT-------TTPTTTT 3245

Qy        380 PVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEA 439
              |     :||  ::  |     || |  |  |:                       | ::   :
Db       3246 PTTSGSTVTPSSI-PGTTHTARVLTTTTTTV------------------ATGSMATPSS 3285

Qy        440 GTTKAGYPYNYNTTASDQLLVENAAGH---------RVAISTYTTSLGAGPVSISAVAVL 490
               |  :| | :  |||:        | |               |     ||:    | : |: |
Db       3286 STQTSGTPPSLTTTAT----TITATGSTTNPSSTPGTTPIPPVLTSMATTPAATSSKATS 3341

Qy        491 APHSALALLEDTLDYPARAHTFDDFCP 517
```

```
Db       3342 SSSPRTATTLPVLTSTATKSTATSFTP 3368


RESULT 12
E86719
hypothetical protein yhgD [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86719
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: E86719
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1180 <STO>
A;Cross-references: UNIPROT:Q9CHH4; GB:AE005176; PID:g12723674; PIDN:AAK04855.1; GSPDB:G
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: yhgD

  Query Match             4.4%;  Score 122;  DB 2;  Length 1180;
  Best Local Similarity   19.8%;  Pred. No. 3;
  Matches  124;  Conservative   76;  Mismatches  205;  Indels  220;  Gaps   31;

Qy          26 NLSTSPLT-----SSVATGTNLVLYAAPLSPLLP----LQDGTNTHIMATE---ASNYAQ 73
               ||:  | |      :||::||           |:|        | :|:    ||   :|||| 
Db          49 NLAFQPKTEKAQAASVSSGT-----------LVPGNTSYDTGGHTY-SGTEFANSSNYAL 96

Qy          74 YRVARATIRYRPLVPNAVGGYAI-----SISFWPQTT--TTPTSVDMNSITS-TD----- 120
               |  |     :  || :      :     |:|    ||  |  ::: ::| :| ||     
Db          97 YGKAVVASNWINLVSSTANSVGLGIFNGSVSAISATTGFTLKSTIKVDSGSSLTDFTKSG 156

Qy         121 --VRILVQPGIASELVIPSE---------------------RLHYRN------------- 144
                 : :::     ::|   ::                     |  | |             
Db         157 DAIGVILTGASKAQLAANAQSSQATNDGLGIRGLPNTVFLGRDLYSNLSNVSTGSLTGID 216

Qy         145 -----QGW----------RSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLL 189
                   ||           |: ::||  :       |      :  : |:   | ||     
Db         217 GSATVNGWTDGPGVVMAIRNTDSSGTLQAANYPSLGSAAPYSPVTNTQNGTAYT------ 270

Qy         190 DFALELEFR-----------------NLTPGNTNTRVSRYSSTARHRLRRGADGTAELTT 232
               || : :                   ||  |||  : |:|            ||      
Db         271 -FATDTSYALGVASPITSSVQEPITVTWTPDATNTASTGYTS----------GTLTFNL 318

Qy         233 TAATRFMKDLYFTSTNGV--------GEIGRGIALTLFNLADTLLGGLPTELISSAGGQL 284
               |          |::||         |  |      |  || ::|  |      :   ||   
Db         319 IAQ---------TTSNGALIGASAVNGGTGGYTLTTHTNLQNSLTVG----FVGGTGGN- 364

Qy         285 FYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPS 344
               |    || ||         ::  ::  : : |             :| |     : |   
Db         365 -YGNLSVSLNG-------ATITGSKGTEPVPI-------------NYLN-----KVTGQ 397

Qy         345 PAPSRPFSVLRA--NDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARS 402
               | ||   | : |  || :  :|||        ||| |   : :   :      || || : :
Db         398 PIPSMAQSSITANVNDTIGAALTAP--------SSTSPDNNTYTYVVPAAPTGYQANSAT 449

Qy         403 LDWTKVTLDGRPLSTIQQYSKT---FFV------------LPLRGKLSF-W--EAGTTKA 444
                 |   |  | ||    : |   | |              | :  : | |   :||| |  
Db         450 ---TTTVLAANPASTTNTSATTVSNFIVGTTNPNALNVSYTPSQQTVLFNWAKASGTTLA 506

Qy         445 GYP----YNYNTTASDQLLVENAAGHRVAISTYTTSL------------GAGPVSISAV 487
                  |    |          :: :|   :   :|:| |:|           |  ::|     
Db         507 NLPNQIAYGATGITDASVVTDNPFSNTTLLSSYATALSNAVPTGYNITQISNGTTTVSGA 566

Qy         488 AVLAPHSALALLEDTLDYPARAHTF 512
                 |  :|      |:   :  :|: 
Db         567 TTAATLAAFTSQNPTVGATSTLNTY 591


RESULT 13
```

```
B85547
probable RTX family exoprotein [imported] - Escherichia coli (strain O157:H7, substrain E
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85547
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85547
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5188 <STO>
A;Cross-references: UNIPROT:Q8X4H5; GB:AE005174; NID:g12513368; PIDN:AAG54838.1; GSPDB:GN
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z0615

  Query Match             4.4%;  Score 122;  DB 2;  Length 5188;
  Best Local Similarity   21.8%;  Pred. No. 26;
  Matches  114;  Conservative   68;  Mismatches  208;  Indels  134;  Gaps   24;

Qy           1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
               ||| : :|   || :     :  ||: |  || : :|  :                :  |
Db        2535 AVAISINTVASDDVINAA---EKGTNLTLSGSTSGIESGQTVT----------VTFGGK 2580

Qy          61 THIMATEASNYAQYRVARATIRYRP--------LVPNAVGGYAISISFWPQTTTTPTSVD 112
               |:  :  |:       |  | :   |                | :| |  |  :   : || :
Db        2581 TYTASVAANGSWSVNVPAADLATLPEGAANVQASVSSASGNSASATHAYSVDASAPT-LT 2639

Qy         113 MNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGS 172
               :|:| | |:    :  |  | | |                  || :  | |   | : ::|:
Db        2640 INTIASDDILNAAEAG--SPLTI----------------SGTSTAE-TGQTVTVTLNGA 2679

Qy         173 LVNSYTNTPY----------TGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRR 222
                 :|| |             | ||| |: :      |  |    |    :  :| | |  
Db        2680 ---TYTGTVQADGSWSVSVPTSALGALNAS------NYTVSATVNDKAGNPGSASHNL-- 2728

Qy         223 GADGTA---ELTTTAATRFMKD------LYFTSTNGVGEIGRGIALTLFNLADTLLGGLP 273
                 | ||    :  | |    : |       |  : |:  || |  ::: |           
Db        2729 AVDTTAPVLTINTVAGDDIINDAEHAQALVISGTSSGGEXGDVVSVVL------------ 2776

Qy         274 TELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIP-HDID-LGESRVVIQD 331
                              ||    | ||:  :|  :  : :|  |:  ||      |      
Db        2777 --------------------NG----KTYTTTLDASGNWSVGVPAADVTALGSGAQTI-- 2810

Qy         332 YDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAE---------YDQSTYGSSTGPVY 382
                        ||   |   ||  :| :  |: ::  | :             |  :|  |  
Db        2811 --TASVSDRAGNSDDASRTVTVSLSAPVISINTIAGDDVINATEKGSDLALSGTSDQPAG 2868

Qy         383 VSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ--YSKTFFVLPLRGKLSF---- 436
                : :||| |     :      | :|: ||:    :| : :  || |  |   :|     
Db        2869 TAITVTL-NGQNYSATTDASGNWS-VTVPASAVSALGEATYSVTASVTNAQGNSSTASHN 2926

Qy         437 WEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
                 :  |   |      |  |:| ::  : ||    ||   |   ||
Db        2927 VQVNTALPG--ITINPVATDDIINASEAGSAQTISGQVTGAAAG 2968


RESULT 14
F90696
hypothetical protein ECs0542 [imported] - Escherichia coli (strain O157:H7, substrain RIM
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F90696
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.,
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90696
A;Status: preliminary
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A;Molecule type: DNA
A;Residues: 1-5291 <HAY>
A;Cross-references: UNIPROT:Q8X2T1; GB:BA000007; PIDN:BAB33965.1; PID:g13360000; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0542

  Query Match             4.4%;  Score 122;  DB 2;  Length 5291;
  Best Local Similarity   21.8%;  Pred. No. 27;
  Matches  114;  Conservative   68;  Mismatches  208;  Indels  134;  Gaps   24;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||| : :|    || :     :  ||: |  || : :|  :           :  |
Db       2535 AVAISINTVASDDVINAA---EKGTNLTLSGSTSGIESGQTVT----------VTFGGK 2580

Qy         61 THIMATEASNYAQYRVARATIRYRP--------LVPNAVGGYAISISFWPQTTTTPTSVD 112
              |:  :  |:      |  | :   |         | :| |  | :   :    : || :
Db       2581 TYTASVAANGSWSVNVPAADLATLPEGAANVQASVSSASGNSASATHAYSVDASAPT-LT 2639

Qy        113 MNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGS 172
              :|:| | |:    : |  | | |                  || :  | |    | : ::|:
Db       2640 INTIASDDILNAAEAG--SPLTI----------------SGTSTAE-TGQTVTVTLNGA 2679

Qy        173 LVNSYTNTPY----------TGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRR 222
                :|| |             | ||| |: :      | |   |    :   :| | |
Db       2680 ---TYTGTVQADGSWSVSVPTSALGALNAS------NYTVSATVNDKAGNPGSASHNL-- 2728

Qy        223 GADGTA---ELTTTAATRFMKD------LYFTSTNGVGEIGRGIALTLFNLADTLLGGLP 273
               | ||    : | |    : |       |  : |:  || |  ::: |
Db       2729 AVDTTAPVLTINTVAGDDIINDAEHAQALVISGTSSGGEAGDVVSVVL------------ 2776

Qy        274 TELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIP-HDID-LGESRVVIQD 331
                                 ||    | ||:  :|  :  : :|  |:  ||      |
Db       2777 --------------------NG----KTYTTTLDASGNWSVGVPAADVTALGSGAQTI-- 2810

Qy        332 YDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAE---------YDQSTYGSSTGPVY 382
                       ||    |   ||  :|  :  |: ::  | :          |  :  |:|  |
Db       2811 --TASVSDRAGNSDDASRTVTVSLSAPVISINTIAGDDVINATEKGSDLALSGTSDQPAG 2868

Qy        383 VSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ--YSKTFFVLPLRGKLSF---- 436
               : :||| |    :     | :|: ||:    :| : :  || |  |   :|  |
Db       2869 TAITVTL-NGQNYSATTDASGNWS-VTVPASAVSALGEATYSVTASVTNAQGNSSTASHN 2926

Qy        437 WEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
                :  |   |      |  |:| ::  : ||    ||   |   ||
Db       2927 VQVNTALPG--ITINPVATDDIINASEAGSAQTISGQVTGAAAG 2968


RESULT 15
A47001
transcription factor Oct-1 - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Sep-1999
C;Accession: A47001; A31754
R;Sturm, R.A.; Cassady, J.L.; Das, G.; Romo, A.; Evans, G.A.
Genomics 16, 333-341, 1993
A;Title: Chromosomal structure and expression of the human OTF1 locus encoding the oct-1
A;Reference number: A47001; MUID:93300505; PMID:8314572
A;Accession: A47001
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-766 <STU>
A;Note: the sequence in GenBank entry HSOCT1, release 111.0, begins with Met-24
R;Sturm, R.A.; Das, G.; Herr, W.
Genes Dev. 2, 1582-1599, 1988
A;Title: The ubiquitous octamer-binding protein Oct-1 contains a POU domain with a homeo
A;Reference number: A31754; MUID:89107993; PMID:2905684
A;Accession: A31754
A;Molecule type: mRNA
A;Residues: 'P',8-400,'R',402-766 <ST2>
A;Cross-references: GB:X13403; NID:g35126; PIDN:CAA31767.1; PID:g35127
C;Genetics:
A;Gene: GDB:POU2F1; OTF1; OCT1
A;Cross-references: GDB:120254; OMIM:164175
A;Map position: 1q22-1q23
C;Superfamily: transcription factor Oct-1; homeobox homology; POU domain homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;310-377/Domain: POU domain homology <POU>
F;403-459/Domain: homeobox homology <HOX>

  Query Match             4.4%;  Score 121.5;  DB 1;  Length 766;
  Best Local Similarity   25.7%;  Pred. No. 1.8;
  Matches   78;  Conservative   40;  Mismatches  136;  Indels   49;  Gaps   13;

Qy         28 STSPL-------TSSVATGTNLVLYAA----PLSPLLPLQDGTNTHIMATEASNYAQYRV 76
              |:||:       || |||  :||  :|     :||:|||      |::  |  |:
Db        469 SSSPIKAIFPSPTSLVATTPSLVTSSAATTLTVSPVLPLTSAAVTNLSVTGTSDTTSNNT 528

Qy         77 ARATIRYRPLVPNAVGGYAISISFWPQ---TTTTPTSVDMNSITSTDVRILVQPGIASEL 133
              |   |    |   :||   ::| |  |     :|:  :|    | | |    |  |   |::
Db        529 A-TVISTAPPASSAVTSPSLSPS--PSASASTSEASSASETSTTQTTSTPLSSPLGTSQV 585

Qy        134 VIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFAL 193
              :: :  |     |   :    | |:  | : |  :      |  |          | | |
Db        586 MVTASGL----QTAAAAALQGAAQLPANASLAAMAAAAGLNPSLMAPSQFAAGGAL---- 637

Qy        194 ELEFRNLTPGNTNTRVS---RYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGV 250
                 :| ||  :  :|     :||        : |:  :|:  ||    :| | :  |
Db        638 ----LSLNPGTLSGALSPALMSNSTLATIQALASGGSLPITSLDAT---GNLVFANAGGA 690

Qy        251 GEIGRGIALTLF----NLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVE 306
              |   :   ||    ||  :||   |  |:|:|      | || | :         || |
Db        691 PNI---VTAPLFLNPQNL--SLLTSNPVSLVSAAAASAGNSAPVASLHATS-----TSAE 740

Qy        307 NAQ 309
              : |
Db        741 SIQ 743


Search completed: July 14, 2005, 15:51:38
Job time : 11.3396 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 14, 2005, 01:31:43 ; Search time 39.3962 Seconds
(without alignments)
7019.016 Million cell updates/sec

Title: US-09-769-066-25
Perfect score: 2769
Sequence: 1 AVAPAHDTPPVPDVDSRGAI.....PLGLQGCAFQSTVAELQRLK 540

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2769	100.0	660	1	VST2_HEVBU	P29326 hepatitis e
2	2762	99.7	660	2	Q9E8G5	Q9e8g5 hepatitis e
3	2758	99.6	660	2	Q9W7W9	Q9w7w9 hepatitis e
4	2758	99.6	660	2	Q9WQA0	Q9wqa0 hepatitis e
5	2756	99.5	660	1	VST2_HEVPA	P33426 hepatitis e
6	2756	99.5	660	2	Q77EC8	Q77ec8 hepatitis e
7	2756	99.5	660	2	Q89468	Q89468 hepatitis e
8	2752	99.4	660	2	Q69419	Q69419 hepatitis e
9	2751	99.3	660	2	Q81871	Q81871 hepatitis e
10	2750	99.3	660	2	O91855	O91855 hepatitis e
11	2749	99.3	660	2	O91856	O91856 hepatitis e
12	2744	99.1	660	2	Q81878	Q81878 hepatitis e
13	2741	99.0	660	2	Q69411	Q69411 hepatitis e
14	2741	99.0	660	2	Q6XXV0	Q6xxv0 hepatitis e
15	2735	98.8	660	2	Q9WLL4	Q9wll4 hepatitis e
16	2731	98.6	660	2	Q68985	Q68985 hepatitis e
17	2730	98.6	659	2	Q8JT32	Q8jt32 hepatitis e
18	2728	98.5	660	1	VST2_HEVMY	Q04611 hepatitis e
19	2660	96.1	660	2	Q80IY5	Q80iy5 hepatitis e
20	2656	95.9	660	2	Q8JJM8	Q8jjm8 hepatitis e
21	2655	95.9	660	2	O36613	O36613 swine hepat
22	2655	95.9	660	2	Q6J8F7	Q6j8f7 hepatitis e
23	2654	95.8	660	2	Q8JJM4	Q8jjm4 hepatitis e
24	2652	95.8	660	2	Q8AZM3	Q8azm3 hepatitis e
25	2652	95.8	660	2	Q9YLQ9	Q9ylq9 hepatitis e
26	2649	95.7	660	2	Q8V729	Q8v729 swine hepat
27	2649	95.7	660	2	Q6J8G3	Q6j8g3 hepatitis e
28	2649	95.7	660	2	Q80IR7	Q80ir7 hepatitis e
29	2648	95.6	550	2	Q8JVV3	Q8jvv3 hepatitis e
30	2648	95.6	671	2	Q8JJM1	Q8jjm1 hepatitis e
31	2648	95.6	674	2	Q8JJN6	Q8jjn6 hepatitis e
32	2646	95.6	660	2	Q911I4	Q911i4 hepatitis e
33	2646	95.6	674	2	Q8JJN2	Q8jjn2 hepatitis e
34	2646	95.6	674	2	Q6BD83	Q6bd83 hepatitis e
35	2646	95.6	674	2	Q7TGF1	Q7tgf1 hepatitis e
36	2645	95.5	674	2	Q6BD78	Q6bd78 hepatitis e
37	2645	95.5	674	2	Q806D7	Q806d7 hepatitis e
38	2645	95.5	674	2	Q806E0	Q806e0 swine hepat
39	2645	95.5	674	2	Q80IR5	Q80ir5 hepatitis e
40	2642	95.4	660	2	Q9YLR2	Q9ylr2 hepatitis e
41	2642	95.4	674	2	Q6PMR3	Q6pmr3 swine hepat
42	2641	95.4	660	2	Q8BB05	Q8bb05 swine hepat
43	2617.5	94.5	659	1	VST2_HEVME	Q03500 hepatitis e
44	2614	94.4	672	2	Q9IVZ8	Q9ivz8 hepatitis e
45	2484	89.7	605	2	Q9YWL0	Q9ywl0 hepatitis e

ALIGNMENTS

RESULT 1
VST2_HEVBU
ID VST2_HEVBU STANDARD; PRT; 660 AA.
AC P29326;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Structural protein 2 precursor.
GN ORFNames=ORF2;
OS Hepatitis E virus (strain Burma) (HEV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=31767;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92024067; PubMed=1926770;
RA Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
RA Fry K.E., Reyes G.R.;
RT "Hepatitis E virus (HEV): molecular cloning and sequencing of the
RT full-length viral genome.";
RL Virology 185:120-131(1991).
CC -!- FUNCTION: Contains a high basic amino acid content suggesting that
CC it may be involved in the encapsidation of the genomic RNA by
CC effectively neutralizing the negatively charged RNA.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; M73218; AAA45736.1; -.
DR PIR; C40778; VHWWH2.
DR InterPro; IPR004261; SP2.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF03014; SP2; 1.
KW Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 660 Structural protein 2.
SQ SEQUENCE 660 AA; 70978 MW; 5832A013CCC4A61C CRC64;

Query Match 100.0%; Score 2769; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 1.7e-186;
Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231
```

```
Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651
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RESULT 2
Q9E8G5
ID Q9E8G5 PRELIMINARY; PRT; 660 AA.
AC Q9E8G5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Structural protein.
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Abb-2B;
RX MEDLINE=20271579; PubMed=10813471;
RA van Cuyck-Gandre H., Zhang H.Y., Tsarev S.A., Warren R.L.,
RA Caudill J.D., Snellings N.J., Begot L., Innis B.L., Longer C.F.;
RT "Phylogenetically distinct hepatitis E viruses in Pakistan.";
RL Am. J. Trop. Med. Hyg. 62:187-189(2000).
DR EMBL; AF185822; AAG16766.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70903 MW; 1F506BE3CFB3BACE CRC64;

Query Match 99.7%; Score 2762; DB 2; Length 660;
Best Local Similarity 99.8%; Pred. No. 5.2e-186;
Matches 539; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
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Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651
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RESULT 3
Q9W7W9
ID Q9W7W9 PRELIMINARY; PRT; 660 AA.
AC Q9W7W9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Structural protein 2 (Structural viral protein).
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HEV-Morocco;
RX MEDLINE=99107414; PubMed=9892396;
RX DOI=10.1002/(SICI)1096-9071(199902)57:2<126::AID-JMV7>3.3.CO;2-F;
RA Meng J., Cong M., Dai X., Pillot J., Purdy M.A., Fields H.A.,
RA Khudyakov Y.E.;
RT "Primary structure of open reading frame 2 and 3 of the hepatitis E
RT virus isolated from Morocco.";
RL J. Med. Virol. 57:126-133(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen G., Meng J.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF065061; AAD10627.1; -.
DR EMBL; AY230202; AAO72992.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70943 MW; 9719D30CCD932950 CRC64;

Query Match 99.6%; Score 2758; DB 2; Length 660;
Best Local Similarity 99.6%; Pred. No. 9.9e-186;
Matches 538; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291
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Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 4
Q9WQA0
ID   Q9WQA0      PRELIMINARY;      PRT;   660 AA.
AC   Q9WQA0;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   ORF-2..
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99350000; PubMed=10423137;
RA   Arankalle V.A., Paranjape S., Emerson S.U., Purcell R.H.,
RA   Walimbe A.M.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from India (1976-
RT   1993).";
RL   J. Gen. Virol. 80:1691-1700(1999).
DR   EMBL; AF124407; AAD45493.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71040 MW;  03B72DDF0AB7B521 CRC64;

  Query Match             99.6%;  Score 2758;  DB 2;  Length 660;
  Best Local Similarity   99.6%;  Pred. No. 9.9e-186;
  Matches  538;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVFAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 5
VST2_HEVPA
ID   VST2_HEVPA     STANDARD;      PRT;   660 AA.
AC   P33426;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   Structural protein 2 precursor.
GN   ORFNames=ORF2;
OS   Hepatitis E virus (strain Pakistan) (HEV).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=33774;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92115700; PubMed=1731327;
RA   Tsarev S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J.,
RA   Malik I.A., Iqbal M., Purcell R.H.;
RT   "Characterization of a prototype strain of hepatitis E virus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).
CC   -!- FUNCTION: Contains a high basic amino acid content suggesting that
CC       it may be involved in the encapsidation of the genomic RNA by
CC       effectively neutralizing the negatively charged RNA.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M80581; AAA45727.1; -.
DR   InterPro; IPR004261; SP2.
DR   InterPro; IPR008975; Viral_cap_coat.
DR   Pfam; PF03014; SP2; 1.
KW   Signal.
FT   SIGNAL        1     22       By similarity.
FT   CHAIN        23    660       Structural protein 2.
SQ   SEQUENCE   660 AA;  70980 MW;  8085BC53CFB46FD3 CRC64;

  Query Match             99.5%;  Score 2756;  DB 1;  Length 660;
  Best Local Similarity   99.4%;  Pred. No. 1.4e-185;
  Matches  537;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291
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Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540

Db        592 PVSISAVAVLAPHSVLALLEDTMDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651
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RESULT 6
Q77EC8
ID Q77EC8 PRELIMINARY; PRT; 660 AA.
AC Q77EC8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Capsid protein.
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sar-55;
RX MEDLINE=21625046; PubMed=11742081; DOI=10.1073/pnas.251555098;
RA Emerson S.U., Zhang M., Meng X.-J., Nguyen H., St Claire M.,
RA Govindarajan S., Huang Y.K., Purcell R.H.;
RT "Recombinant hepatitis E virus genomes infectious for primates:
RT importance of capping and discovery of a cis-reactive element.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:15270-15275(2001).
DR EMBL; AF444003; AAL50059.1; -.
DR EMBL; AF444002; AAL50056.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70979 MW; 8085BC53CFB46FD3 CRC64;

Query Match 99.5%; Score 2756; DB 2; Length 660;
Best Local Similarity 99.4%; Pred. No. 1.4e-185;
Matches 537; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180

Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540

Db        592 PVSISAVAVLAPHSVLALLEDTMDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651
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RESULT 7
Q89468
ID Q89468 PRELIMINARY; PRT; 660 AA.
AC Q89468;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Unnamed protein product (ORFs 1-3).
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RA Yin S.R., Purcell R.H., Emerson S.U.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K52-87;
RX MEDLINE=95176571; PubMed=7871758;
RA Yin S., Purcell R.H., Emerson S.U.;
RT "A new Chinese isolate of hepatitis E virus: comparison with strains
RT recovered from different geographical regions.";
RL Virus Genes 9:23-32(1994).
DR EMBL; L25547; AAA91080.1; -.
DR EMBL; L25595; AAA65490.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70979 MW; DC68116DCD639175 CRC64;

Query Match 99.5%; Score 2756; DB 2; Length 660;
Best Local Similarity 99.4%; Pred. No. 1.4e-185;
Matches 537; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180

Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
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Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              |||||||||| ||||||||||:|||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLTPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 8
Q69419
ID   Q69419      PRELIMINARY;      PRT;   660 AA.
AC   Q69419;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ORF1, ORF2 & ORF3.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   von Brunn A., Seebach J., Thyagarajan S.P., Mohanavalli B., Menon T.,
RA   Froesner G.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X99441; CAA67804.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70960 MW;  DAC3DF95F91689F8 CRC64;

  Query Match             99.4%;  Score 2752;  DB 2;  Length 660;
  Best Local Similarity   99.4%;  Pred. No. 2.6e-185;
  Matches  537;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              || ||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        412 LYRSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSALRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 9
Q81871
ID   Q81871      PRELIMINARY;      PRT;   660 AA.
AC   Q81871;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   ORF 2 precursor.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92024067; PubMed=1926770;
RA   Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
RA   Fry K.E., Reyes G.R.;
RT   "Hepatitis E virus (HEV): molecular cloning and sequencing of the
RT   full-length viral genome.";
RL   Virology 185:120-131(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92115700; PubMed=1731327;
RA   Tsarev S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J.,
RA   Malik I.A., Iqbal M., Purcell R.H.;
RT   "Characterization of a prototype strain of hepatitis E virus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92261377; PubMed=1584074;
RA   Uchida T., Suzuki K., Hayashi N., Iida F., Hara T., Oo S.S., Wang C.,
RA   Shikata T., Ichikawa M., Rikihisa T., Mizuno K., Win K.M.;
RT   "Hepatitis E virus: cDNA cloning and expression.";
RL   Microbiol. Immunol. 36:67-79(1992).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92335008; PubMed=1630924;
RA   Aye T.T., Uchida T., Ma M.Z., Iida F., Shikata T., Zhuang H.,
RA   Win K.M.;
RT   "Complete nucleotide sequence of a hepatitis E virus isolated from the
RT   Xinjiang epidemic (1986-1988) of China.";
RL   Nucleic Acids Res. 20:3512-3512(1992).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92271462; PubMed=1589964;
RA   Fry K.E., Tam A.W., Smith M.W., Kim J.P., Luk K.-C., Young L.M.,
RA   Piatak M., Feldman R.A., Yun K.Y., Purdy M.A., McCaustland K.A.,
RA   Bradley D.W., Reyes G.R.;
RT   "Hepatitis E virus (HEV): strain variation in the nonstructural gene
RT   region encoding consensus motifs for an RNA-dependent RNA polymerase
RT   and an ATP/GTP binding site.";
RL   Virus Genes 6:173-185(1992).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93348763; PubMed=8346669; DOI=10.1016/0168-1702(93)90024-H;
RA   Bi S-L., Purdy M.A., McCaustland K.A., Margolis H.S., Bradley D.W.;
RT   "The sequence of hepatitis E virus isolated directly from a single
RT   source during an outbreak in China.";
RL   Virus Res. 28:233-247(1993).
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DR   EMBL; L08816; AAA03191.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
KW   Signal.
FT   SIGNAL       1     19       Potential.
SQ   SEQUENCE   660 AA;  70979 MW;  B58F23955FDD6614 CRC64;

  Query Match             99.3%;  Score 2751;  DB 2;  Length 660;
  Best Local Similarity   99.3%;  Pred. No. 3.1e-185;
  Matches  536;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASEHVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTTQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 10
O91855
ID   O91855      PRELIMINARY;      PRT;   660 AA.
AC   O91855;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Structural protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=93-Egypt;
RX   MEDLINE=99105430; PubMed=9890424;
RX   DOI=10.1002/(SICI)1096-9071(199901)57:1<68::AID-JMV10>3.0.CO;2-E;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
RL   J. Med. Virol. 57:68-74(1999).
DR   EMBL; AF051351; AAC35761.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71039 MW;  044FF5EA7C492791 CRC64;

  Query Match             99.3%;  Score 2750;  DB 2;  Length 660;
  Best Local Similarity   99.1%;  Pred. No. 3.6e-185;
  Matches  535;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||:|||||:||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTSSDQLLIENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 11
O91856
ID   O91856      PRELIMINARY;      PRT;   660 AA.
AC   O91856;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Structural protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=94-Egypt;
RX   MEDLINE=99105430; PubMed=9890424;
RX   DOI=10.1002/(SICI)1096-9071(199901)57:1<68::AID-JMV10>3.0.CO;2-E;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
RL   J. Med. Virol. 57:68-74(1999).
DR   EMBL; AF051352; AAC35764.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71025 MW;  16C560FA16941F2A CRC64;

  Query Match             99.3%;  Score 2749;  DB 2;  Length 660;
  Best Local Similarity   99.1%;  Pred. No. 4.3e-185;
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  Matches  535;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||:||| ||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLIENATGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 12
Q81878
ID   Q81878      PRELIMINARY;      PRT;   660 AA.
AC   Q81878;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Complete genome sequence.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Uchida T.;
RL   Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; D11093; BAA01867.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70937 MW;  5412313F1A2EF4A9 CRC64;

  Query Match           99.1%;  Score 2744;  DB 2;  Length 660;
  Best Local Similarity   98.9%;  Pred. No. 9.6e-185;
  Matches  534;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYGISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||:|||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        292 PYTGALGVLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGTDGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YCKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 13
Q69411
ID   Q69411      PRELIMINARY;      PRT;   660 AA.
AC   Q69411;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Structural protein.
GN   Name=ORF2;
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Donati M.C., Fagan E.A., Harrison T.J.;
RT   "Sequence analysis of full length HEV clones derived directly from
RT   human liver in fulminant hepatitis E.";
RL   (In) Rizzetto M., Purcell R.H., Gerin J.L., Verme G (eds.);
RL   VIRAL HEPATITIS AND LIVER DISEASE, pp.313-316, Edizioni Minerva
RL   Medica, Torino (1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Harrison T.J.;
RL   Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X98292; CAA66937.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71024 MW;  F37E3FEFF7A4EAD1 CRC64;

  Query Match           99.0%;  Score 2741;  DB 2;  Length 660;
  Best Local Similarity   98.7%;  Pred. No. 1.6e-184;
  Matches  533;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSPVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
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Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGLPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALEFEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||:|||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVAISAVAVLAPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 14
Q6XXV0
ID   Q6XXV0      PRELIMINARY;      PRT;   660 AA.
AC   Q6XXV0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Structural protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RX   MEDLINE=98071272; PubMed=9407381;
RX   DOI=10.1002/(SICI)1096-9071(199712)53:4<340::AID-JMV5>3.0.CO;2-7;
RA   van Cuyck-Gandre H., Zhang H.Y., Tsarev S.A., Clements N.J.,
RA   Cohen S.J., Caudill J.D., Buisson Y., Coursaget P., Warren R.L.,
RA   Longer C.F.;
RT   "Characterization of hepatitis E virus (HEV) from Algeria and Chad by
RT   partial genome sequence.";
RL   J. Med. Virol. 53:340-347(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RX   MEDLINE=99105430; PubMed=9890424;
RX   DOI=10.1002/(SICI)1096-9071(199901)57:1<68::AID-JMV10>3.0.CO;2-E;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
RL   J. Med. Virol. 57:68-74(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RX   MEDLINE=22987819; PubMed=14625096; DOI=10.1016/S0928-8244(03)00241-4;
RA   van Cuyck H., Juge F., Roques P.;
RT   "Phylogenetic analysis of the first complete hepatitis E virus (HEV)
RT   genome from Africa.";
RL   FEMS Immunol. Med. Microbiol. 39:133-139(2003).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RA   Van Cuyck-Gandre H., Zhang H.Y., Tsarev S.A., Clements N.J.,
RA   Cohen S.J., Caudill J.D., Buisson Y., Coursaget P., Warren R.L.,
RA   Longer C.F.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RA   van Cuyck H., Roberston D., Juge F., Roques P., Lemey P.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY204877; AAB61825.2; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70949 MW;  EA56732D458D0AB1 CRC64;

  Query Match             99.0%;  Score 2741;  DB 2;  Length 660;
  Best Local Similarity   98.9%;  Pred. No. 1.6e-184;
  Matches  534;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVSDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
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Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||:|| ||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLIENVAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 15
Q9WLL4
ID   Q9WLL4      PRELIMINARY;      PRT;   660 AA.
AC   Q9WLL4;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Capsid protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
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RP   SEQUENCE FROM N.A.
RC   STRAIN=TK15/92;
RX   MEDLINE=99049628; PubMed=9833882; DOI=10.1016/S0168-1702(98)00079-3;
RA   Gouvea V., Snellings N., Popek M.J., Longer C.F., Innis B.L.;
RT   "Hepatitis E virus: complete genome sequence and phylogenetic analysis
RT   of a Nepali isolate.";
RL   Virus Res. 57:21-26(1998).
DR   EMBL; AF051830; AAC97188.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70798 MW;  A04C0185ACC085DB CRC64;

  Query Match             98.8%;  Score 2735;  DB 2;  Length 660;
  Best Local Similarity   99.1%;  Pred. No. 4.1e-184;
  Matches  535;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||| |||||| ||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVGSRGAILCRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARAAIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASGQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


Search completed: July 14, 2005, 15:50:30
Job time : 41.3962 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 14, 2005, 00:29:03 ; Search time 44.6604 Seconds
(without alignments)
4676.418 Million cell updates/sec

Title: US-09-769-066-26
Perfect score: 2776
Sequence: 1 AVAPAHDTSPVPDVDSRGAI.....ALGLQGCAFQSTVAELQRLK 540

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2776	100.0	540	2	AAR96102	Aar96102 Hepatitis
2	2776	100.0	549	2	AAR96092	Aar96092 Hepatitis
3	2776	100.0	660	2	AAR96090	Aar96090 Hepatitis
4	2749.5	99.0	659	2	AAR38787	Aar38787 HEV ORF2
5	2749.5	99.0	659	2	AAW35827	Aaw35827 Hepatitis
6	2749.5	99.0	659	2	AAW93387	Aaw93387 Human HEV
7	2746.5	98.9	659	2	AAR39308	Aar39308 Mexico st
8	2713.5	97.7	659	5	ABJ04808	Abj04808 Hepatitis
9	2701	97.3	525	2	AAR96104	Aar96104 Hepatitis
10	2654	95.6	549	2	AAW76367	Aaw76367 Hepatitis
11	2654	95.6	660	2	AAR70323	Aar70323 Hepatitis
12	2654	95.6	660	2	AAW76369	Aaw76369 Hepatitis
13	2650	95.5	660	2	AAR91814	Aar91814 Hepatitis
14	2650	95.5	660	2	AAW93386	Aaw93386 Human HEV
15	2650	95.5	660	2	AAW93388	Aaw93388 Human HEV
16	2650	95.5	660	5	ABB81670	Abb81670 Hepatitis
17	2650	95.5	660	6	ADA50060	Ada50060 Hepatitis
18	2650	95.5	660	7	ADB97807	Adb97807 HEV ORF2
19	2644	95.2	540	2	AAR96101	Aar96101 Hepatitis
20	2644	95.2	549	2	AAR96091	Aar96091 Hepatitis
21	2644	95.2	660	2	AAR38785	Aar38785 HEV ORF2
22	2644	95.2	660	2	AAR39306	Aar39306 Burma str
23	2644	95.2	660	2	AAR96089	Aar96089 Hepatitis
24	2644	95.2	660	2	AAW35826	Aaw35826 Hepatitis
25	2644	95.2	660	2	AAW80197	Aaw80197 Protein e
26	2644	95.2	660	2	AAW93389	Aaw93389 Human HEV
27	2644	95.2	660	2	AAW93390	Aaw93390 Human HEV
28	2644	95.2	660	3	AAB24120	Aab24120 Hepatitis
29	2644	95.2	660	4	AAB62523	Aab62523 HEV-Burma
30	2644	95.2	660	5	AAO15699	Aao15699 Hepatitis
31	2644	95.2	660	7	ADD24376	Add24376 Hepatitis
32	2643	95.2	660	2	AAW93392	Aaw93392 Human HEV
33	2641	95.1	660	2	AAR51265	Aar51265 HEV strai
34	2641	95.1	660	2	AAW81520	Aaw81520 Hepatitis
35	2639	95.1	660	5	ABJ04811	Abj04811 Hepatitis
36	2638	95.0	660	2	AAW93391	Aaw93391 Human HEV
37	2637	95.0	660	2	AAW71210	Aaw71210 Protein e
38	2635	94.9	660	4	AAE12980	Aae12980 Hepatitis
39	2635	94.9	660	5	ABJ04820	Abj04820 Hepatitis
40	2635	94.9	660	5	ABJ04807	Abj04807 Hepatitis
41	2635	94.9	660	5	ABJ04809	Abj04809 Hepatitis
42	2635	94.9	660	5	ABJ04819	Abj04819 Hepatitis
43	2632	94.8	660	5	ABJ04822	Abj04822 Hepatitis
44	2630	94.7	660	2	AAW93395	Aaw93395 Human HEV
45	2630	94.7	660	7	ADE06700	Ade06700 Hepatitis

ALIGNMENTS

RESULT 1
AAR96102
ID AAR96102 standard; protein; 540 AA.
XX
AC AAR96102;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Mexico strain) recombinant 62K antigen.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid.
XX
OS Hepatitis E virus; Mexico strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Claim 6; Page 93-95; 125pp; English.
XX
CC DNA (AAT27110) coding for the 62K antigen (AAR96092) of hepatitis E virus
CC (HEV) Mexico strain capsid protein was cloned into baculovirus expression
CC vector pBluBacIII and recombinant 62K was expressed in Sf9 insect cells.
CC High levels of expression were obtd. and the recombinant 62K was obtd. in
CC over 95% purity. However, C-terminal processing resulted in the deletion
CC of 9 or 23 amino acids from 62K, giving 2 related polypeptide species
CC (AAR96102 and AAR96104). Similar results were obtd. with HEV Burma 62K
CC antigen (see also AAR96101 and AAR96103). Recombinant 62K represents an
CC improved antigen, in comparison to bacterial expressed proteins, for use
CC in HEV diagnostic assays, and also has excellent immunogenic properties.
CC (Updated on 16-OCT-2003 to standardise OS field)

XX
SQ Sequence 540 AA;

Query Match 100.0%; Score 2776; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 3e-232;
Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
```

RESULT 2
AAR96092
ID AAR96092 standard; protein; 549 AA.
XX
AC AAR96092;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Mexico strain) 62K antigen.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid.
XX
OS Hepatitis E virus; Mexico strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
DR N-PSDB; AAT27110.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Claim 4; Page 84-86; 125pp; English.
XX
CC 62K antigen (AAR96092) comprises the C-terminal 549 amino acids of
CC hepatitis E virus (HEV) Mexico strain capsid protein (see also AAR96090).
CC It is obtd. by PCR amplification of HEV Mexico ORF-2 (AAT27108),
CC insertion of amplified DNA (AAT27110) into vector pGEX and expression in
CC E. coli cells. Expression of full-length ORF-2 in Sf9 insect cells using
CC a baculovirus system also results in prodn. of 62K antigen (see also
CC AAR96102 and AAR96104). 62K represents an improved antigen, in comparison
CC to bacterial expressed proteins, for use in HEV diagnostic assays, and
CC also has excellent immunogenic properties. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 549 AA;

Query Match 100.0%; Score 2776; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 3.1e-232;
Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
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RESULT 3
AAR96090
ID AAR96090 standard; protein; 660 AA.
XX
AC AAR96090;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Mexico strain) capsid protein.

```
XX
KW   HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW   diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW   capsid.
XX
OS   Hepatitis E virus; Mexico strain.
XX
PN   WO9612807-A2.
XX
PD   02-MAY-1996.
XX
PF   23-OCT-1995;   95WO-US013703.
XX
PR   24-OCT-1994;   94US-00327952.
PR   13-OCT-1995;   95US-00542634.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fuerst TR,  Mcatee CP,  Yarbough PO,  Zhang Y;
XX
DR   WPI; 1996-230608/23.
DR   N-PSDB; AAT27108.
XX
PT   Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT   diagnostic reagents for determining HEV infection and in vaccines.
XX
PS   Disclosure; Page 80-82; 125pp; English.
XX
CC   The putative capsid protein (AAR96090) of hepatitis E virus (HEV) Mexico
CC   strain is encoded by ORF-2 (AAT27108) of the virus. PCR amplification of
CC   ORF-2 allows prodn. of capsid protein or of C-terminal regions of the
CC   capsid protein (see also AAR96092, AAR96094 and AAR96096) and expression
CC   in Spodoptera frugiperda Sf9 insect cells using a baculovirus vector
CC   provides recombinant C-terminal regions (see also AAR96102 and AAR96104)
CC   useful as diagnostic reagents and in vaccines. The HEV Burma strain
CC   capsid protein (AAR96089) may similarly be used. (Updated on 16-OCT-2003
CC   to standardise OS field)
XX
SQ   Sequence 660 AA;

  Query Match           100.0%;  Score 2776;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 4e-232;
  Matches  540;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 651


RESULT 4
AAR38787
ID   AAR38787 standard; protein; 659 AA.
XX
AC   AAR38787;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   11-JAN-1994  (first entry)
XX
DE   HEV ORF2 protein.
XX
KW   Enterically transmitted non-A non-B hepatitis; ET-NANB; vaccine.
XX
OS   Hepatitis E virus; Mexico strain.
XX
FH   Key             Location/Qualifiers
FT   Peptide          225. .659
FT                    /label= C2
FT   Peptide          333. .659
FT                    /label= SG3
FT   Peptide          612. .659
FT                    /label= 406.3-2
XX
PN   WO9314116-A1.
XX
PD   22-JUL-1993.
XX
PF   15-JAN-1993;   93WO-US000459.
XX
PR   17-JAN-1992;   92US-00822335.
PR   01-MAY-1992;   92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
PA   (USSH ) US SEC DEPT HEALTH.
XX
PI   Reyes GR,  Bradley DW,  Tam AW,  Carl M;
XX
DR   WPI; 1993-243144/30.
DR   N-PSDB; AAQ47130.
XX
PT   New immunogenic hepatitis E virus (HEV) peptide(s) - are from the ORF1,
PT   ORF2 and ORF3 regions of HEV, useful as a vaccine against HEV infection.
XX
PS   Disclosure; Fig 8; 48pp; English.
XX
CC   Immunogenic hepatitis E virus (HEV) peptides are selected from the ORF1,
CC   ORF2 and ORF3 regions of HEV. The peptides can be used in vaccines to
CC   prevent infection by HEV. The antibodies can neutralise and block HEV
CC   infection and can be used to prevent or treat HEV infection. The peptides
CC   and antibodies can also be used as diagnostic reagents. (Updated on 25-
CC   MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS
CC   field)
XX
SQ   Sequence 659 AA;

  Query Match           99.0%;  Score 2749.5;  DB 2;  Length 659;
  Best Local Similarity   99.4%;  Pred. No. 8.1e-230;
  Matches  537;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
                ||||||||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 650
```

RESULT 5
AAW35827
ID AAW35827 standard; protein; 659 AA.
XX
AC AAW35827;
XX
DT 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 26-FEB-1998 (first entry)
XX
DE Hepatitis E virus Mexico strain protein from ORF2.
XX
KW Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
KW diagnosis; HEV.
XX
OS Hepatitis E virus; - Mexico strain.
XX
PN US5686239-A.
XX
PD 11-NOV-1997.
XX
PF 09-MAY-1994; 94US-00240049.
XX
PR 17-JUN-1988; 88US-00208997.
PR 11-APR-1989; 89US-00336672.
PR 16-JUN-1989; 89US-00367486.
PR 13-OCT-1989; 89US-00420921.
PR 05-APR-1990; 90US-00505888.
PR 05-APR-1991; 91US-00681078.
PR 17-JAN-1992; 92US-00822335.
PR 20-APR-1992; 92US-00870985.
PR 01-MAY-1992; 92US-00876941.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Tam AW, Reyes GR, Yarbough PO;
XX
DR WPI; 1997-558132/51.
DR N-PSDB; AAT96960.
XX
PT Diagnosis of hepatitis E virus Burma and Mexico strain infection - by
PT immunoassay with hepatitis E virus peptide antigens.
XX
PS Disclosure; Col 43-46; 36pp; English.
XX
CC A method has been developed for detecting hepatitis E virus (HEV)
CC antibodies (Ab). The method comprises: (a) reacting a serum sample with a
CC HEV peptide antigen; and (b) examining the peptide for the presence of
CC bound Ab, where the presence of bound Ab indicates the presence of HEV
CC Ab. The present sequence represents the protein from the open reading
CC frame, ORF2, from HEV Mexico strain. The method can be used to diagnose
CC infection with the enterically transmitted non-A/non-B viral hepatitis
CC agent HEV, specifically the HEV Burma and Mexico strains. (Updated on 25-
CC MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 659 AA;

Query Match 99.0%; Score 2749.5; DB 2; Length 659;
Best Local Similarity 99.4%; Pred. No. 8.1e-230;
Matches 537; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
                ||||||||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 650
```

RESULT 6
AAW93387
ID AAW93387 standard; protein; 659 AA.
XX
AC AAW93387;
XX
DT 11-JUN-1999 (first entry)
XX
DE Human HEV ORF 2 protein from strain Mexico.
XX
KW Swine hepatitis E virus; HEV; cross-reaction; antibody; human; therapy;
KW vaccine; immunise; infection; detection; diagnosis; prevention.
XX
OS Hepatitis E virus.
XX

PN WO9904029-A2.
XX
PD 28-JAN-1999.
XX
PF 17-JUL-1998; 98WO-US014665.
XX
PR 18-JUL-1997; 97US-0053069P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Meng X, Emerson SU, Purcell RH;
XX
DR WPI; 1999-132270/11.
XX
PT New isolated swine hepatitis E virus - used to develop products for the
PT diagnosis, prevention and treatment of hepatitis E virus infection in
PT mammals, particularly humans.
XX
PS Example 1; Fig 3A; 70pp; English.
XX
CC This invention describes a swine hepatitis E virus (HEV) and its natural
CC mutants which are capable of cross-reacting with antibodies reactive with
CC a human HEV strain or natural mutants. The HEV and the proteins can be
CC used in vaccines for immunising against HEV infection. The swine HEV can
CC be used in humans to prevent possible infection by human HEV. The swine
CC HEV can also be used as a therapeutic treatment for infection by other
CC strains of HEV. The swine HEV can also be used for the production of
CC antibodies which can be used in therapy, detection and diagnosis. The
CC products can also be used for determining the susceptibility of cells or
CC organs to infection with swine HEV. The swine HEV is particularly useful
CC for the development of agents for the prevention, treatment and detection
CC of human HEV because it is not a human virus and thus can be handled both
CC experimentally and clinically without fear of severe infection and/or
CC contamination
XX
SQ Sequence 659 AA;

Query Match 99.0%; Score 2749.5; DB 2; Length 659;
Best Local Similarity 99.4%; Pred. No. 8.1e-230;
Matches 537; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```
Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590
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Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 650
```

RESULT 7
AAR39308
ID AAR39308 standard; protein; 659 AA.
XX
AC AAR39308;
XX
DT 25-MAR-2003 (revised)
DT 14-FEB-1994 (first entry)
XX
DE Mexico strain HEV ORF2 puative virus capsid protein.
XX
KW Hepatitis E virus; vaccine; neutralising antibodies; infection; block;
KW open reading frame; antibodies.
XX
OS Hepatitis E virus.
XX
PN WO9314208-A2.
XX
PD 22-JUL-1993.
XX
PF 19-JAN-1993; 93WO-US000475.
XX
PR 17-JAN-1992; 92US-00822335.
PR 20-APR-1992; 92US-00870985.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Reyes GR, Bradley DW, Twu J, Purdy MA, Tam AW, Krawczynski KZ;
XX
DR WPI; 1993-243223/30.
DR N-PSDB; AAQ46814.
XX
PT Antigen and antibody vaccines against hepatitis E virus infection -
PT contain peptide(s) derived from capsid protein C-terminal or antibodies
PT against protein.
XX
PS Disclosure; Fig 7; 43pp; English.
XX
CC The sequence is that of the putative virus capsid protein encoded by
CC Mexico strain hepatitis E virus (HEV) open reading frame ORF2. This
CC protein or peptide fragments of it may be used in a vaccine composition
CC for immunising an individual against HEV. Antibodies raised against these
CC peptides can also be used in such vaccines. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 659 AA;

Query Match 98.9%; Score 2746.5; DB 2; Length 659;
Best Local Similarity 99.3%; Pred. No. 1.5e-229;
Matches 536; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

```
Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350
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```
Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKLTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 650
```

RESULT 8
ABJ04808
ID ABJ04808 standard; protein; 659 AA.
XX
AC ABJ04808;
XX
DT 07-NOV-2002 (first entry)
XX
DE Hepatitis E virus Mexico strain ORF2 capsid gene.
XX
KW Avian hepatitis E virus; vaccine; hepatitis E; ORF2; zoonosis; virucide;
KW avian hepatitis-splenomegaly syndrome; HEV; HS syndrome.
XX
OS Hepatitis E virus.
XX
PN WO200253712-A2.
XX
PD 11-JUL-2002.
XX
PF 04-JAN-2002; 2002WO-US000215.
XX
PR 05-JAN-2001; 2001US-0259846P.
PR 31-DEC-2001; 2001US-00029840.
XX
PA (VIRG) VIRGINIA TECH INTELLECTUAL PROPERTIES.
XX
PI Meng X, Haqshenas G, Huang F;
XX
DR WPI; 2002-548085/58.
XX
PT Novel isolated avian hepatitis E virus useful in a vaccine for protecting
PT an avian or mammalian species from viral infection or hepatitis-
PT splenomegaly syndrome caused by the avian or mammalian hepatitis E virus.
XX
PS Example 11; Fig 5; 95pp; English.
XX
CC The present invention relates to an isolated avian hepatitis E virus
CC having the nucleic acid sequence shown in ABT05872. Vaccines against the
CC virus are also described, and can be used for protecting an avian or
CC mammalian species from viral infection or hepatitis-splenomegaly syndrome
CC caused by the avian or mammalian HEV. The present sequence is a hepatitis
CC E virus protein described in the exemplification of the invention
XX
SQ Sequence 659 AA;

```
  Query Match             97.7%;  Score 2713.5;  DB 5;  Length 659;
  Best Local Similarity   98.0%;  Pred. No. 1.1e-226;
  Matches  529;  Conservative    3;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||| ||||||||||||||||||   |||||||||||||||||| |
Db        292 PYTGALGLLDFALELEFRMLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFHK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              |||||| |||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGTNGVGEIGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWTKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||:||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 PVSISAVAVLAPHSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 650
```

RESULT 9
AAR96104
ID AAR96104 standard; protein; 525 AA.
XX
AC AAR96104;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Mexico strain) recombinant 62K antigen.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid.
XX
OS Hepatitis E virus; Mexico strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Claim 8; Page 97-98; 125pp; English.
XX
CC DNA (AAT27110) coding for the 62K antigen (AAR96092) of hepatitis E virus
CC (HEV) Mexico strain capsid protein was cloned into baculovirus expression

```
CC   vector pBluBacIII and recombinant 62K was expressed in Sf9 insect cells.
CC   High levels of expression were obtd. and the recombinant 62K was obtd. in
CC   over 95% purity. However, C-terminal processing resulted in the deletion
CC   of 9 or 23 amino acids from 62K, giving 2 related polypeptide species
CC   (AAR96102 and AAR96104). Similar results were obtd. with HEV Burma 62K
CC   antigen (see also AAR96101 and AAR96103). Recombinant 62K represents an
CC   improved antigen, in comparison to bacterial expressed proteins, for use
CC   in HEV diagnostic assays, and also has excellent immunogenic properties.
CC   (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 525 AA;

  Query Match             97.3%;  Score 2701;  DB 2;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-226;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525


RESULT 10
AAW76367
ID   AAW76367 standard; protein; 549 AA.
XX
AC   AAW76367;
XX
DT   03-DEC-1998  (first entry)
XX
DE   Hepatitis E virus hollow particle protein ORF2.
XX
KW   Hollow particle protein; virus; antibody; detection; immunoassay;
KW   infection.
XX
OS   Hepatitis virus.
XX
FH   Key             Location/Qualifiers
FT   Protein         1. .549
FT                   /label= ORF2
FT                   /note= "partial sequence"
XX
PN   JP10234383-A.
XX
PD   08-SEP-1998.
XX
PF   28-FEB-1997;   97JP-00062445.
XX
PR   28-FEB-1997;   97JP-00062445.
XX
PA   (DENK-) DENKA SEIKEN KK.
PA   (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR   WPI; 1998-535037/46.
DR   N-PSDB; AAV61686.
XX
PT   Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids
PT   encoding it - useful for more accurate detection of HEV in samples, using
PT   immuno-assays and nucleic acid hybridisation.
XX
PS   Claim 1; Page 15-17; 29pp; Japanese.
XX
CC   This sequence represents a Hepatitis E viral hollow particle protein
CC   described as ORF2. This polypeptide can be used to raise antibodies to
CC   detect HEV infection in samples, e.g. by immuno-assay based techniques,
CC   and the nucleic acid can be used for the same in nucleic acid
CC   hybridisation assays. The polypeptide and nucleic acid allow more
CC   accurate detection of HEV than previously possible
XX
SQ   Sequence 549 AA;

  Query Match             95.6%;  Score 2654;  DB 2;  Length 549;
  Best Local Similarity   95.0%;  Pred. No. 1.3e-221;
  Matches  513;  Conservative   13;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| ||||||||||||||||||||||||||:||||||||||:| |||||||||
Db          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||:|||||||:|||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||:|||||||||||||||||||||:|||||||| |::|
Db        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||:|:|||||||||||| ||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||:||| ||||| ||||||||| ||| |||||||||||| ||||||||||||||||||||
Db        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 540


RESULT 11
AAR70323
ID   AAR70323 standard; protein; 660 AA.
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XX
AC   AAR70323;
XX
DT   25-MAR-2003  (revised)
DT   28-SEP-1995  (first entry)
XX
DE   Hepatitis E virus ORF2 protein.
XX
KW   HEV; ORF2; antigen; vaccine; immunogen.
XX
OS   Hepatitis E virus.
XX
PN   WO9508632-A1.
XX
PD   30-MAR-1995.
XX
PF   23-SEP-1994;   94WO-AU000572.
XX
PR   24-SEP-1993;   93AU-00001423.
PR   15-DEC-1993;   93AU-00002964.
XX
PA   (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX
PI   Anderson DA,  Locarnini SA,  Torresi J,  Li F,  Hui Z;
XX
DR   WPI; 1995-139601/18.
DR   N-PSDB; AAQ86592.
XX
PT   Antigens of hepatitis E virus (HEV) - selectively immuno:reactive to
PT   convalescent and/or acute phase circulating antibodies to HEV.
XX
PS   Disclosure; Page 39-41; 78pp; English.
XX
CC   RNA from an HEV strain isolated in the Xinjiang region of China was
CC   subjected to RT-PCR to obtain fragments corresp. to ORF2 (given in
CC   AAQ86592) and ORF3 (AAQ86593) that encoded antigenic proteins (AAR70323-
CC   24, respectively). DNA fragments were manipulated into pGEX vectors for
CC   production of GST fusion proteins in E. coli. Applications include HEV
CC   infection diagnosis, therapy and vaccine development. (Updated on 25-MAR-
CC   2003 to correct PN field.)
XX
SQ   Sequence 660 AA;

  Query Match             95.6%;  Score 2654;  DB 2;  Length 660;
  Best Local Similarity   95.0%;  Pred. No. 1.6e-221;
  Matches  513;  Conservative   13;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:|||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||:||||||||||||||||||:||||||||| |::|
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Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||:||| ||||| |||||||||| ||| ||||||||||||| ||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 12
AAW76369
ID   AAW76369 standard; protein; 660 AA.
XX
AC   AAW76369;
XX
DT   03-DEC-1998  (first entry)
XX
DE   Hepatitis E virus hollow particle protein #2.
XX
KW   Hollow particle protein; virus; antibody; detection; immunoassay;
KW   infection.
XX
OS   Hepatitis virus.
XX
PN   JP10234383-A.
XX
PD   08-SEP-1998.
XX
PF   28-FEB-1997;   97JP-00062445.
XX
PR   28-FEB-1997;   97JP-00062445.
XX
PA   (DENK-) DENKA SEIKEN KK.
PA   (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR   WPI; 1998-535037/46.
DR   N-PSDB; AAV61688.
XX
PT   Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids
PT   encoding it - useful for more accurate detection of HEV in samples, using
PT   immuno-assays and nucleic acid hybridisation.
XX
PS   Claim 13; Page 24-26; 29pp; Japanese.
XX
CC   This sequence represents a Hepatitis E viral hollow particle protein.
CC   This polypeptide can be used to raise antibodies to detect HEV infection
CC   in samples, e.g. by immuno-assay based techniques, and the nucleic acid
CC   can be used for the same in nucleic acid hybridisation assays. The
CC   polypeptides and nucleic acids allow more accurate detection of HEV than
CC   previously possible
XX
SQ   Sequence 660 AA;

  Query Match             95.6%;  Score 2654;  DB 2;  Length 660;
  Best Local Similarity   95.0%;  Pred. No. 1.6e-221;
  Matches  513;  Conservative   13;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:|||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
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Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||:|||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||:||| ||||| |||||||| ||| |||||||||||| ||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651
```

RESULT 13
AAR91814
ID AAR91814 standard; protein; 660 AA.
XX
AC AAR91814;
XX
DT 26-NOV-1996 (first entry)
XX
DE Hepatitis E virus strain SAR-55 ORF-2.
XX
KW Hepatitis E virus; HEV; SAR-55 strain; enteric transmission;
KW structural region; antigen; detection; antibody; vaccine; immunisation;
KW infection.
XX
OS Hepatitis E virus.
XX
PN WO9610580-A2.
XX
PD 11-APR-1996.
XX
PF 03-OCT-1995; 95WO-US013102.
XX
PR 03-OCT-1994; 94US-00316765.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Tsarev SA, Emerson SU, Purcell RH;
XX
DR WPI; 1996-209320/21.
DR N-PSDB; AAT27394.
XX
PT Isolated and purified hepatitis E virus strain SAR-55 DNA - encodes
PT antigenic protein useful in diagnosis, prophylaxis and treatment of
PT hepatitis E virus infection.
XX
PS Claim 6; Page 13-15; 121pp; English.
XX
CC The present sequence is the protein prod. of ORF-2 from the hepatitis E
CC virus (HEV) strain SAR-55, which was implicated in an enterically
CC transmitted non-A, non-B hepatitis in Pakistan. The protein encoded by
CC the structural region of the virus (i.e. ORF-2), which is capable of
CC forming HEV like particles, is useful for the detection of HEV antibodies
CC (pref. IgG or IgM) in blood, plasma, sera, cerebrospinal fluid, tissue,
CC urine or pleural fluid. The protein, and anti-HEV antibodies generated
CC using the protein, can also be used in vaccines for immunising an animal
CC against HEV infection. The protein is identified as a band of greater
CC than 50 kD following SDS-PAGE of cell lysates of insect cells infected
CC with a HEV ORF-2 contg. baculovirus, i.e. the claimed recombinant
CC expression vectors pPIC9-1779, -1780 and -1781
XX

SQ Sequence 660 AA;

Query Match 95.5%; Score 2650; DB 2; Length 660;
Best Local Similarity 94.8%; Pred. No. 3.7e-221;
Matches 512; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
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Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||:|||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
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Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||:||| ||||| | ||||||| ||| |||||||||||| ||||||||||||||||||||
Db        592 PVSISAVAVLAPHSVLALLEDTMDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651
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RESULT 14
AAW93386
ID AAW93386 standard; protein; 660 AA.
XX
AC AAW93386;
XX
DT 11-JUN-1999 (first entry)
XX
DE Human HEV ORF 2 protein from strain Sar55.
XX
KW Swine hepatitis E virus; HEV; cross-reaction; antibody; human; therapy;
KW vaccine; immunise; infection; detection; diagnosis; prevention.
XX
OS Hepatitis E virus.
XX
PN WO9904029-A2.
XX
PD 28-JAN-1999.
XX
PF 17-JUL-1998; 98WO-US014665.
XX
PR 18-JUL-1997; 97US-0053069P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Meng X, Emerson SU, Purcell RH;
XX
DR WPI; 1999-132270/11.
XX
PT New isolated swine hepatitis E virus - used to develop products for the

PT diagnosis, prevention and treatment of hepatitis E virus infection in
PT mammals, particularly humans.
XX
PS Example 1; Fig 3A; 70pp; English.
XX
CC This invention describes a swine hepatitis E virus (HEV) and its natural
CC mutants which are capable of cross-reacting with antibodies reactive with
CC a human HEV strain or natural mutants. The HEV and the proteins can be
CC used in vaccines for immunising against HEV infection. The swine HEV can
CC be used in humans to prevent possible infection by human HEV. The swine
CC HEV can also be used as a therapeutic treatment for infection by other
CC strains of HEV. The swine HEV can also be used for the production of
CC antibodies which can be used in therapy, detection and diagnosis. The
CC products can also be used for determining the susceptibility of cells or
CC organs to infection with swine HEV. The swine HEV is particularly useful
CC for the development of agents for the prevention, treatment and detection
CC of human HEV because it is not a human virus and thus can be handled both
CC experimentally and clinically without fear of severe infection and/or
CC contamination
XX
SQ Sequence 660 AA;

Query Match 95.5%; Score 2650; DB 2; Length 660;
Best Local Similarity 94.8%; Pred. No. 3.7e-221;
Matches 512; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||| |||||||||||||||||||||||:|||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||:|||||||||||||||||||:||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

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              ||||||||||||||||||||||||||||||||||:|:|||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||:||| ||||| | ||||||| ||| |||||||||||| ||||||||||||||||||||
Db        592 PVSISAVAVLAPHSVLALLEDTMDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651
```

RESULT 15
AAW93388
ID AAW93388 standard; protein; 660 AA.
XX
AC AAW93388;
XX
DT 11-JUN-1999 (first entry)
XX
DE Human HEV ORF 2 protein from strain KS2-87.
XX
KW Swine hepatitis E virus; HEV; cross-reaction; antibody; human; therapy;
KW vaccine; immunise; infection; detection; diagnosis; prevention.
XX
OS Hepatitis E virus.
XX
PN WO9904029-A2.
XX
PD 28-JAN-1999.
XX
PF 17-JUL-1998; 98WO-US014665.
XX
PR 18-JUL-1997; 97US-0053069P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Meng X, Emerson SU, Purcell RH;
XX
DR WPI; 1999-132270/11.
XX
PT New isolated swine hepatitis E virus - used to develop products for the
PT diagnosis, prevention and treatment of hepatitis E virus infection in
PT mammals, particularly humans.
XX
PS Example 1; Fig 3A; 70pp; English.
XX
CC This invention describes a swine hepatitis E virus (HEV) and its natural
CC mutants which are capable of cross-reacting with antibodies reactive with
CC a human HEV strain or natural mutants. The HEV and the proteins can be
CC used in vaccines for immunising against HEV infection. The swine HEV can
CC be used in humans to prevent possible infection by human HEV. The swine
CC HEV can also be used as a therapeutic treatment for infection by other
CC strains of HEV. The swine HEV can also be used for the production of
CC antibodies which can be used in therapy, detection and diagnosis. The
CC products can also be used for determining the susceptibility of cells or
CC organs to infection with swine HEV. The swine HEV is particularly useful
CC for the development of agents for the prevention, treatment and detection
CC of human HEV because it is not a human virus and thus can be handled both
CC experimentally and clinically without fear of severe infection and/or
CC contamination
XX
SQ Sequence 660 AA;

Query Match 95.5%; Score 2650; DB 2; Length 660;
Best Local Similarity 94.8%; Pred. No. 3.7e-221;
Matches 512; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
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Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
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Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
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Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||:|||||||||||||||||||:||||||||| |::|
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```

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Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
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Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||:||| ||| | ||||||||| ||| |||||||||||| ||||||||||||||||||
Db        592 PVSISAVAVLTPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651
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Search completed: July 14, 2005, 15:46:30
Job time : 45.6604 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 14, 2005, 02:26:53 ; Search time 9.33962 Seconds
(without alignments)
5563.078 Million cell updates/sec

Title: US-09-769-066-26
Perfect score: 2776
Sequence: 1 AVAPAHDTSPVPDVDSRGAI.....ALGLQGCAFQSTVAELQRLK 540

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2749.5	99.0	659	1	B44212	structural protein
2	2644	95.2	660	1	VHWWH2	structural protein
3	128.5	4.6	5188	2	B85547	probable RTX famil
4	128.5	4.6	5291	2	F90696	hypothetical prote
5	127	4.6	1367	1	S48478	glucan 1,4-alpha-g
6	125	4.5	3282	2	E82750	hemagglutinin-like
7	125	4.5	3442	2	E82589	hemagglutinin-like
8	125	4.5	3455	2	B82519	hemagglutinin-like
9	122.5	4.4	1077	2	H96007	probable acriflavi
10	121	4.4	725	2	A41258	a-agglutinin core
11	120	4.3	1041	2	S55862	probable membrane
12	120	4.3	1975	2	B81192	hemagglutinin/hemo
13	120	4.3	1995	2	G81044	hemagglutinin/hemo
14	119	4.3	2015	2	B81989	hypothetical prote
15	118.5	4.3	547	2	T41213	probable zinc fing
16	118.5	4.3	2130	2	AB0821	probable exported
17	118	4.3	1104	2	S59310	probable membrane
18	116.5	4.2	583	2	S67571	hypothetical prote
19	116	4.2	351	1	VCVETC	coat protein - tur
20	115.5	4.2	2054	2	T46612	multi PDZ domain p
21	115	4.1	3083	2	AH2493	hypothetical prote
22	113.5	4.1	1213	2	T51032	hypothetical prote
23	113.5	4.1	1483	2	C97012	probably celluloso
24	113	4.1	797	1	VGBEX1	glycoprotein X pre
25	113	4.1	1350	2	AF2005	RNA polymerase bet
26	112.5	4.1	1643	2	D71630	outer membrane pro
27	112	4.0	1180	2	E86719	hypothetical prote
28	112	4.0	1345	2	H90975	hypothetical prote
29	112	4.0	1377	2	I54632	tsh protein - Esch
30	112	4.0	2505	1	XYRTFA	enoyl-[acyl-carrie
31	112	4.0	2660	2	E85822	probable invasin Z
32	111.5	4.0	962	2	S03818	carboxymethylcellu
33	111.5	4.0	1374	2	AE3259	extracellular seri
34	111.5	4.0	3570	2	T45025	mucin MUC5B, trach
35	111	4.0	1014	1	NMCLSS	exo-alpha-sialidas
36	111	4.0	3972	2	S75251	hypothetical prote
37	110.5	4.0	1306	2	S25370	MSB2 protein - yea
38	110.5	4.0	1746	1	S19694	tenascin precursor
39	110.5	4.0	3624	2	AD0835	large repetitive p
40	110	4.0	1112	2	T32733	AMPA glutamate rec
41	110	4.0	1131	2	T41144	hypothetical serin
42	109.5	3.9	1016	2	H71460	probable outer mem
43	109.5	3.9	1802	2	S69703	HKR1 protein precu
44	109.5	3.9	4199	2	S76412	hypothetical prote
45	109	3.9	507	2	F72382	glutamate synthase

ALIGNMENTS

RESULT 1
B44212
structural protein 2 precursor - hepatitis E virus (strain Mexico)
C;Species: hepatitis E virus
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: B44212
R;Huang, C.C.; Nguyen, D.; Fernandez, J.; Yun, K.Y.; Fry, K.E.; Bradley, D.W.; Tam, A.W.,
Virology 191, 550-558, 1992
A;Title: Molecular cloning and sequencing of the Mexico isolate of hepatitis E virus (HEV
A;Reference number: A44212; MUID:93079857; PMID:1448913
A;Accession: B44212
A;Molecule type: genomic RNA
A;Residues: 1-659 <HUA>
A;Cross-references: UNIPROT:Q03500; GB:M74506; NID:g330017; PIDN:AAA45732.1; PID:g330020
C;Superfamily: hepatitis E virus structural protein 2
C;Keywords: structural protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-659/Product: structural protein 2 #status predicted <SP2>

Query Match 99.0%; Score 2749.5; DB 1; Length 659;
Best Local Similarity 99.4%; Pred. No. 5.6e-184;
Matches 537; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
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Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
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Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
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Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
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Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
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Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 650


RESULT 2
VHWWH2
structural protein 2 precursor - hepatitis E virus (strain Burma)
C;Species: hepatitis E virus
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: C40778
R;Tam, A.W.; Smith, M.M.; Guerra, M.E.; Huang, C.C.; Bradley, D.W.; Fry, K.E.; Reyes, G.
Virology 185, 120-131, 1991
A;Title: Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length vi
A;Reference number: A40778; MUID:92024067; PMID:1926770
A;Accession: C40778
A;Molecule type: genomic RNA
A;Residues: 1-660 <TAM>
A;Cross-references: UNIPROT:P29326; GB:M73218; NID:g330023; PIDN:AAA45736.1; PID:g330026
A;Note: the authors translated the codon CGC for residue 2 as Ala
C;Superfamily: hepatitis E virus structural protein 2
C;Keywords: structural protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-660/Product: structural protein 2 #status predicted <SP2>

  Query Match             95.2%;  Score 2644;  DB 1;  Length 660;
  Best Local Similarity   94.8%;  Pred. No. 1.3e-176;
  Matches  512;  Conservative   13;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| ||||||||||||||||||||||||||:||||||||||:| |||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              |||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||:||| ||||| ||||||||| ||| |||||||||||| ||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 3
B85547
probable RTX family exoprotein [imported] - Escherichia coli (strain O157:H7, substrain
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85547
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85547
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5188 <STO>
A;Cross-references: UNIPROT:Q8X4H5; GB:AE005174; NID:g12513368; PIDN:AAG54838.1; GSPDB:GN
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z0615

  Query Match              4.6%;  Score 128.5;  DB 2;  Length 5188;
  Best Local Similarity   21.2%;  Pred. No. 8.4;
  Matches  122;  Conservative   70;  Mismatches  242;  Indels  141;  Gaps   27;

Qy         11 VPDVDSRGAILRRQYNLSTS--PLTSSVASGTNLVLYAAPLNPPLPLQDG-----TNTHI 63
              | |          |  ::|    :| :  || | :| |      || :  |     |   :
Db       2215 VTDAGGNSGSATHQVTVNTGLPTITFNAISGDN-ILNADEKGQPLTISGGSTGLATGAQV 2273

Qy         64 MAT-EASNYAQYRVARA----TIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITS 118
                |    ||:    |          |:    |        | :| |          ||   |:  |
Db       2274 TVTLNGHNYSATTDASGNWTLTVPVSDLAALGQANYTVSAS--------ATSAAGNT-AS 2324

Qy        119 TDVRILVQPGIASELV--IPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNS 176
              :   :||  |:    :  :  : :    :        |||    |    | : : |   |:
Db       2325 SQANLLVDSGLPDVTINTVAGDDIINAAEAGADQTISGVVTRAAAGDTVTVTLGG---NT 2381

Qy        177 YTNTPYTG-------------ALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRG 223
              || |  :                |||  |  :    ::|  | ||
Db       2382 YTATVQSNLSWSVSVPTADLQALGNGDLTIT---ASVTNANGNT---------------- 2422

Qy        224 ADGTAELTTTAATRFMKDLHFTGLNGVGEVGRGIALTLLNLADTL-LGGLPTELISSAGG 282
                || ::|  |    ::      | : |  :  | || :   :  |  | : |  |:|
Db       2423 GSGTRDITIDANLPGLRVDTVAGDDIVNSIEHGQALVITGGSSGLNAGAVLTVTINSVA- 2481

Qy        283 QLFYSRPVVSANGEPTVKLYTSVENAQQDKGVAIP-HDIDLGDSRVVIQDYDNQHEQDRP 341
                                |::   |      | ||  ::    :  :  : | |   : |
Db       2482 -------------------YSATVQADGSWSVGIPAANVSAWPAGPLTVEVDGQSSANNP 2522

Qy        342 TPSPAPSRPFSV-----------LRANDVLWLSLTAAEYDQS-TYGSSTGPVYISDSVTL 389
                : | ||:|           : ::||    : |||   : |   ||  :     :|||:
Db       2523 V---SVSHPFTVDLTAVAISINTVASDDV----INAAEKGTNLTLSGSTSGIESGQTVTV 2575

Qy        390 V-NVATGAQAVARSLDWSKVTLDGRPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPY 448
                |   :|| :  || | :      | |: : :       ::  :|     :  | : |
Db       2576 TFGGKTYTASVAANGSWS-VNVPAADLATLPEGAAN-----VQASVSSASGNSASATHAY 2629

Qy        449 N---------YNTTASDQILIENAAGHRVAIS-TYTTRLG-----------AGPV-AIS 485
              :           || ||| ||     ||  : || | |   |              | | |
Db       2630 SVDASAPTLTINTIASDDILNAAEAGSPLTISGTSTAETGQTVTVTLNGATYTGTVQADG 2689

Qy        486 AAAVLAPRSAL-----------ALLEDTFDYPGRA 509
              : :|  | |||           | : |    || |
Db       2690 SWSVSVPTSALGALNASNYTVSATVNDKAGNPGSA 2724


RESULT 4
F90696
hypothetical protein ECs0542 [imported] - Escherichia coli (strain O157:H7, substrain RIM
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F90696
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90696
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5291 <HAY>
A;Cross-references: UNIPROT:Q8X2T1; GB:BA000007; PIDN:BAB33965.1; PID:g13360000; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0542

  Query Match             4.6%;  Score 128.5;  DB 2;  Length 5291;
  Best Local Similarity   21.2%;  Pred. No. 8.6;
  Matches  122;  Conservative   70;  Mismatches  242;  Indels  141;  Gaps   27;

Qy         11 VPDVDSRGAILRRQYNLSTS--PLTSSVASGTNLVLYAAPLNPPLPLQDG-----TNTHI 63
              |  |          |  ::|    :| :  || | :| |      || :  |     |   :
Db       2215 VTDAGGNSGSATHQVTVNTGLPTITFNAISGDN-ILNADEKGQPLTISGGSTGLATGAQV 2273

Qy         64 MAT-EASNYAQYRVARA----TIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITS 118
                |    ||:    |      |:     |       | :| |          ||   |: |
Db       2274 TVTLNGHNYSATTDASGNWTLTVPVSDLAALGQANYTVSAS--------ATSAAGNT-AS 2324

Qy        119 TDVRILVQPGIASELV--IPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNS 176
              :   :||  |:    :  :  : :    :        |||     |    | : : |   |:
Db       2325 SQANLLVDSGLPDVTINTVAGDDIINAAEAGADQTISGVVTRAAAGDTVTVTLGG---NT 2381

Qy        177 YTNTPYTG------------ALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRG 223
              || | :             |||  |  :     ::|  | ||
Db       2382 YTATVQSNLSWSVSVPTADLQALGNGDLTIT---ASVTNANGNT---------------- 2422

Qy        224 ADGTAELTTTAATRFMKDLHFTGLNGVGEVGRGIALTLLNLADTL-LGGLPTELISSAGG 282
                || ::|  |    ::     | : |  :  | || :   :  |  | : |  |:|
Db       2423 GSGTRDITIDANLPGLRVDTVAGDDIVNSIEHGQALVITGGSSGLNAGAVLTVTINSVA- 2481

Qy        283 QLFYSRPVVSANGEPTVKLYTSVENAQQDKGVAIP-HDIDLGDSRVVIQDYDNQHEQDRP 341
                            |::   |      | ||  ::    :  :  : | |   : |
Db       2482 -------------------YSATVQADGSWSVGIPAANVSAWPAGPLTVEVDGQSSANNP 2522

Qy        342 TPSPAPSRPFSV-----------LRANDVLWLSLTAAEYDQS-TYGSSTGPVYISDSVTL 389
              :  | ||:|           : ::||    : |||   :  |   ||  :    :||:
Db       2523 V---SVSHPFTVDLTAVAISINTVASDDV----INAAEKGTNLTLSGSTSGIESGQTVTV 2575

Qy        390 V-NVATGAQAVARSLDWSKVTLDGRPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPY 448
                 |   :|| :  || | :     | |: : :       ::  :|     :  | : |
Db       2576 TFGGKTYTASVAANGSWS-VNVPAADLATLPEGAAN-----VQASVSSASGNSASATHAY 2629

Qy        449 N---------YNTTASDQILIENAAGHRVAIS-TYTTRLG-----------AGPV-AIS 485
              :          || ||| ||    ||  : || | |   |             | | |
Db       2630 SVDASAPTLTINTIASDDILNAAEAGSPLTISGTSTAETGQTVTVTLNGATYTGTVQADG 2689

Qy        486 AAAVLAPRSAL----------ALLEDTFDYPGRA 509
              : :|  | |||           | : |    || |
Db       2690 SWSVSVPTSALGALNASNYTVSATVNDKAGNPGSA 2724


RESULT 5
S48478
glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae)
N;Alternate names: extracellular glucoamylase; mucin-like protein MUC1; protein YIR019c
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S48478; A26877; B26877; S27281; JC6123
R;Rowley, K.
submitted to the EMBL Data Library, October 1994
A;Reference number: S48478
A;Accession: S48478
A;Molecule type: DNA
A;Residues: 1-1367 <ROW>
A;Cross-references: UNIPROT:P08640; GB:Z47047; EMBL:Z38061; NID:g603997; PID:g763364; GS
R;Yamashita, I.; Nakamura, M.; Fukui, S.
J. Bacteriol. 169, 2142-2149, 1987
A;Title: Gene fusion is a possible mechanism underlying the evolution of STA1.
A;Reference number: A91831; MUID:87194600; PMID:3106330
A;Accession: A26877
A;Molecule type: DNA
A;Residues: 1-242 <YAM>
A;Cross-references: EMBL:M16164; NID:g172522; PIDN:AAA35014.1; PID:g172525
A;Accession: B26877
A;Molecule type: DNA
A;Residues: 762-1331 <YA2>
A;Cross-references: EMBL:M16165; NID:g172523; PIDN:AAA35015.1; PID:g172526
R;Pardo, J.M.; Ianez, E.; Zalacain, M.; Claros, M.G.; Jimenez, A.
FEBS Lett. 239, 179-184, 1988
A;Title: Similar short elements in the 5' regions of the STA2 and SGA genes from Saccharc
A;Reference number: S27281; MUID:89031230; PMID:3141213
A;Accession: S27281
A;Molecule type: DNA
A;Residues: 1-31 <PAR>
A;Cross-references: EMBL:X13857; NID:g4551; PIDN:CAA32069.1; PID:g4552
R;Lambrechts, M.G.; Bauer, F.F.; Marmur, J.; Pretorius, I.S.
Proc. Natl. Acad. Sci. U.S.A. 93, 8419-8424, 1996
A;Title: Muc1, a mucin-like protein that is regulated by Mss10, is critical for pseudohyp
A;Reference number: JC6123; MUID:96323237; PMID:8710886
A;Accession: JC6123
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1367 <LAM>
A;Cross-references: GB:U30626; NID:g1304386; PIDN:AAC49609.1; PID:g1304387
C;Genetics:
A;Gene: SGD:MUC1; STA2; MAL5; DEX2; SGD:S0001458
A;Cross-references: MIPS:YIR019c; SGD:S0001458
A;Map position: 9R
C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase h
C;Keywords: glycosidase; hydrolase; polysaccharide degradation; transmembrane protein
F;5-21/Domain: transmembrane #status predicted <TM1>
F;1350-1366/Domain: transmembrane #status predicted <TM2>

  Query Match             4.6%;  Score 127;  DB 1;  Length 1367;
  Best Local Similarity   20.0%;  Pred. No. 1.6;
  Matches  121;  Conservative   69;  Mismatches  258;  Indels  156;  Gaps   23;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              :|||     | |                |:| :|||  | |          : |:|    :
Db        805 SVAPV----PTPS-------------SSSNITSSAPSSTPFSSSTESSSVPVPTPSSST 846

Qy         61 TH------IMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDM- 113
              |          :|  |: |       ::        |:::   : : ||   || ||:|
Db        847 TESSSAPVSSSTTESSVAPVPTPSSSSNITSSAPSSIPFSSTTESPSTGTTVTPSSSKYP 906

Qy        114 -----NSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLC 168
                  |::||    :|     : :  ||                ::|    | |||    |
Db        907 GSQTETSVSSTTETTIVPTKTTTSVTTPSTTTITTTVCSTGTNSAG----ETTSG----C 958

Qy        169 IHGSPVNSYTNTPYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADG-- 226
              ||     |  | |                ::|| :| |  :   ||  :        |
Db        959 ---SPKTVTTTVPTTTT-----------TSVTTSSTTTITTTVCSTGTNSAGETTSGCS 1003

Qy        227 -------------------------TAELTTTAATRFMKDLHFTGLNGVGE-----VGR 255
                                      |  :|| :|  :   :  |      ||      | :
Db       1004 PKTITTTVPCSTSPSETASESTTTSPTTPVTTVVSTTVVTTEYSTSTKPGGEITTTFVTK 1063

Qy        256 GIALTLLNL------ADTLLGGLPTEL--------ISSAG--------GQLFYSRPVVSA 293
              |  | |          |:    || :          :|||           :  : | :
Db       1064 NIPTTYLTTIAPTPSVTTVTNFTPTTITTTVCSTGTNSAGETTSGCSPKTVTTTVPCSTG 1123

Qy        294 NGEPTVKLYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSV 353
              || | :  | | |          |          :       |  :       : ||| |  |
Db       1124 TGEYTTEATTLVTTAVTTTVVTTESSTGTNSAGKTTTGYTTKSVPTTYVTTLAPSAP--V 1181

Qy        354 LRANDVLWLSLTAAEYDQST--YGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLD 411
              | : :  ::|  |    :|    | :|    :  : |:|: |:  :  | |       |
Db       1182 TPATNAVPTTITTTECSAATNAAGETTS---VCSAKTIVSSASAGENTAPSATTPVTT-- 1236

Qy        412 GRPLPTVEQYSKTPFVLPLRGKLSFWEAGTTKAGY-----PYNYNTTASDQILIENAAGH 466
              :||          |:     :    || |  ||      |  | ||     ||  : |
Db       1237 --AIPTT--------VITTESSVGTNSAGETTTGYTTKSIPTTYITT-----LIPGSNGA 1281

Qy        467 R-----------VAISTYTTRLGAGPVAISAAAVLAPRSALALLED-------TFDYPGR 508
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Db       1282 KNYETVATATNPISIKT-TSQLATTASASSVAPVVTSPSLTGPLQSASGSAVATYSVPSI 1340

Qy        509 AHTF 512
Db       1341 SSTY 1344
```

RESULT 6
E82750
hemagglutinin-like secreted protein XF0889 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82750
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82750
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3282 <SIM>
A;Cross-references: UNIPROT:Q9PEY9; GB:AE003928; GB:AE003849; NID:g9105798; PIDN:AAF8369
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0889

  Query Match   4.5%; Score 125; DB 2; Length 3282;
  Best Local Similarity   21.2%; Pred. No. 7.6;
  Matches 128; Conservative   63; Mismatches 212; Indels 200; Gaps   27;

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Qy          1 AVAPAHD------TSPVP-----------------DVDSRGAILRRQYNLSTSPLTSSV 36
Db        439 SVPPATDTPPSTGTMPIPSHPQTAPVLAAGRLTLENDIDNRGGHITAGGAIDAILTTLDN 498

Qy         37 ASGTNLVLYAAPLNPPLPLQDG--TNTH---IMATEA-------SNYAQYRVARATIRYR 84
Db        499 RDGT------AALN-RLTLQGQRLDNQHGILTLATEATIHTHTLNNAAGQLHVNGTLDLT 551

Qy         85 PLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRN 144
Db        552 AQHLNNASGHLLTTG--PQSATL-TIADLLDNTSGTL------ASAGSLTLTAATL---- 598

Qy        145 QGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTTCN 204
Db        599 -------------DTTDGTVQSGQGPLHMDAATLTAHRGTLTSQD--------TLTLTG 636

Qy        205 TNTRVSRYSSTARHRLRRGADGTAELTT-------------------------TAATRF 238
Db        637 THTDLSHATTTAQQITLH----TGDLTTAGGHLTAYGTHTLQLEARTRLDNTGGTIATNG 692

Qy        239 MKDLHFTGLNGVGEVGRGIAL---------TLLNLADTLLGGLPTELI----SSAGGQLF 285
Db        693 TLDLHTAALDNTGGTLHSTATGPNRLDITDTLTNTAGHLLLNGPTTLTTGTWTNTGGHLQ 752

Qy        286 YSRPVV-------------SANGEPTVKLYTSVENAQQDKGVAIPHD-IDLGDSRVVIQ 330
Db        753 ITGPATLHATTLDNRGGILHTATGPLDLRITGTLNN--QDNGLLTTTDALTLTAASLL-- 808
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Qy        331 DYDNQH-EQDRPTPSPAP-----SRPFSVLRANDVLWL----------SLTAAEYDQST- 373
Db        809 ---NQHGTLDAAGPAHLTLTGLLDNTAGLLQTAHTLWLTSAGLTNRSGTLTASQLTLDTQ 865

Qy        374 ----------YGSSTGPVYI--------------------SDSVTLVNVATGAQAVARS 402
Db        866 GHTLDNTRGRLGTTTGNLTLHSGPLDNTAGLLQTAAALTIDTGAATLTNRDGGALLAATA 925

Qy        403 LDWSKVTLDGRPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIEN 462
Db        926 LDLTTATLDNRG-GTIDSQTAT--------HLHTTTLDNTTAGHISSSGTLQIDGTTLTN 976

Qy        463 AAG 465
Db        977 TGG 979
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RESULT 7
E82589
hemagglutinin-like secreted protein XF2196 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82589
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82589
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3442 <SIM>
A;Cross-references: UNIPROT:Q9PBE8; GB:AE004032; GB:AE003849; NID:g9107324; PIDN:AAF8499
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2196

  Query Match   4.5%; Score 125; DB 2; Length 3442;
  Best Local Similarity   21.2%; Pred. No. 8.2;
  Matches 128; Conservative   63; Mismatches 212; Indels 200; Gaps   27;

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Qy          1 AVAPAHD------TSPVP-----------------DVDSRGAILRRQYNLSTSPLTSSV 36
Db        439 SVPPATDTPPSTGTMPIPSHPQTAPVLAAGRLTLENDIDNRGGHITAGGAIDAILTTLDN 498

Qy         37 ASGTNLVLYAAPLNPPLPLQDG--TNTH---IMATEA-------SNYAQYRVARATIRYR 84
Db        499 RDGT------AALN-RLTLQGQRLDNQHGILTLATEATIHTHTLNNAAGQLHVNGTLDLT 551

Qy         85 PLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRN 144
Db        552 AQHLNNASGHLLTTG--PQSATL-TIADLLDNTSGTL------ASAGSLTLTAATL---- 598

Qy        145 QGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTTCN 204
Db        599 -------------DTTDGTVQSGQGPLHMDAATLTAHRGTLTSQD--------TLTLTG 636

Qy        205 TNTRVSRYSSTARHRLRRGADGTAELTT-------------------------TAATRF 238
```

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            |:| :|  ::||:        | :|||                                  | ||
Db        637 THTDLSHATTTAQQITLH----TGDLTTAGGHLTAYGTHTLQLEARTRLDNTGGTIATNG 692

Qy        239 MKDLHFTGLNGVGEVGRGIAL---------TLLNLADTLLGGLPTELI----SSAGGQLF 285
              |||   |: |       |           || | |  ||   || |      :: || |
Db        693 TLDLHTAALDNTGGTLHSTATGPNRLDITDTLTNTAGHLLLNGPTTLTTGTWTNTGGHLQ 752

Qy        286 YSRPVV--------------SANGEPTVKLYTSVENAQQDKGVAIPHD-IDLGDSRVVIQ 330
              : |                :| |  :::  :: |  || |:    | : |  : ::
Db        753 ITGPATLHATTLDNRGGILHTATGPLDLRITGTLNN--QDNGLLTTTDALTLTAASLL-- 808

Qy        331 DYDNQH-EQDRPTPSPAP-----SRPFSVLRANDVLWL----------SLTAAEYDQST- 373
                 |||    |   |:             :|:    |||          :|||::    |
Db        809 ---NQHGTLDAAGPAHLTLTGLLDNTAGLLQTAHTLWLTSAGLTNRSGTLTASQLTLDTQ 865

Qy        374 ----------YGSSTGPVYI--------------------SDSVTLVNVATGAQAVARS 402
                       |::|| : :                    : : || |   ||   | :
Db        866 GHTLDNTRGRLGTTTGNLTLHSGPLDNTAGLLQTAAALTIDTGAATLTNRDGGALLAATA 925

Qy        403 LDWSKVTLDGRPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIEN 462
              || :  ||| |   |:: : |          |       | ||:  :  |   |   : |
Db        926 LDLTTATLDNRG-GTIDSQTAT--------HLHTTTLDNTTAGHISSSGTLQIDGTTLTN 976

Qy        463 AAG 465
                |
Db        977 TGG 979


RESULT 8
B82519
hemagglutinin-like secreted protein XF2775 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82519
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: B82519
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3455 <SIM>
A;Cross-references: UNIPROT:Q9P9U6; GB:AE004082; GB:AE003849; NID:g9108003; PIDN:AAF8556
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2775

  Query Match             4.5%;  Score 125;  DB 2;  Length 3455;
  Best Local Similarity   21.2%;  Pred. No. 8.2;
  Matches  128;  Conservative   63;  Mismatches  212;  Indels  200;  Gaps   27;

Qy          1 AVAPAHD------TSPVP-----------------DVDSRGAILRRQYNLSTSPLTSSV 36
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Db        439 SVPPATDTPPSTGTMPIPSHPQTAPVLAAGRLTLENDIDNRGGHITAGGAIDAILTTLDN 498

Qy         37 ASGTNLVLYAAPLNPPLPLQDG--TNTH---IMATEA-------SNYAQYRVARATIRYR 84
                ||     | ||  | ||     | |    :||||       :| |     |:
Db        499 RDGT------AALN-RLTLQGQRLDNQHGILTLATEATIHTHTLNNAAGQLHVNGTLDLT 551
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Qy         85 PLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRN 144
                  |   |: ::    ||: |  |  |:   ||  :         |  | : :  |
Db        552 AQHLNNASGHLLTTG--PQSATL-TIADLLDNTSGTL------ASAGSLTLTAATL---- 598

Qy        145 QGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTTCN 204
                        : | | |       ::: | | : | |   |             ||
Db        599 -------------DTTDGTVQSGQGPLHMDAATLTAHRGTLTSQD--------TLTLTG 636

Qy        205 TNTRVSRYSSTARHRLRRGADGTAELTT-------------------------TAATRF 238
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Db        637 THTDLSHATTTAQQITLH----TGDLTTAGGHLTAYGTHTLQLEARTRLDNTGGTIATNG 692

Qy        239 MKDLHFTGLNGVGEVGRGIAL---------TLLNLADTLLGGLPTELI----SSAGGQLF 285
              |||   |:  |       |           || | |  ||   || |      :: || |
Db        693 TLDLHTAALDNTGGTLHSTATGPNRLDITDTLTNTAGHLLLNGPTTLTTGTWTNTGGHLQ 752

Qy        286 YSRPVV--------------SANGEPTVKLYTSVENAQQDKGVAIPHD-IDLGDSRVVIQ 330
              : |                :| |  :::  :: |  || |:    | : |  : ::
Db        753 ITGPATLHATTLDNRGGILHTATGPLDLRITGTLNN--QDNGLLTTTDALTLTAASLL-- 808

Qy        331 DYDNQH-EQDRPTPSPAP-----SRPFSVLRANDVLWL----------SLTAAEYDQST- 373
                 |||    |   |:             :|:    |||          :|||::    |
Db        809 ---NQHGTLDAAGPAHLTLTGLLDNTAGLLQTAHTLWLTSAGLTNRSGTLTASQLTLDTQ 865

Qy        374 ----------YGSSTGPVYI--------------------SDSVTLVNVATGAQAVARS 402
                       |::|| : :                    : : || |   ||   | :
Db        866 GHTLDNTRGRLGTTTGNLTLHSGPLDNTAGLLQTAAALTIDTGAATLTNRDGGALLAATA 925

Qy        403 LDWSKVTLDGRPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIEN 462
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Db        926 LDLTTATLDNRG-GTIDSQTAT--------HLHTTTLDNTTAGHISSSGTLQIDGTTLTN 976

Qy        463 AAG 465
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Db        977 TGG 979


RESULT 9
H96007
probable acriflavin resistence protein [imported] - Sinorhizobium meliloti (strain 1021)
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: H96007
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernanc
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endos
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: H96007
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1077 <KUR>
A;Cross-references: UNIPROT:Q92U15; GB:AL591985; PIDN:CAC49728.1; PID:g15141215; GSPDB:GN
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: acrF; SMb21498
A;Genome: plasmid
C;Superfamily: acriflavin resistance protein

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Db        375 PVALVGTFAVILAMGFSLNTVSLLALVLAIGIVVDDAIVVVENVERVMEENPGMSAAQAA 434

Qy         70 NYAQYRVARATIRYRPLVPNAVGGYAISISFWP-------QTTTTPTSVDMNSITSTDVR 122

Db        435 RLAMGEITGAIVAITLVLLSVF----VPVAFIPGLSGQLFQQFAVAVSVSM--VISAINA 488

Qy        123 ILVQPGIASELVIPSERLHYRNQGWRS----------VETSGVAEEEATSGLVMLCIH-G 171

Db        489 LTLSPALCAILLKPHHGPKRGILGWISRGIDRTRNGYAHVAGSIARRAIIGVILLAVAIG 548

Qy        172 SPVNSYTNTPYTGALGLLD---FALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTA 228

Db        549 ASGWLFRIVP-TGFLPSEDQGAFFAEIRLPEGASFNRTDAVVREVET----MLGGIEGVA 603

Qy        229 ELTTTAATRFMKDL---------------------------------------------- 242

Db        604 NVTTVTGYSFLDGIAKSSSAFAIVTMKPFAERQDESASVNAAIGTVMAKGAAIRNAQVFA 663

Qy        243 -HFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGE----P 297

Db        664 FNLPPIIGLG-TGSGFEYQLLDLQ----GRSPAELAATAGGLM------VAANQNPQLGP 712

Qy        298 TVKLYTSVE-----NAQQDKGVAIPHDIDLGDSRVVIQD-----YDNQHEQDRPTPSPAP 347

Db        713 TFSTYSASSPQLYLNLDRDRLQAL--GVSVSDLFATLQGTLGSYYVND------------ 758

Qy        348 SRPFSVLRANDVLW-LSLTAAEYDQSTYG--------SSTGPVYISDSVTLVNVATGAQA 398

Db        759 ---FNLFGRS---WKVTMQAAEADRDAVDDISRLHVRNAAGDMVPVASVARVDYIVGPQS 812

Qy        399 VARSLDWSKVTLDGRPLP---------TVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPYN 449

Db        813 IVRYNNYRSITLNGQPAPGISSGQALAAMEQVS----------------AATLPPGYSFE 856

Qy        450 YNTTASDQILIENAAGHRVAI 470

Db        857 WTGTALQEL---EAAGQTTVI 874
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RESULT 10
A41258
a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: a-agglutinin attachment protein AGA1; protein N3431; protein YNR044w
C;Species: Saccharomyces cerevisiae
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C;Accession: A41258; S63375; S17031
R;Roy, A.; Lu, C.F.; Marykwas, D.L.; Lipke, P.N.; Kurjan, J.
Mol. Cell. Biol. 11, 4196-4206, 1991
A;Title: The AGA1 product is involved in cell surface attachment of the Saccharomyces ce
A;Reference number: A41258; MUID:91304412; PMID:2072914
A;Accession: A41258
A;Molecule type: DNA
A;Residues: 1-725 <ROY>
A;Cross-references: UNIPROT:P32323; GB:M60590; NID:g170963; PIDN:AAA34382.1; PID:g170964
R;Pohl, T.M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63346
A;Accession: S63375
A;Molecule type: DNA
A;Residues: 1-725 <POH>
A;Cross-references: EMBL:Z71659; NID:g1302551; PIDN:CAA96325.1; PID:e239834; PID:g130255
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:AGA1
A;Cross-references: SGD:S0005327; MIPS:YNR044w
A;Map position: 14R
C;Keywords: glycoprotein; transmembrane protein
F;8-24/Domain: transmembrane #status predicted <TM1>
F;708-724/Domain: transmembrane #status predicted <TM2>

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Qy          8 TSPVPDVDSRGAILRRQYNLSTSP-LTSSVASGTNLVLYAAPLNPPLPLQDGTNTHIMAT 66

Db        275 TSPSSKSTSASSTSTSSYSTSTSPSLTSS-------------SPTLASTSPSSTSISST 320

Qy         67 EASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTT------TTPTSVDMNSITSTD 120

Db        321 FTDSTSS-------------LGSSIASSSTSVSLYSPSTPVYSVPSTSSNVATPSMTSST 367

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVET-------------SGV----------A 156

Db        368 VETTVSSQSSSEYITKS-----------SISTTIPSFSMSTYFTTVSGVTTMYTTWCPYS 416

Qy        157 EEEATSGLVML----------CIHGSPVNSYTNTPYTGALGLLDFALELEFRNL-TTCNT 205

Db        417 SESETSTLTSMHETVTTDATVCTHESCMPSQTTS-------LITSSIKMSTKNVATSVST 469

Qy        206 NTRVSRY-------SSTARHRLRRGADGTAELTTTAATRFMKDL---------HFTGLNG 249

Db        470 STVESSYACSTCAETSHSYSSVQTASSSSVTQQTTSTKSWVSSMTTSDEDFNKHATGKYH 529

Qy        250 VGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSA-------NGEPTVKLY 302

Db        530 VTSSGTSTISTSVSEA-TSTSSIDSE--SQEQSSHLLSTSVLSSSSLSATLSSDSTILLF 586

Qy        303 TSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWL 362

Db        587 SSVSS------------LSVEQSPVTTLQISSTSEILQPTSSTA---------------- 618

Qy        363 SLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQYS 422

Db        619 --------IATISAST------SSLSATSISTPSTSVESTIESSSLT------PTVSSIF 658

Qy        423 KTFFVLP--LRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480

Db        659 LSSSSAPSSLQTSVTTTEVSTTSISIQYQ----TSSMVTISQYMG-----SGSQTRLPLG 709

Qy        481 PVAISAAAV 489

Db        710 KLVFAIMAV 718
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RESULT 11
S55862
probable membrane protein YNL327w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N0320
C;Species: Saccharomyces cerevisiae
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55862; S63308; S51288
R;Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin, C.
Yeast 11, 567-572, 1995
A;Title: Sequencing analysis of a 15.4 kb fragment of yeast chromosome XIV identifies the
A;Reference number: S55859; MUID:95373280; PMID:7645347
A;Accession: S55862
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1041 <MAF>
A;Cross-references: UNIPROT:P42835; EMBL:Z46259; NID:g633655; PIDN:CAA86371.1; PID:g6336
R;Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin, C.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63287
A;Accession: S63308
A;Molecule type: DNA
A;Residues: 1-1041 <MAW>
A;Cross-references: EMBL:Z71603; NID:g1302444; PID:e239572; PID:g1302445; MIPS:YNL327w
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:EGT2
A;Cross-references: SGD:S0005271; MIPS:YNL327w
A;Map position: 14L
C;Keywords: transmembrane protein
F;4-20/Domain: transmembrane #status predicted <TM1>

F;1025-1041/Domain: transmembrane #status predicted <TM2>

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Db        405 TTPSSSLSATETYSIISSASISVTQASYIDNSTTTAVTQSTSTIAVSSAEKLSSTLSY-- 462

Qy         86 LVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQ 145
Db        463 -----TSNVTISVSSATQHTTTPSYVS-NSTTLSSSSVL---------------------- 495

Qy        146 GWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTPY---------TGALGLLDFALELE 196
Db        496 --ESVISSPYLANTTVSG-------ASSASQSTNPPYVSNSTTSSATQLATIAPFAINIT 546

Qy        197 FRNLTTCNTNTRVSRYSSTARHRLRRG--------ADGTAELTTTAATRFMKDL------ 242
Db        547 GTSISSSITNT--SSVSSTT-SSLSSGPFVSNTAVASGSYILTTTTESAQLTEIGSLIPI 603

Qy        243 ----HFTGLNGVGEVGRG-------IALTLLNLADTLLGGLPTELISSA----------- 280
Db        604 STITTSTTTSGTDKTGSNKVASSTEIAQSIVNNSSLSVSTINTNAATAAANARNATFTHA 663

Qy        281 --GGQL---FYSRPVVSANGEPTVKLYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQ 335
Db        664 THSGSLQPSYHSSSLLSSTID--TKVTTATTSTSRDGSSSLAFTTGLNQSVVTGTD---- 717

Qy        336 HEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQ---STY------GSSTGPVYISD 385
Db        718 -----------KSDTYSVISSTE----SAQVTEYDSLLPISTLKPTVVTGTSRNSTFSMV 762

Qy        386 SVTLVNVATG-----AQAVARSLDWSKVTLDGRPLP--TVE------------------- 419
Db        763 SSTKLTEATATDKGDAYSVISSTQSAQVTEYGSMLPISTLETPTVIMSTDESGYFTLTTC 822

Qy        420 -------QYSKTFFVLPLRGKLSFWEAG--------TTKAGYPYNYNTTASDQILIENAA 464
Db        823 TESGQATEYGSLIPISTLDGSVIYTFTGESVVVGYSTTVGAAQYAQHTSL---VPVSTIK 879

Qy        465 GHRVAIST-------YTTRLGAGPVA-----ISAAAVLAPRSALALLE----------DT 502
Db        880 GSKTSLSTEESVVAGYSTTVGAAQYAQHTSLVPVSTIKGSKTSLSTEESVVAGYSTTVDS 939

Qy        503 FDYPGRAH---------------TFDDFCPECRAL 522
Db        940 AQYAEHTNLVAIDTLKTSTFQKATATEVCVTCTAL 974
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RESULT 12
B81192
hemagglutinin/hemolysin-related protein NMB0497 [imported] - Neisseria meningitidis (str
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: B81192
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: B81192
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1975 <TET>
A;Cross-references: UNIPROT:Q9K0S7; GB:AE002406; GB:AE002098; NID:g7225720; PIDN:AAF4092
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0497

Query Match 4.3%; Score 120; DB 2; Length 1975;
Best Local Similarity 21.1%; Pred. No. 8.2;
Matches 142; Conservative 92; Mismatches 226; Indels 214; Gaps 35;

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Qy         13 DVDSR-GAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTNTHIMATEASNY 71
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Qy         72 AQYR--VARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNS--------ITSTDV 121
Db        418 ADGRTVIKEASI--------------------QTGTTVYSSSKGNAELGNNTRITGADV 456

Qy        122 RILVQPGIASELVIPS-ERLHYRNQGWRSVETSGVAEEEATSG--------LVMLCIH-- 170
Db        457 TVLSNGTISSSAVIDAKDTAHIEAGKPLSLEASTVTSDIRLNGGSIKGGKQLALLADDNI 516

Qy        171 -------GSPVNSYTNT------------------------PYTGALGLLDFALEL--E 196
Db        517 TAKTTNLNTPGNLYVHTGKDLNLNVDKDLSAASIHLKSDNAAHITGTSKTLTASKDMGVE 576

Qy        197 FRNLTTCNTNTRVSR-----YSSTARHRLRRGADGTAELTTTAATR--FMKD-LH----- 243
Db        577 AGSLNVTNTNLRTNSGNLHIQAAKGNIQLRNTKLNAAKALETTALQGNIVSDGLHAVSAD 636

Qy        244 -----------FTGLN--------GVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQ 283
Db        637 GHVSLLANGNADFTGHNTLTAKADVNAGSVGKG-RLKADNTNITSSSGDIT-LVAGNGIQ 694

Qy        284 LFYSRPVVSANGEP---------------TVKLYTSVENAQQDKGVAI-------PHDID 321
Db        695 LGDGKQRNSINGKHISIKNNGGNADLKNLNVHAKSGALNIHSDRALSIENTKLESTHNTH 754

Qy        322 LG--DSRVVIQDYD-----------NQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAE 368
Db        755 LNAQHERVTLNQVDAYAHRHLSITGSQIWQNDKLPSA------NKLVANGVLALN---AR 805

Qy        369 YDQSTYGSSTGPVYISDSVTL----VNVATGAQAVAR-SLDWSKVTLDGRPLPTVEQYSK 423
Db        806 YSQ-----------IADNTTLRAGAINLTAGTALVKRGNINWSTVS-----TKTLEDNAE 849

Qy        424 TFFVLPLRGKLSFWEAGT-TKAGYPYNYNTTASD-------QILIENAAGHRVAISTYTT 475
Db        850 ---LKPLAGRLNI-EAGSGTLTIEPANRISAHTDLSIKTGGKLLLSAKGGNAGAPSAQVS 905

Qy        476 --------RLGAGPVAISAAAVLAPRS-ALALLEDTFDYPGRAHTFDDFCPECRA--LGL 524
Db        906 SLEAKGNIRLVTGETDLRGSKITAGKNLVVATTKGKLNIEAVNNSFSNYFPTQKAAELNQ 965

Qy        525 QGCAFQSTVAELQR 538
Db        966 KSKELEQQIAQLKK 979
```

RESULT 13
G81044
hemagglutinin/hemolysin-related protein NMB1779 [imported] - Neisseria meningitidis (stra
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: G81044
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: G81044
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1995 <TET>
A;Cross-references: UNIPROT:Q9JY23; GB:AE002527; GB:AE002098; NID:g7227023; PIDN:AAF4211
A;Experimental source: serogroup B, strain MC58
C;Genetics:

A;Gene: NMB1779

Query Match 4.3%; Score 120; DB 2; Length 1995;
Best Local Similarity 21.1%; Pred. No. 8.3;
Matches 142; Conservative 92; Mismatches 226; Indels 214; Gaps 35;

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Qy         13 DVDSR-GAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTNTHIMATEASNY 71
              |:  | ||:::   |  : | |: : :| |||           ::  || :     |:
Db        375 DISLRNGAVVQ---NNGSRPATTVLNAGHNLV----------IESKTNVNNAKGPATLS 420

Qy         72 AQYR--VARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNS--------ITSTDV 121
              |  |  :  |:|                        || ||  |    :        ||  ||
Db        421 ADGRTVIKEASI--------------------QTGTTVYSSSKGNAELGNNTRITGADV 459

Qy        122 RILVQPGIASELVIPS-ERLHYRNQGWRSVETSGVAEEEATSG--------LVMLCIH-- 170
               :|    |:|  || : :  |        |:| | |  :   :|       | :|
Db        460 TVLSNGTISSSAVIDAKDTAHIEAGKPLSLEASTVTSDIRLNGGSIKGGKQLALLADDNI 519

Qy        171 -------GSPVNSYTNT-------------------------PYTGALGLLDFALEL--E 196
                    :| | | :|                          ||    |  : ::  |
Db        520 TAKTTNLNTPGNLYVHTGKDLNLNVDKDLSAASIHLKSDNAAHITGTSKTLTASKDMGVE 579

Qy        197 FRNLTTCNTNTRVSR-----YSSTARHRLRRGADGTAELTTTAATR--FMKD-LH----- 243
               :|   ||| | :       ::    :||       |:   | | :   : | ||
Db        580 AGSLNVTNTNLRTNSGNLHIQAAKGNIQLRNTKLNAAKALETTALQGNIVSDGLHAVSAD 639

Qy        244 ------------FTGLN--------GVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQ 283
                         ||| |          | ||:|  |    |    |  | | |::  | ||
Db        640 GHVSLLANGNADFTGHNTLTAKADVNAGSVGKG-RLKADNTNITSSSGDIT-LVAGNGIQ 697

Qy        284 LFYSRPVVSANGEP---------------TVKLYTSVENAQQDKGVAI-------PHDID 321
              |   :   | ||:              |   :    |   |: ::|          |:
Db        698 LGDGKQRNSINGKHISIKNNGGNADLKNLNVHAKSGALNIHSDRALSIENTKLESTHNTH 757

Qy        322 LG--DSRVVIQDYD-----------NQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAE 368
              |     || :   |           :|  |:   ||       : | || || |:   |
Db        758 LNAQHERVTLNQVDAYAHRHLSITGSQIWQNDKLPSA------NKLVANGVLALN---AR 808

Qy        369 YDQSTYGSSTGPVYISDSVTL----VNVATGAQAVAR-SLDWSKVTLDGRPLPTVEQYSK 423
              | |           |:|: ||    :|:  |   | | :::|| |:       |:|  ::
Db        809 YSQ-----------IADNTTLRAGAINLTAGTALVKRGNINWSTVS-----TKTLEDNAE 852

Qy        424 TFFVLPLRGKLSFWEAGT-TKAGYPYNYNTTASD-------QILIENAAGHRVAISTYTT 475
               : || |:|:  |||: |   | |  :  :|       ::|:   | |   :
Db        853 ---LKPLAGRLNI-EAGSGTLTIEPANRISAHTDLSIKTGGKLLLSAKGGNAGAPSAQVS 908

Qy        476 --------RLGAGPVAISAAAVLAPRS-ALALLEDTFDYPGRAHTFDDFCPECRA--LGL 524
                     ||  |   :  : : | ::  :|  :   :     ::| :: |  :|  |
Db        909 SLEAKGNIRLVTGETDLRGSKITAGKNLVVATTKGKLNIEAVNNSFSNYFPTQKAAELNQ 968

Qy        525 QGCAFQSTVAELQR 538
              :   :  :|:|::
Db        969 KSKELEQQIAQLKK 982
```

RESULT 14
B81989
hypothetical protein NMA0688 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: B81989
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: B81989
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2015 <PAR>
A;Cross-references: UNIPROT:Q9JRD2; GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB8397
A;Experimental source: serogroup A, strain Z2491
C;Genetics:

A;Gene: NMA0688

Query Match 4.3%; Score 119; DB 2; Length 2015;
Best Local Similarity 21.4%; Pred. No. 9.9;
Matches 144; Conservative 94; Mismatches 224; Indels 210; Gaps 37;

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Qy         13 DVDSR-GAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTNTHIMATEASNY 71
              |:  | ||:::   |  : | |: : :| |||           ::  || :     |:
Db        375 DISLRNGAVVQ---NNGSRPATTVLNAGHNLV----------IESKTNVNNAKGSANLS 420

Qy         72 AQYR--VARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNS-ITSTDVRILVQPG 128
              |  |  :  |||:          |    |       :|   | :  |: | : :| :|
Db        421 AGGRTTINDATIQ--------AGSSVYS------STKGDTELGENTRIIAENVTVLSNGS 466

Qy        129 IASELVIPS-ERLHYRNQGWRSVETSGV-------------------AEEEATSGLVML 167
              | |  || : :  |  :    |:||| |                  |::  |:    |
Db        467 IGSAAVIEAKDTAHIESGKPLSLETSTVASNIRLNNGNIKGGKQLALLADDNITAKTTNL 526

Qy        168 CIHGSPVNSYTNT-------------------------PYTGALGLL----DFALELEFR 198
                 :| | | :|                          ||    |    | :|
Db        527 ---NTPGNLYVHTGKDLNLNVDKDLSAASIHLKSDNAAHITGTSKTLTASKDMGVEAGLL 583

Qy        199 NLTTCNTNTRVSR-----YSSTARHRLRRGADGTAELTTTAATR--FMKD-LH------- 243
              |:|  ||| | :       ::    :||       |:   | | :   : | ||
Db        584 NVT--NTNLRTNSGNLHIQAAKGNIQLRNTKLNAAKALETTALQGNIVSDGLHAVSADGH 641

Qy        244 ----------FTGLN--------GVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLF 285
                       ||| |          | ||:|  |    |    |  | | |::  | ||
Db        642 VSLLANGNADFTGHNTLTAKADVNAGSVGKG-RLKADNTNITSSSGDIT-LVAGNGIQLG 699

Qy        286 YSRPVVSANGEP---------------TVKLYTSVENAQQDKGVAI-------PHDIDLG 323
               :   | ||:                |   :    |   |: ::|         |:  |
Db        700 DGKQRNSINGKHISIKNNGGNADLKNLNVHAKSGALNIHSDRALSIENTKLESTHNTHLN 759

Qy        324 --DSRVVIQDYD-----------NQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYD 370
                 || :   |           :|  |:   ||       : | || || |:   | |
Db        760 AQHERVTLNQVDAYAHRHLSITGSQIWQNDKLPSA------NKLVANGVLALN---ARYS 810

Qy        371 QSTYGSSTGPVYISDSVTL----VNVATGAQAVAR-SLDWSKVTLDGRPLPTVEQYSKTF 425
              |          |:|: ||    :|:  |   | | :::|| |:       |:|  ::
Db        811 Q-----------IADNTTLRAGAINLTAGTALVKRGNINWSTVS-----TKTLEDNAE-- 852

Qy        426 FVLPLRGKLSFWEAGT-TKAGYPYNYNTTASD-------QILIENAAGHRVAISTYTT-- 475
               : || |:|:  |||: |   | |  :  :|       ::|:   | |   :
Db        853 -LKPLAGRLNI-EAGSGTLTIEPANRISAHTDLSIKTGGKLLLSAKGGNAGAPSAQVSSL 910

Qy        476 ------RLGAGPVAISAAAVLAPRS-ALALLEDTFDYPGRAHTFDDFCPECRA--LGLQG 526
                   ||  |   :  : : | ::  :|  :   :     ::| :: |  :|  | :
Db        911 EAKGNIRLVTGETDLRGSKITAGKNLVVATTKGKLNIEAVNNSFSNYFPTQKAAELNQKS 970

Qy        527 CAFQSTVAELQR 538
                :  :|:|::
Db        971 KELEQQIAQLKK 982
```

RESULT 15
T41213
probable zinc finger protein SPCC1906.05 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 20-Oct-2000 #sequence_revision 08-Dec-2000 #text_change 09-Jul-2004
C;Accession: T41213; T41109
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z21969
A;Accession: T41213
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-379 <LYN1>
A;Cross-references: UNIPROT:O74463; EMBL:AL031538; NID:g3581923; PIDN:CAA20774.1; PID:g35
A;Experimental source: strain 972h-; cosmid c1906
A;Accession: T41109
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA

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A;Residues: 320-547 <LYN2>
A;Cross-references: EMBL:AL031540; NID:g3581876; PIDN:CAA20775.1; PID:g3581877; GSPDB:GN
A;Experimental source: strain 972h-; cosmid c1739
C;Genetics:
A;Gene: SPDB:SPCC1906.05; SPDB:SPCC1739.01
A;Map position: 3

  Query Match             4.3%;  Score 118.5;  DB 2;  Length 547;
  Best Local Similarity   21.8%;  Pred. No. 1.6;
  Matches  109;  Conservative   66;  Mismatches  187;  Indels  139;  Gaps   21;

Qy          45 YAAPLNPPLPLQDGTNTHIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQT 104
               :| | |  ||  :||:|: ||: |:|     ||           :|   || |   :|
Db          92 HALPGNTNLP--NGTSTNTMASMAANGGASSVA----------SKQMGANQISPSLSSKT 139

Qy         105 TTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVE---------TSGV 155
                  |     |: |:||||       |:    |  |   |: |  ::          :|||
Db         140 MKNPAD-KANNTTATDVR----GNTATSPYFPFSRSPGRHSGNSTINGMMTTPNFLSSGV 194

Qy         156 AE------EEATSGLVMLCIHGSPV--------------NSYTNTPYTGALGLLDFALE 194
                     ::||     ::| |:                :| ::|   |: |||
Db         195 NSRSVDEFNNSSSGFPS-SLNGIPIASPPLATSPTSFSLASSASSTNLGGSKGLL----- 248

Qy         195 LEFRNLTTCNT----------NTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLH 243
                 |: :|: |            ||  :| |||           : ||:    :    |
Db         249 --FQQMTSENNRDYFSRRPTLLNTYGNRCSSTDT------LSSLSRLTSQDPLKASLPLQ 300

Qy         244 FTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYT 303
                  |    : |  ::   | | |  || |      | |  :   | |  :|       :
Db         301 SPPL--APKTGVSLSRPRLTL-DQSLGNL------SLGSGINQRRQVPRSNS--YAGAFP 349

Qy         304 SVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLS 363
               || :|     | : | :|: |           |: |   :|  |    |:| :: :  ||
Db         350 SVVSASLPTKVDLNHQMDVSD----------EEQRFLSTPLGSFDESILGSSPINRLS 397

Qy         364 LTAAEYDQS----------------------TYGSSTGPVYISDSVTLVNVATGAQ--- 397
                :  :|  |                    | | :  |  | |::   :||
Db         398 SSFKQYTSSLKSPGLSTRTSSTMNSLNSSRFGAYFSKSRYVEGSGSMSTTPLATSVNNSY 457

Qy         398 ------AVARSLDWSKVTLDG-RPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNY 450
                    :|     :|  | :| ||:      |:  |        |   :  | ||
Db         458 KLPSGFSVREEAVFSSPTTEGSRPVSLARLKSEPIF-------RSDTASPETIAG----L 506

Qy         451 NTTASDQILIENAAGHRVAIS 471
                 | :| ::  | :  |: ::
Db         507 GDTKNDPVVSTNNSVSRITVA 527


Search completed: July 14, 2005, 15:51:41
Job time : 12.3396 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 14, 2005, 01:31:43 ; Search time 39.3962 Seconds
(without alignments)
7019.016 Million cell updates/sec

Title: US-09-769-066-26
Perfect score: 2776
Sequence: 1 AVAPAHDTSPVPDVDSRGAI.....ALGLQGCAFQSTVAELQRLK 540

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2749.5	99.0	659	1	VST2_HEVME	Q03500 hepatitis e
2	2654	95.6	660	2	Q9E8G5	Q9e8g5 hepatitis e
3	2650	95.5	660	1	VST2_HEVPA	P33426 hepatitis e
4	2650	95.5	660	2	Q77EC8	Q77ec8 hepatitis e
5	2650	95.5	660	2	Q89468	Q89468 hepatitis e
6	2650	95.5	660	2	Q9W7W9	Q9w7w9 hepatitis e
7	2650	95.5	660	2	Q9WQA0	Q9wqa0 hepatitis e
8	2644	95.2	660	1	VST2_HEVBU	P29326 hepatitis e
9	2644	95.2	660	2	O91855	O91855 hepatitis e
10	2644	95.2	660	2	Q69419	Q69419 hepatitis e
11	2643	95.2	660	2	O91856	O91856 hepatitis e
12	2643	95.2	660	2	Q69411	Q69411 hepatitis e
13	2638	95.0	660	2	Q81878	Q81878 hepatitis e
14	2635	94.9	660	2	Q6XXV0	Q6xxv0 hepatitis e
15	2633	94.8	660	2	Q80IY5	Q80iy5 hepatitis e
16	2630	94.7	660	2	Q8JJM8	Q8jjm8 hepatitis e
17	2630	94.7	660	2	Q81871	Q81871 hepatitis e
18	2628	94.7	660	2	Q8JJM4	Q8jjm4 hepatitis e
19	2627	94.6	660	2	O36613	O36613 swine hepat
20	2627	94.6	660	2	Q8V729	Q8v729 swine hepat
21	2627	94.6	660	2	Q6J8F7	Q6j8f7 hepatitis e
22	2627	94.6	660	2	Q9WLL4	Q9wll4 hepatitis e
23	2626	94.6	660	2	Q8AZM3	Q8azm3 hepatitis e
24	2626	94.6	660	2	Q9YLQ9	Q9ylq9 hepatitis e
25	2624	94.5	660	2	Q80IR7	Q80ir7 hepatitis e
26	2623	94.5	660	2	Q68985	Q68985 hepatitis e
27	2622	94.5	659	2	Q8JT32	Q8jt32 hepatitis e
28	2621	94.4	660	2	Q911I4	Q911i4 hepatitis e
29	2621	94.4	660	2	Q6J8G3	Q6j8g3 hepatitis e
30	2620	94.4	660	1	VST2_HEVMY	Q04611 hepatitis e
31	2617	94.3	660	2	Q8BB05	Q8bb05 swine hepat
32	2616	94.2	660	2	Q9YLR2	Q9ylr2 hepatitis e
33	2607	93.9	674	2	Q8JJN2	Q8jjn2 hepatitis e
34	2607	93.9	674	2	Q7TGF1	Q7tgf1 hepatitis e
35	2606	93.9	674	2	Q6BD78	Q6bd78 hepatitis e
36	2604	93.8	550	2	Q8JVV3	Q8jvv3 hepatitis e
37	2604	93.8	671	2	Q8JJM1	Q8jjm1 hepatitis e
38	2604	93.8	674	2	Q8JJN6	Q8jjn6 hepatitis e
39	2603	93.8	674	2	Q6BD83	Q6bd83 hepatitis e
40	2601	93.7	674	2	Q806D7	Q806d7 hepatitis e
41	2601	93.7	674	2	Q806E0	Q806e0 swine hepat
42	2601	93.7	674	2	Q80IR5	Q80ir5 hepatitis e
43	2600	93.7	674	2	Q6PMR3	Q6pmr3 swine hepat
44	2577	92.8	672	2	Q9IVZ8	Q9ivz8 hepatitis e
45	2395	86.3	605	2	Q9YWL0	Q9ywl0 hepatitis e

ALIGNMENTS

RESULT 1
VST2_HEVME
ID VST2_HEVME STANDARD; PRT; 659 AA.
AC Q03500;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Structural protein 2 precursor.
GN ORFNames=ORF2;
OS Hepatitis E virus (strain Mexico) (HEV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=31768;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93079857; PubMed=1448913;
RA Huang C.C., Nguyen D., Fernandez J., Yun K.Y., Fry K.E., Bradley D.W.,
RA Tam A.W., Reyes G.R.;
RT "Molecular cloning and sequencing of the Mexico isolate of hepatitis E
RT virus (HEV).";
RL Virology 191:550-558(1992).
CC -!- FUNCTION: Contains a high basic amino acid content suggesting that
CC it may be involved in the encapsidation of the genomic RNA by
CC effectively neutralizing the negatively charged RNA.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; M74506; AAA45732.1; -.
DR PIR; B44212; B44212.
DR InterPro; IPR004261; SP2.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF03014; SP2; 1.
KW Signal.
FT SIGNAL 1 22 By similarity.
FT CHAIN 23 659 Structural protein 2.
SQ SEQUENCE 659 AA; 70640 MW; CF75E75EFD8FBE2C CRC64;

Query Match 99.0%; Score 2749.5; DB 1; Length 659;
Best Local Similarity 99.4%; Pred. No. 1.6e-182;
Matches 537; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231
```

```
Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 650
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RESULT 2
Q9E8G5
ID Q9E8G5 PRELIMINARY; PRT; 660 AA.
AC Q9E8G5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Structural protein.
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Abb-2B;
RX MEDLINE=20271579; PubMed=10813471;
RA van Cuyck-Gandre H., Zhang H.Y., Tsarev S.A., Warren R.L.,
RA Caudill J.D., Snellings N.J., Begot L., Innis B.L., Longer C.F.;
RT "Phylogenetically distinct hepatitis E viruses in Pakistan.";
RL Am. J. Trop. Med. Hyg. 62:187-189(2000).
DR EMBL; AF185822; AAG16766.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70903 MW; 1F506BE3CFB3BACE CRC64;

Query Match 95.6%; Score 2654; DB 2; Length 660;
Best Local Similarity 95.0%; Pred. No. 6.8e-176;
Matches 513; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||:|||||||||||||||||||||||:|||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||:||| ||||| |||||||| ||| |||||||||||| ||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651
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RESULT 3
VST2_HEVPA
ID VST2_HEVPA STANDARD; PRT; 660 AA.
AC P33426;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Structural protein 2 precursor.
GN ORFNames=ORF2;
OS Hepatitis E virus (strain Pakistan) (HEV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=33774;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92115700; PubMed=1731327;
RA Tsarev S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J.,
RA Malik I.A., Iqbal M., Purcell R.H.;
RT "Characterization of a prototype strain of hepatitis E virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).
CC -!- FUNCTION: Contains a high basic amino acid content suggesting that
CC it may be involved in the encapsidation of the genomic RNA by
CC effectively neutralizing the negatively charged RNA.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; M80581; AAA45727.1; -.
DR InterPro; IPR004261; SP2.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF03014; SP2; 1.
KW Signal.
FT SIGNAL 1 22 By similarity.
FT CHAIN 23 660 Structural protein 2.
SQ SEQUENCE 660 AA; 70980 MW; 8085BC53CFB46FD3 CRC64;

Query Match 95.5%; Score 2650; DB 1; Length 660;
Best Local Similarity 94.8%; Pred. No. 1.3e-175;
Matches 512; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171
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Qy          61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy         121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy         181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
               ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db         292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy         241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
               ||:||  |||||:||||||| ||||||||||||||||||||||||||||||||||||||||
Db         352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy         301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
               ||||||||||||:|||||||:||||||||||||||||||||||||||||||||||||||||
Db         412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy         361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
               ||||||||||||||||||||||:||||||||||||||||||:|||||||| |::|
Db         472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy         421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
               ||||||||||||||||||||||||||||||||||||||:|:|||||||||||| ||||
Db         532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy         481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
               ||:||| ||||| | ||||||| ||| |||||||||||| ||||||||||||||||||||
Db         592 PVSISAVAVLAPHSVLALLEDTMDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651
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RESULT 4
Q77EC8
ID Q77EC8 PRELIMINARY; PRT; 660 AA.
AC Q77EC8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Capsid protein.
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sar-55;
RX MEDLINE=21625046; PubMed=11742081; DOI=10.1073/pnas.251555098;
RA Emerson S.U., Zhang M., Meng X.-J., Nguyen H., St Claire M.,
RA Govindarajan S., Huang Y.K., Purcell R.H.;
RT "Recombinant hepatitis E virus genomes infectious for primates:
RT importance of capping and discovery of a cis-reactive element.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:15270-15275(2001).
DR EMBL; AF444003; AAL50059.1; -.
DR EMBL; AF444002; AAL50056.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70979 MW; 8085BC53CFB46FD3 CRC64;

Query Match 95.5%; Score 2650; DB 2; Length 660;
Best Local Similarity 94.8%; Pred. No. 1.3e-175;
Matches 512; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

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Qy           1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
               |||||||| |||||||||||||||||||||||||:||||||||||:| ||||||||
Db         112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy          61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy         121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy         181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
               ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db         292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy         241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
               ||:||  |||||:||||||| ||||||||||||||||||||||||||||||||||||||||
Db         352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy         301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
               ||||||||||||:|||||||:||||||||||||||||||||||||||||||||||||||||
Db         412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy         361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
               ||||||||||||||||||||||:||||||||||||||||||:|||||||| |::|
Db         472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy         421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
               ||||||||||||||||||||||||||||||||||||||:|:|||||||||||| ||||
Db         532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy         481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
               ||:||| ||||| | ||||||| ||| |||||||||||| ||||||||||||||||||||
Db         592 PVSISAVAVLAPHSVLALLEDTMDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651
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RESULT 5
Q89468
ID Q89468 PRELIMINARY; PRT; 660 AA.
AC Q89468;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Unnamed protein product (ORFs 1-3).
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RA Yin S.R., Purcell R.H., Emerson S.U.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K52-87;
RX MEDLINE=95176571; PubMed=7871758;
RA Yin S., Purcell R.H., Emerson S.U.;
RT "A new Chinese isolate of hepatitis E virus: comparison with strains
RT recovered from different geographical regions.";
RL Virus Genes 9:23-32(1994).
DR EMBL; L25547; AAA91080.1; -.
DR EMBL; L25595; AAA65490.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70979 MW; DC68116DCD639175 CRC64;

Query Match 95.5%; Score 2650; DB 2; Length 660;
Best Local Similarity 94.8%; Pred. No. 1.3e-175;
Matches 512; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

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Qy           1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
               |||||||| |||||||||||||||||||||||||:||||||||||:| ||||||||
Db         112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy          61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy         121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
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Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||:|||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||:||| ||| | |||||||| ||| ||||||||||||| ||||||||||||||||||||
Db        592 PVSISAVAVLTPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 6
Q9W7W9
ID   Q9W7W9      PRELIMINARY;      PRT;   660 AA.
AC   Q9W7W9;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Structural protein 2 (Structural viral protein).
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HEV-Morocco;
RX   MEDLINE=99107414; PubMed=9892396;
RX   DOI=10.1002/(SICI)1096-9071(199902)57:2<126::AID-JMV7>3.3.CO;2-F;
RA   Meng J., Cong M., Dai X., Pillot J., Purdy M.A., Fields H.A.,
RA   Khudyakov Y.E.;
RT   "Primary structure of open reading frame 2 and 3 of the hepatitis E
RT   virus isolated from Morocco.";
RL   J. Med. Virol. 57:126-133(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Chen G., Meng J.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF065061; AAD10627.1; -.
DR   EMBL; AY230202; AAO72992.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70943 MW;  9719D30CCD932950 CRC64;

  Query Match             95.5%;  Score 2650;  DB 2;  Length 660;
  Best Local Similarity   94.8%;  Pred. No. 1.3e-175;
  Matches  512;  Conservative   14;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||:|||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:|:  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||:|||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||:||| ||||| ||||||||| ||| ||||||||||||| ||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 7
Q9WQA0
ID   Q9WQA0      PRELIMINARY;      PRT;   660 AA.
AC   Q9WQA0;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   ORF-2.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99350000; PubMed=10423137;
RA   Arankalle V.A., Paranjape S., Emerson S.U., Purcell R.H.,
RA   Walimbe A.M.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from India (1976-
RT   1993).";
RL   J. Gen. Virol. 80:1691-1700(1999).
DR   EMBL; AF124407; AAD45493.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71040 MW;  03B72DDF0AB7B521 CRC64;

  Query Match             95.5%;  Score 2650;  DB 2;  Length 660;
  Best Local Similarity   94.8%;  Pred. No. 1.3e-175;
  Matches  512;  Conservative   13;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||:|||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
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Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||:|||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||:|||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||:||| || || |||||||| ||| |||||||||||| ||||||||||||||||||||||
Db        592 PVSISAVAVFAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 8
VST2_HEVBU
ID   VST2_HEVBU     STANDARD;      PRT;   660 AA.
AC   P29326;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   Structural protein 2 precursor.
GN   ORFNames=ORF2;
OS   Hepatitis E virus (strain Burma) (HEV).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=31767;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92024067; PubMed=1926770;
RA   Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
RA   Fry K.E., Reyes G.R.;
RT   "Hepatitis E virus (HEV): molecular cloning and sequencing of the
RT   full-length viral genome.";
RL   Virology 185:120-131(1991).
CC   -!- FUNCTION: Contains a high basic amino acid content suggesting that
CC       it may be involved in the encapsidation of the genomic RNA by
CC       effectively neutralizing the negatively charged RNA.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M73218; AAA45736.1; -.
DR   PIR; C40778; VHWWH2.
DR   InterPro; IPR004261; SP2.
DR   InterPro; IPR008975; Viral_cap_coat.
DR   Pfam; PF03014; SP2; 1.
KW   Signal.
FT   SIGNAL       1     19       Potential.
FT   CHAIN       20    660       Structural protein 2.
SQ   SEQUENCE   660 AA;  70978 MW;  5832A013CCC4A61C CRC64;

  Query Match             95.2%;  Score 2644;  DB 1;  Length 660;
  Best Local Similarity   94.8%;  Pred. No. 3.4e-175;
  Matches  512;  Conservative   13;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| ||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||:|||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||:|||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||:||| ||||| |||||||| ||| |||||||||||| ||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 9
O91855
ID   O91855      PRELIMINARY;      PRT;   660 AA.
AC   O91855;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Structural protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=93-Egypt;
RX   MEDLINE=99105430; PubMed=9890424;
RX   DOI=10.1002/(SICI)1096-9071(199901)57:1<68::AID-JMV10>3.0.CO;2-E;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
RL   J. Med. Virol. 57:68-74(1999).
DR   EMBL; AF051351; AAC35761.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71039 MW;  044FF5EA7C492791 CRC64;

  Query Match             95.2%;  Score 2644;  DB 2;  Length 660;
  Best Local Similarity   94.6%;  Pred. No. 3.4e-175;
  Matches  511;  Conservative   14;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| ||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231
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Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:|:  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||||||||:|||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||:|||:|||||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTSSDQLLIENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||:||| ||||| ||||||||| ||| |||||||||||| ||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 10
Q69419
ID   Q69419      PRELIMINARY;      PRT;   660 AA.
AC   Q69419;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ORF1, ORF2 & ORF3.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   von Brunn A., Seebach J., Thyagarajan S.P., Mohanavalli B., Menon T.,
RA   Froesner G.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X99441; CAA67804.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70960 MW;  DAC3DF95F91689F8 CRC64;

  Query Match             95.2%;  Score 2644;  DB 2;  Length 660;
  Best Local Similarity   94.6%;  Pred. No. 3.4e-175;
  Matches  511;  Conservative   13;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
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Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:|:  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              || |||||||||:|||||||:||||||||||||||||||||||||||||| |||||||
Db        412 LYRSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSALRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||||:||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||:||| ||||| ||||||||| ||| |||||||||||| ||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 11
O91856
ID   O91856      PRELIMINARY;      PRT;   660 AA.
AC   O91856;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Structural protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=94-Egypt;
RX   MEDLINE=99105430; PubMed=9890424;
RX   DOI=10.1002/(SICI)1096-9071(199901)57:1<68::AID-JMV10>3.0.CO;2-E;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
RL   J. Med. Virol. 57:68-74(1999).
DR   EMBL; AF051352; AAC35764.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71025 MW;  16C560FA16941F2A CRC64;

  Query Match             95.2%;  Score 2643;  DB 2;  Length 660;
  Best Local Similarity   94.6%;  Pred. No. 3.9e-175;
  Matches  511;  Conservative   13;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:|:  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLSTIQQ 420
              |||||||||||||||||||||:|||||||||||||||||||||:||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||:||| ||||| ||||||||| ||| |||||||||||| ||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||:||| ||||| ||||||||| ||| |||||||||||| ||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYRSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSALRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||||:||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||:||| ||||| ||||||||| ||| |||||||||||| ||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||||:||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||:||| ||||| ||||||||| ||| |||||||||||| ||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||:||| ||||| ||||||||| ||| |||||||||||| ||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651
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Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||:||||||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||:||||| |||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLIENATGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              ||:||| ||||| ||||||||| ||| |||||||||||| ||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 12
Q69411
ID   Q69411      PRELIMINARY;      PRT;   660 AA.
AC   Q69411;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Structural protein.
GN   Name=ORF2;
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Donati M.C., Fagan E.A., Harrison T.J.;
RT   "Sequence analysis of full length HEV clones derived directly from
RT   human liver in fulminant hepatitis E.";
RL   (In) Rizzetto M., Purcell R.H., Gerin J.L., Verme G (eds.);
RL   VIRAL HEPATITIS AND LIVER DISEASE, pp.313-316, Edizioni Minerva
RL   Medica, Torino (1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Harrison T.J.;
RL   Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X98292; CAA66937.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71024 MW;  F37E3FEFF7A4EAD1 CRC64;

  Query Match           95.2%;  Score 2643;  DB 2;  Length 660;
  Best Local Similarity   94.8%;  Pred. No. 3.9e-175;
  Matches  512;  Conservative   11;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||| ||:|||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSPVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGLPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||| |||||| ||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALEFEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||||||:||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||:||||| |||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
              |||||| ||||| |||||||||| ||| |||||||||||| ||||||||||||||||||||
Db        592 PVAISAVAVLAPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 13
Q81878
ID   Q81878      PRELIMINARY;      PRT;   660 AA.
AC   Q81878;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Complete genome sequence.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Uchida T.;
RL   Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; D11093; BAA01867.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70937 MW;  5412313F1A2EF4A9 CRC64;

  Query Match           95.0%;  Score 2638;  DB 2;  Length 660;
  Best Local Similarity   94.3%;  Pred. No. 8.8e-175;
  Matches  509;  Conservative   14;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||| ||:|||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYGISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||:|||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGVLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGTDGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||||||:||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              | ||||||||||||||||||||||||||||||||||:|:||||||||||||| ||||
Db        532 YCKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
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                ||:||| ||||| ||||||||| ||| |||||||||||| ||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 14
Q6XXV0
ID   Q6XXV0      PRELIMINARY;      PRT;   660 AA.
AC   Q6XXV0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Structural protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RX   MEDLINE=98071272; PubMed=9407381;
RX   DOI=10.1002/(SICI)1096-9071(199712)53:4<340::AID-JMV5>3.0.CO;2-7;
RA   van Cuyck-Gandre H., Zhang H.Y., Tsarev S.A., Clements N.J.,
RA   Cohen S.J., Caudill J.D., Buisson Y., Coursaget P., Warren R.L.,
RA   Longer C.F.;
RT   "Characterization of hepatitis E virus (HEV) from Algeria and Chad by
RT   partial genome sequence.";
RL   J. Med. Virol. 53:340-347(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RX   MEDLINE=99105430; PubMed=9890424;
RX   DOI=10.1002/(SICI)1096-9071(199901)57:1<68::AID-JMV10>3.0.CO;2-E;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
RL   J. Med. Virol. 57:68-74(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RX   MEDLINE=99105430; PubMed=9890424; DOI=10.1016/S0928-8244(03)00241-4;
RA   van Cuyck H., Juge F., Roques P.;
RT   "Phylogenetic analysis of the first complete hepatitis E virus (HEV)
RT   genome from Africa.";
RL   FEMS Immunol. Med. Microbiol. 39:133-139(2003).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RA   Van Cuyck-Gandre H., Zhang H.Y., Tsarev S.A., Clements N.J.,
RA   Cohen S.J., Caudill J.D., Buisson Y., Coursaget P., Warren R.L.,
RA   Longer C.F.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RA   van Cuyck H., Roberston D., Juge F., Roques P., Lemey P.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY204877; AAB61825.2; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70949 MW;  EA56732D458D0AB1 CRC64;

  Query Match             94.9%;  Score 2635;  DB 2;  Length 660;
  Best Local Similarity   94.4%;  Pred. No. 1.4e-174;
  Matches  510;  Conservative   13;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
                |||||||| || |||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVSDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
               ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
               ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
               ||:|:  |||||:|||||||| ||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
               |||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
               ||||||||||||||||||:||||||||||||||||||:||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
               ||||||||||||||||||||||||||||||||||||:|||| |||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLIENVAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
               ||:||| ||||| |||||||||| ||| |||||||||||| ||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK 651


RESULT 15
Q80IY5
ID   Q80IY5      PRELIMINARY;      PRT;   660 AA.
AC   Q80IY5;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Structural protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Osh 205;
RA   Robertson B.H., Lu L., Drobeniuc J., Favorov M., Usmanov R.,
RA   Kobylnilkov N., Balayan M.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF455784; AAO67359.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70881 MW;  AB83CAC3F181164E CRC64;

  Query Match             94.8%;  Score 2633;  DB 2;  Length 660;
  Best Local Similarity   94.1%;  Pred. No. 2e-174;
  Matches  508;  Conservative   14;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||:|| ||:|||||||||||||||||||||||||||||||||||||||| ||||||||
Db        112 AVSPAPDTAPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
               ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
                |||||||||||||||||||||  |||||||||:|||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
                ||||||  ||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        352 DLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
                |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
                ||||||||||:|||||| |:|:||:|| |||||||||||||||||||||||||||| |::|
Db        472 WLSLTAAEYDQTTYGSSTNPMYVSDTVTFVNVATGAQAVARSLDWSKVTLDGRPLTTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
                |||||:|||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        532 YSKTFYVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLK 540
                ||::||  |||| |||| |||| ||| |||||||||||| ||||||||||:|||||||
Db        592 PVSVSAVGVLAPHSALAALEDTIDYPARAHTFDDFCPECRNLGLQGCAFQSTIAELQRLK 651
```

Search completed: July 14, 2005, 15:50:31
Job time : 40.3962 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 14, 2005, 00:29:03 ; Search time 43.4198 Seconds
(without alignments)
4676.418 Million cell updates/sec

Title: US-09-769-066-27
Perfect score: 2694
Sequence: 1 AVAPAHDTPPVPDVDSRGAI.....PARAHTFDDFCPECRPLGLQ 525

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2694	100.0	525	2	AAR96103	Aar96103 Hepatitis
2	2694	100.0	540	2	AAR96101	Aar96101 Hepatitis
3	2694	100.0	549	2	AAR96091	Aar96091 Hepatitis
4	2694	100.0	660	2	AAR38785	Aar38785 HEV ORF2
5	2694	100.0	660	2	AAR39306	Aar39306 Burma str
6	2694	100.0	660	2	AAR96089	Aar96089 Hepatitis
7	2694	100.0	660	2	AAW35826	Aaw35826 Hepatitis
8	2694	100.0	660	2	AAW80197	Aaw80197 Protein e
9	2694	100.0	660	2	AAW93389	Aaw93389 Human HEV
10	2694	100.0	660	3	AAB24120	Aab24120 Hepatitis
11	2694	100.0	660	4	AAB62523	Aab62523 HEV-Burma
12	2694	100.0	660	5	AAO15699	Aao15699 Hepatitis
13	2694	100.0	660	7	ADD24376	Add24376 Hepatitis
14	2687	99.7	549	2	AAW76367	Aaw76367 Hepatitis
15	2687	99.7	660	2	AAW76369	Aaw76369 Hepatitis
16	2687	99.7	660	2	AAW71210	Aaw71210 Protein e
17	2685	99.7	660	2	AAR70323	Aar70323 Hepatitis
18	2685	99.7	660	4	AAE12980	Aae12980 Hepatitis
19	2681	99.5	660	2	AAR91814	Aar91814 Hepatitis
20	2681	99.5	660	2	AAW93386	Aaw93386 Human HEV
21	2681	99.5	660	2	AAW93388	Aaw93388 Human HEV
22	2681	99.5	660	5	ABB81670	Abb81670 Hepatitis
23	2681	99.5	660	6	ADA50060	Ada50060 Hepatitis
24	2681	99.5	660	7	ADB97807	Adb97807 HEV ORF2
25	2679	99.4	660	5	ABJ04803	Abj04803 Hepatitis
26	2677	99.4	660	2	AAW93390	Aaw93390 Human HEV
27	2676	99.3	660	2	AAW93395	Aaw93395 Human HEV
28	2672	99.2	660	2	AAR51265	Aar51265 HEV strai
29	2672	99.2	660	2	AAW81520	Aaw81520 Hepatitis
30	2670	99.1	660	5	ABJ04811	Abj04811 Hepatitis
31	2669	99.1	660	2	AAW93391	Aaw93391 Human HEV
32	2668	99.0	660	5	ABJ04820	Abj04820 Hepatitis
33	2668	99.0	660	5	ABJ04819	Abj04819 Hepatitis
34	2666	99.0	660	2	AAW93392	Aaw93392 Human HEV
35	2666	99.0	660	5	ABJ04807	Abj04807 Hepatitis
36	2666	99.0	660	5	ABJ04809	Abj04809 Hepatitis
37	2663	98.8	660	5	ABJ04822	Abj04822 Hepatitis
38	2662	98.8	660	5	ABJ04818	Abj04818 Hepatitis
39	2662	98.8	660	5	ABJ04805	Abj04805 Hepatitis
40	2661	98.8	660	5	ABJ04806	Abj04806 Hepatitis
41	2659	98.7	660	2	AAR14619	Aar14619 Protein e
42	2659	98.7	660	5	ABJ04821	Abj04821 Hepatitis
43	2658	98.7	660	2	AAW93394	Aaw93394 Human HEV
44	2656	98.6	660	2	AAW93393	Aaw93393 Human HEV
45	2656	98.6	660	4	ADH13471	Adh13471 Hepatitis

ALIGNMENTS

RESULT 1
AAR96103
ID AAR96103 standard; protein; 525 AA.
XX
AC AAR96103;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Burma strain) recombinant 62K antigen.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid.
XX
OS Hepatitis E virus; Burma strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Claim 7; Page 95-97; 125pp; English.
XX
CC DNA (AAT27109) coding for the 62K antigen (AAR96091) of hepatitis E virus
CC (HEV) Burma strain capsid protein was cloned into baculovirus expression
CC vector pBluBacIII and recombinant 62K was expressed in Sf9 insect cells.
CC High levels of expression were obtd. and the recombinant 62K was obtd. in
CC over 95% purity. However, C-terminal processing resulted in the deletion
CC of 9 or 23 amino acids from 62K, giving 2 related polypeptide species
CC (AAR96101 and AAR96103). Similar results were obtd. with HEV Mexico 62K
CC antigen (see also AAR96102 and AAR96104). Recombinant 62K represents an
CC improved antigen, in comparison to bacterial expressed proteins, for use
CC in HEV diagnostic assays, and also has excellent immunogenic properties.
CC (Updated on 16-OCT-2003 to standardise OS field)

XX
SQ Sequence 525 AA;

Query Match 100.0%; Score 2694; DB 2; Length 525;
Best Local Similarity 100.0%; Pred. No. 7.4e-218;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
```

RESULT 2
AAR96101
ID AAR96101 standard; protein; 540 AA.
XX
AC AAR96101;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Burma strain) recombinant 62K antigen.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid.
XX
OS Hepatitis E virus; Burma strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Claim 5; Page 92-93; 125pp; English.
XX
CC DNA (AAT27109) coding for the 62K antigen (AAR96091) of hepatitis E virus
CC (HEV) Burma strain capsid protein was cloned into baculovirus expression
CC vector pBluBacIII and recombinant 62K was expressed in Sf9 insect cells.
CC High levels of expression were obtd. and the recombinant 62K was obtd. in
CC over 95% purity. However, C-terminal processing resulted in the deletion
CC of 9 or 23 amino acids from 62K, giving 2 related polypeptide species
CC (AAR96101 and AAR96103). Similar results were obtd. with HEV Mexico 62K
CC antigen (see also AAR96102 and AAR96104). Recombinant 62K represents an
CC improved antigen, in comparison to bacterial expressed proteins, for use
CC in HEV diagnostic assays, and also has excellent immunogenic properties.
CC (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 540 AA;

Query Match 100.0%; Score 2694; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 7.7e-218;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
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RESULT 3
AAR96091
ID AAR96091 standard; protein; 549 AA.
XX
AC AAR96091;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Burma strain) 62K antigen.

```
XX
KW   HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW   diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW   capsid.
XX
OS   Hepatitis E virus; Burma strain.
XX
PN   WO9612807-A2.
XX
PD   02-MAY-1996.
XX
PF   23-OCT-1995;   95WO-US013703.
XX
PR   24-OCT-1994;   94US-00327952.
PR   13-OCT-1995;   95US-00542634.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fuerst TR,  Mcatee CP,  Yarbough PO,  Zhang Y;
XX
DR   WPI; 1996-230608/23.
DR   N-PSDB; AAT27109.
XX
PT   Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT   diagnostic reagents for determining HEV infection and in vaccines.
XX
PS   Claim 3; Page 83-84; 125pp; English.
XX
CC   62K antigen (AAR96091) comprises the C-terminal 549 amino acids of
CC   hepatitis E virus (HEV) Burma strain capsid protein (see also AAR96089).
CC   It is obtd. by PCR amplification of HEV Burma ORF-2 (AAT27107), insertion
CC   of amplified DNA (AAT27109) into vector pGEX and expression in E. coli
CC   cells. Expression of full-length ORF-2 in Sf9 insect cells using a
CC   baculovirus system also results in prodn. of 62K antigen (see also
CC   AAR96101 and AAR96103). 62K represents an improved antigen, in comparison
CC   to bacterial expressed proteins, for use in HEV diagnostic assays, and
CC   also has excellent immunogenic properties. (Updated on 16-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 549 AA;

  Query Match             100.0%;  Score 2694;  DB 2;  Length 549;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-218;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525


RESULT 4
AAR38785
ID   AAR38785 standard; protein; 660 AA.
XX
AC   AAR38785;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   11-JAN-1994  (first entry)
XX
DE   HEV ORF2 protein.
XX
KW   Enterically transmitted non-A non-B hepatitis; ET-NANB; vaccine.
XX
OS   Hepatitis E virus; Burma strain.
XX
FH   Key             Location/Qualifiers
FT   Peptide          225. .660
FT                    /label= C2
FT   Peptide          334. .660
FT                    /label= SG3
FT   Peptide          613. .660
FT                    /label= 406.3-2
XX
PN   WO9314116-A1.
XX
PD   22-JUL-1993.
XX
PF   15-JAN-1993;   93WO-US000459.
XX
PR   17-JAN-1992;   92US-00822335.
PR   01-MAY-1992;   92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
PA   (USSH ) US SEC DEPT HEALTH.
XX
PI   Reyes GR,  Bradley DW,  Tam AW,  Carl M;
XX
DR   WPI; 1993-243144/30.
DR   N-PSDB; AAQ47129.
XX
PT   New immunogenic hepatitis E virus (HEV) peptide(s) - are from the ORF1,
PT   ORF2 and ORF3 regions of HEV, useful as a vaccine against HEV infection.
XX
PS   Disclosure; Fig 8; 48pp; English.
XX
CC   Immunogenic hepatitis E virus (HEV) peptides are selected from the ORF1,
CC   ORF2 and ORF3 regions of HEV. The peptides can be used in vaccines to
CC   prevent infection by HEV. The antibodies can neutralise and block HEV
CC   infection and can be used to prevent or treat HEV infection. The peptides
CC   and antibodies can also be used as diagnostic reagents. (Updated on 25-
CC   MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS
CC   field)
XX
SQ   Sequence 660 AA;

  Query Match             100.0%;  Score 2694;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1e-217;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171
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Qy          61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy         121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy         181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy         241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy         301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy         361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy         421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy         481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
               |||||||||||||||||||||||||||||||||||||||||||||
Db         592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
```

RESULT 5
AAR39306
ID AAR39306 standard; protein; 660 AA.
XX
AC AAR39306;
XX
DT 25-MAR-2003 (revised)
DT 14-FEB-1994 (first entry)
XX
DE Burma strain HEV ORF2 puative virus capsid protein.
XX
KW Hepatitis E virus; vaccine; neutralising antibodies; infection; block;
KW open reading frame; antibodies.
XX
OS Hepatitis E virus.
XX
PN WO9314208-A2.
XX
PD 22-JUL-1993.
XX
PF 19-JAN-1993; 93WO-US000475.
XX
PR 17-JAN-1992; 92US-00822335.
PR 20-APR-1992; 92US-00870985.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Reyes GR, Bradley DW, Twu J, Purdy MA, Tam AW, Krawczynski KZ;
XX
DR WPI; 1993-243223/30.
DR N-PSDB; AAQ46813.
XX
PT Antigen and antibody vaccines against hepatitis E virus infection -
PT contain peptide(s) derived from capsid protein C-terminal or antibodies
PT against protein.
XX
PS Disclosure; Fig 7; 43pp; English.
XX
CC The sequence is that of the putative virus capsid protein encoded by
CC Burma strain hepatitis E virus (HEV) open reading frame ORF2. This
CC protein or peptide fragments of it may be used in a vaccine composition
CC for immunising an individual against HEV. Antibodies raised against these
CC peptides can also be used in such vaccines. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 660 AA;

Query Match 100.0%; Score 2694; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 1e-217;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy           1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy          61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy         121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy         181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy         241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy         301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy         361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy         421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy         481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
               |||||||||||||||||||||||||||||||||||||||||||||
Db         592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
```

RESULT 6
AAR96089
ID AAR96089 standard; protein; 660 AA.
XX
AC AAR96089;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Burma strain) capsid protein.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid.
XX
OS Hepatitis E virus; Burma strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.

```
PR   13-OCT-1995;   95US-00542634.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fuerst TR,  Mcatee CP,  Yarbough PO,  Zhang Y;
XX
DR   WPI; 1996-230608/23.
DR   N-PSDB; AAT27107.
XX
PT   Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT   diagnostic reagents for determining HEV infection and in vaccines.
XX
PS   Disclosure; Page 78-80; 125pp; English.
XX
CC   The putative capsid protein (AAR96089) of hepatitis E virus (HEV) Burma
CC   strain is encoded by ORF-2 (AAT27107) of the virus. PCR amplification of
CC   ORF-2 allows prodn. of capsid protein or of C-terminal regions of the
CC   capsid protein (see also AAR96091, AAR96093 and AAR96095) and expression
CC   in Spodoptera frugiperda Sf9 insect cells using a baculovirus vector
CC   provides recombinant C-terminal regions (see also AAR96101 and AAR96103)
CC   useful as diagnostic reagents and in vaccines. The HEV Mexico strain
CC   capsid protein (AAR96090) may similarly be used. (Updated on 16-OCT-2003
CC   to standardise OS field)
XX
SQ   Sequence 660 AA;

  Query Match             100.0%;  Score 2694;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1e-217;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 7
AAW35826
ID   AAW35826 standard; protein; 660 AA.
XX
AC   AAW35826;
XX
DT   17-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   26-FEB-1998  (first entry)
XX
DE   Hepatitis E virus Burma strain protein from ORF2.
XX
KW   Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
KW   diagnosis; HEV.
XX
OS   Hepatitis E virus; - Burma strain.
XX
PN   US5686239-A.
XX
PD   11-NOV-1997.
XX
PF   09-MAY-1994;   94US-00240049.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   17-JAN-1992;   92US-00822335.
PR   20-APR-1992;   92US-00870985.
PR   01-MAY-1992;   92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Tam AW,  Reyes GR,  Yarbough PO;
XX
DR   WPI; 1997-558132/51.
DR   N-PSDB; AAT96959.
XX
PT   Diagnosis of hepatitis E virus Burma and Mexico strain infection - by
PT   immunoassay with hepatitis E virus peptide antigens.
XX
PS   Disclosure; Col 39-42; 36pp; English.
XX
CC   A method has been developed for detecting hepatitis E virus (HEV)
CC   antibodies (Ab). The method comprises: (a) reacting a serum sample with a
CC   HEV peptide antigen; and (b) examining the peptide for the presence of
CC   bound Ab, where the presence of bound Ab indicates the presence of HEV
CC   Ab. The present sequence represents the protein from the open reading
CC   frame, ORF2, from HEV Burma strain. The method can be used to diagnose
CC   infection with the enterically transmitted non-A/non-B viral hepatitis
CC   agent HEV, specifically the HEV Burma and Mexico strains. (Updated on 25-
CC   MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to standardise OS
CC   field)
XX
SQ   Sequence 660 AA;

  Query Match             100.0%;  Score 2694;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1e-217;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
                 |||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
```

RESULT 8
AAW80197
ID AAW80197 standard; protein; 660 AA.
XX
AC AAW80197;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 23-DEC-1998 (first entry)
XX
DE Protein encoded by ORF2 of ET-NANB (HEV) Burma strain DNA sequence.
XX
KW Enterically transmitted non A non B hepatitis virus; ET-NANB;
KW Hepatitis E virus; HEV; Burma HEV isolate; vaccine; diagnostic probe.
XX
OS Non-A.
OS non-B hepatitis virus.
XX
PN US5824649-A.
XX
PD 20-OCT-1998.
XX
PF 07-JUN-1995; 95US-00475807.
XX
PR 17-JUN-1988; 88US-00208997.
PR 11-APR-1989; 89US-00336672.
PR 16-JUN-1989; 89US-00367486.
PR 13-OCT-1989; 89US-00420921.
PR 05-APR-1990; 90US-00505888.
PR 25-JUL-1994; 94US-00279823.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Bradley DW, Reyes GR, Krawczynski KZ, Tam A, Fry KE, Yarbough PO;
XX
DR WPI; 1998-582599/49.
DR N-PSDB; AAV66321.
XX
PT Hepatitis E virus proteins - useful for diagnosis or vaccine production
PT the virus.
XX
PS Claim 6; Col 65-70; 47pp; English.
XX
CC AAW80196-98 are encoded by the genome of the Burma strain of enterically
CC transmitted non A non B hepatitis virus (ET-NANB) (hepatitis E virus
CC (HEV)). The specification describes an isolated protein which is
CC specifically immunoreactive with antibodies present in individuals
CC infected with HEV and encoded by a sequence contained in an open reading
CC frame (ORF) of an HEV genome. The genome has a sequence that is more than
CC 70% identical to the ORF1 sequence from Burma HEV isolate. The protein is
CC used as a vaccine and a diagnostic probe for ET-NANB. (Updated on 25-MAR-
CC 2003 to correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)
XX

SQ Sequence 660 AA;

  Query Match   100.0%; Score 2694; DB 2; Length 660;
  Best Local Similarity 100.0%; Pred. No. 1e-217;
  Matches 525; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
```

RESULT 9
AAW93389
ID AAW93389 standard; protein; 660 AA.
XX
AC AAW93389;
XX
DT 11-JUN-1999 (first entry)
XX
DE Human HEV ORF 2 protein from strain Burma.
XX
KW Swine hepatitis E virus; HEV; cross-reaction; antibody; human; therapy;
KW vaccine; immunise; infection; detection; diagnosis; prevention.
XX
OS Hepatitis E virus.
XX
PN WO9904029-A2.
XX
PD 28-JAN-1999.
XX
PF 17-JUL-1998; 98WO-US014665.
XX
PR 18-JUL-1997; 97US-0053069P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Meng X, Emerson SU, Purcell RH;
XX
DR WPI; 1999-132270/11.
XX
PT New isolated swine hepatitis E virus - used to develop products for the

```
PT   diagnosis, prevention and treatment of hepatitis E virus infection in
PT   mammals, particularly humans.
XX
PS   Example 1; Fig 3A; 70pp; English.
XX
CC   This invention describes a swine hepatitis E virus (HEV) and its natural
CC   mutants which are capable of cross-reacting with antibodies reactive with
CC   a human HEV strain or natural mutants. The HEV and the proteins can be
CC   used in vaccines for immunising against HEV infection. The swine HEV can
CC   be used in humans to prevent possible infection by human HEV. The swine
CC   HEV can also be used as a therapeutic treatment for infection by other
CC   strains of HEV. The swine HEV can also be used for the production of
CC   antibodies which can be used in therapy, detection and diagnosis. The
CC   products can also be used for determining the susceptibility of cells or
CC   organs to infection with swine HEV. The swine HEV is particularly useful
CC   for the development of agents for the prevention, treatment and detection
CC   of human HEV because it is not a human virus and thus can be handled both
CC   experimentally and clinically without fear of severe infection and/or
CC   contamination
XX
SQ   Sequence 660 AA;

  Query Match             100.0%;  Score 2694;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1e-217;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 10
AAB24120
ID   AAB24120 standard; protein; 660 AA.
XX
AC   AAB24120;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Hepatitis E virus Burma strain ORF2 protein sequence SEQ ID NO:8.
XX
KW   Hepatitis E virus; HEV; non-A/non-B viral hepatitis; viral protein;
KW   immunological; diagnosis; hepatitis; infection; identification;
KW   detection; immunoreactive; hepatotropic; antiinflammatory; virucide;
KW   vaccine; antiviral; antigenic; antibody; antigen.
XX
OS   Hepatitis E virus.
XX
PN   US6120988-A.
XX
PD   19-SEP-2000.
XX
PF   07-JUN-1995;   95US-00478507.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   25-JUL-1994;   94US-00279823.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
PA   (USGO ) US GOVERNMENT.
XX
PI   Yarbough PO,  Krawczynski KZ,  Fry KE,  Bradley DW,  Tam A,  Reyes GR;
XX
DR   WPI; 2000-593712/56.
DR   N-PSDB; AAA99259.
XX
PT   Identifying recombinant antigen immunoreactive with antibody induced by
PT   hepatitis E virus (HEV), for detecting HEV infection, comprises
PT   immunoreacting a polypeptide from an HEV genome with an HEV-positive
PT   antiserum.
XX
PS   Claim 6; Col 63-68; 46pp; English.
XX
CC   The present invention describes a method for identifying a recombinant
CC   antigen immunoreactive with a hepatitis E virus (HEV)-induced antibody.
CC   The method comprises producing a polypeptide derived from an HEV genome,
CC   immunoreacting the polypeptide with an HEV-positive antiserum and
CC   selecting the polypeptide as a recombinant antigen if the polypeptide
CC   reacts with the HEV-positive antiserum. The method is useful for
CC   identifying recombinant antigen immunoreactive with antibody induced by
CC   HEV. The enterically transmitted non-A/non-B hepatitis (ET-NANB (also
CC   known as HEV))-specific fragments are useful for identifying ET-NANB-
CC   derived cDNAs, which contain additional sequence information, as primers
CC   for detecting ET-NANB viral genomic material in a patient sample, for the
CC   synthesis of polypeptides for use in immunoassays, and for identifying
CC   similar antigenic regions encoded by related viral strains, e.g. Burmese
CC   strain. The antigens are especially useful in the preparation of vaccine
CC   against ET-NANB infection. These antigens may further be used to prepare
CC   antibodies to ET-NANB virus particles for use directly as antiviral
CC   agents, and to produce antiserum designed for pre- or post-exposure
CC   prophylaxis. The present sequence represents a specifically claimed HEV
CC   Burma strain protein sequence for use in the present invention
XX
SQ   Sequence 660 AA;

  Query Match             100.0%;  Score 2694;  DB 3;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1e-217;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291
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Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
```

RESULT 11
AAB62523
ID AAB62523 standard; protein; 660 AA.
XX
AC AAB62523;
XX
DT 23-JUL-2001 (first entry)
XX
DE HEV-Burma strain viral protein ORF2.
XX
KW HEV; enterically transmitted nonA/nonB viral hepatitis agent; viral;
KW ET-NANB; infection; vaccine.
XX
OS Hepatitis E virus.
XX
PN US6229005-B1.
XX
PD 08-MAY-2001.
XX
PF 03-AUG-1998; 98US-00128275.
XX
PR 17-JUN-1988; 88US-00208997.
PR 11-APR-1989; 89US-00336672.
PR 16-JUN-1989; 89US-00367486.
PR 13-OCT-1989; 89US-00420921.
PR 05-APR-1990; 90US-00505888.
PR 05-APR-1991; 91US-00681078.
PR 25-JUL-1994; 94US-00279823.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Reyes GR, Yarbough PO, Bradley DW, Krawczynski KZ, Tam AW;
PI Fry KE;
XX
DR WPI; 2001-342705/36.
DR N-PSDB; AAF83495.
XX
PT New DNA sequences of enterically transmitted non-A/non-B (ET-NANB)
PT hepatitis viral agent, useful in diagnosing infection by an enterically
PT transmitted agent (e.g. ET-NANB virus), as well as in vaccine production.
XX
PS Disclosure; Col 63-68; 45pp; English.
XX
CC The invention relates to an isolated DNA comprising the genome of an
CC enterically transmitted nonA/nonB (ET-NANB) viral hepatitis agent (also
CC referred as HEV). The DNA sequences or their fragments are useful in
CC preparing ET-NANB viral proteins and as probes for virus detection. These
CC are particularly useful in diagnosing infection by an enterically
CC transmitted agent (e.g. ET-NANB virus), as well as in vaccine production.
CC The present sequence represents a ORF2 protein encoded by a ET-NANB viral
CC DNA sequence from HEV-Burma strain
XX
SQ Sequence 660 AA;

Query Match 100.0%; Score 2694; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 1e-217;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
```

RESULT 12
AAO15699
ID AAO15699 standard; protein; 660 AA.
XX
AC AAO15699;
XX
DT 08-NOV-2002 (first entry)
XX
DE Hepatitis E virus (Burma strain) ORF2 protein.
XX
KW HEV; enterically transmitted nonA/nonB hepatitis viral agent;
KW Burma strain; bile; ORF2.
XX
OS Hepatitis E virus.
XX
PN US6379891-B1.
XX
PD 30-APR-2002.
XX
PF 19-APR-2000; 2000US-00553427.
XX
PR 17-JUN-1988; 88US-00208997.
PR 11-APR-1989; 89US-00336672.
PR 16-JUN-1989; 89US-00367486.

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PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   15-APR-1991;   91US-00681078.
PR   25-JUL-1994;   94US-00279823.
PR   07-JUN-1995;   95US-00478507.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Reyes GR,  Yarbough PO,  Bradley DW,  Krawczynski KZ,  Tam A,  Fry KE;
XX
DR   WPI; 2002-517277/55.
DR   N-PSDB; AAL50386.
XX
PT   Detecting the presence of enterically transmitted nonA/nonB hepatitis
PT   viral (HEV) agents in bile samples from infected humans and monkeys using
PT   polymerase chain reaction.
XX
PS   Disclosure; Col 19-24; 61pp; English.
XX
CC   The invention comprises a method for detecting the presence of
CC   enterically transmitted nonA/nonB hepatitis viral (HEV) agents in a
CC   sample and isolating HEV agents or nucleic acid fragments produced by the
CC   agent. The method utilises PCR - using bile from a human or cynomolgus
CC   monkey actively infected with HEV as a source of the agent. The method of
CC   the invention is used for detecting the presence of a viral agent in a
CC   sample of cultured cells infected with the agent and isolating
CC   enterically transmitted nonA/nonB HEV agents or nucleic acid fragments
CC   produced by the agent. The present amino acid sequence represents the
CC   protein encoded by open reading frame 2 (ORF2) of a DNA sequence isolated
CC   from a Burmese strain of the Hepatitis E virus
XX
SQ   Sequence 660 AA;

  Query Match             100.0%;  Score 2694;  DB 5;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1e-217;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
```

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RESULT 13
ADD24376
ID   ADD24376 standard; protein; 660 AA.
XX
AC   ADD24376;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Hepatitis E virus strain Burma ORF 2.
XX
KW   non-A/non-B viral hepatitis; ET-NANB; HEV; vaccine.
XX
OS   Hepatitis E virus; strain Burma.
XX
PN   US2003124510-A1.
XX
PD   03-JUL-2003.
XX
PF   07-MAY-2001; 2001US-00851410.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   25-JUL-1994;   94US-00279823.
PR   03-AUG-1998;   98US-00128275.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Reyes GR,  Yarbough PO,  Bradley DW,  Krawczynski KZ,  Tam AW;
PI   Fry KE;
XX
DR   WPI; 2003-810978/76.
DR   N-PSDB; ADD24374.
XX
PT   New proteins derived from an enterically transmitted non-A/non-B (ET-
PT   NANB) viral hepatitis agent, useful for diagnosing ET-NANB infection and
PT   producing vaccines for immunizing an individual against ET-NANB hepatitis
PT   viral agent.
XX
PS   Disclosure; SEQ ID NO 8; 81pp; English.
XX
CC   The invention relates to a protein derived from an enterically
CC   transmitted non-A/non-B viral hepatitis agent. The viral proteins are
CC   useful for detecting infection by the enterically transmitted non-A/non-B
CC   (ET-NANB/HEV) hepatitis viral agent. The proteins are also useful for
CC   producing vaccines for immunising an individual against HEV hepatitis
CC   viral agent. The DNA fragments are useful for identifying and sequencing
CC   the entire viral agent and for assaying the viral agent in an infected
CC   sample. The present sequence is used in the exemplification of the
CC   invention.
XX
SQ   Sequence 660 AA;

  Query Match             100.0%;  Score 2694;  DB 7;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 1e-217;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291
```

```
Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
```

RESULT 14
AAW76367
ID AAW76367 standard; protein; 549 AA.
XX
AC AAW76367;
XX
DT 03-DEC-1998 (first entry)
XX
DE Hepatitis E virus hollow particle protein ORF2.
XX
KW Hollow particle protein; virus; antibody; detection; immunoassay;
KW infection.
XX
OS Hepatitis virus.
XX
FH Key   Location/Qualifiers
FT Protein   1. .549
FT   /label= ORF2
FT   /note= "partial sequence"
XX
PN JP10234383-A.
XX
PD 08-SEP-1998.
XX
PF 28-FEB-1997; 97JP-00062445.
XX
PR 28-FEB-1997; 97JP-00062445.
XX
PA (DENK-) DENKA SEIKEN KK.
PA (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR WPI; 1998-535037/46.
DR N-PSDB; AAV61686.
XX
PT Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids
PT encoding it - useful for more accurate detection of HEV in samples, using
PT immuno-assays and nucleic acid hybridisation.
XX
PS Claim 1; Page 15-17; 29pp; Japanese.
XX
CC This sequence represents a Hepatitis E viral hollow particle protein
CC described as ORF2. This polypeptide can be used to raise antibodies to
CC detect HEV infection in samples, e.g. by immuno-assay based techniques,
CC and the nucleic acid can be used for the same in nucleic acid
CC hybridisation assays. The polypeptide and nucleic acid allow more
CC accurate detection of HEV than previously possible
XX

SQ Sequence 549 AA;

```
  Query Match             99.7%;  Score 2687;  DB 2;  Length 549;
  Best Local Similarity   99.8%;  Pred. No. 3.1e-217;
  Matches  524;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
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Db        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
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Db        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
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Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
```

RESULT 15
AAW76369
ID AAW76369 standard; protein; 660 AA.
XX
AC AAW76369;
XX
DT 03-DEC-1998 (first entry)
XX
DE Hepatitis E virus hollow particle protein #2.
XX
KW Hollow particle protein; virus; antibody; detection; immunoassay;
KW infection.
XX
OS Hepatitis virus.
XX
PN JP10234383-A.
XX
PD 08-SEP-1998.
XX
PF 28-FEB-1997; 97JP-00062445.
XX
PR 28-FEB-1997; 97JP-00062445.
XX
PA (DENK-) DENKA SEIKEN KK.
PA (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR WPI; 1998-535037/46.
DR N-PSDB; AAV61688.
XX
PT Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids

PT encoding it - useful for more accurate detection of HEV in samples, using
PT immuno-assays and nucleic acid hybridisation.
XX
PS Claim 13; Page 24-26; 29pp; Japanese.
XX
CC This sequence represents a Hepatitis E viral hollow particle protein.
CC This polypeptide can be used to raise antibodies to detect HEV infection
CC in samples, e.g. by immuno-assay based techniques, and the nucleic acid
CC can be used for the same in nucleic acid hybridisation assays. The
CC polypeptides and nucleic acids allow more accurate detection of HEV than
CC previously possible
XX
SQ Sequence 660 AA;

Query Match 99.7%; Score 2687; DB 2; Length 660;
Best Local Similarity 99.8%; Pred. No. 4e-217;
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
```

Search completed: July 14, 2005, 15:46:31
Job time : 44.4198 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 14, 2005, 02:26:53 ; Search time 9.08019 Seconds
(without alignments)
5563.078 Million cell updates/sec

Title: US-09-769-066-27
Perfect score: 2694
Sequence: 1 AVAPAHDTPPVPDVDSRGAI.....PARAHTFDDFCPECRPLGLQ 525

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2694	100.0	660	1	VHWWH2	structural protein
2	2542.5	94.4	659	1	B44212	structural protein
3	135.5	5.0	1041	2	S55862	probable membrane
4	129.5	4.8	2130	2	AB0821	probable exported
5	127	4.7	583	2	S67571	hypothetical prote
6	125.5	4.7	1306	2	S25370	MSB2 protein - yea
7	125.5	4.7	1879	2	S74915	extracellular nucl
8	125	4.6	3282	2	E82750	hemagglutinin-like
9	125	4.6	3442	2	E82589	hemagglutinin-like
10	125	4.6	3455	2	B82519	hemagglutinin-like
11	124.5	4.6	3570	2	T45025	mucin MUC5B, trach
12	122	4.5	1180	2	E86719	hypothetical prote
13	122	4.5	5188	2	B85547	probable RTX famil
14	122	4.5	5291	2	F90696	hypothetical prote
15	121.5	4.5	766	1	A47001	transcription fact
16	120.5	4.5	687	2	T09994	arginine-tRNA liga
17	120.5	4.5	1483	2	C97012	probably celluloso
18	120	4.5	636	2	S63131	probable membrane
19	120	4.5	1131	2	T41144	hypothetical serin
20	119.5	4.4	948	2	T11678	hypothetical prote
21	118	4.4	725	2	A41258	a-agglutinin core
22	117	4.3	1802	2	S69703	HKR1 protein precu
23	117	4.3	3972	2	S75251	hypothetical prote
24	116.5	4.3	796	2	T21460	hypothetical prote
25	116.5	4.3	918	2	T02759	hypothetical prote
26	116.5	4.3	1161	2	S57180	probable membrane
27	116	4.3	1367	1	S48478	glucan 1,4-alpha-g
28	115.5	4.3	1077	2	H96007	probable acriflavi
29	115.5	4.3	3507	2	T34513	hypothetical prote
30	115	4.3	1213	2	T51032	hypothetical prote
31	115	4.3	3083	2	AH2493	hypothetical prote
32	114.5	4.3	739	2	I56187	transcription fact
33	114	4.2	1350	2	AF2005	RNA polymerase bet
34	114	4.2	2054	2	T46612	multi PDZ domain p
35	113.5	4.2	1419	2	T30531	agglutinin-like ad
36	113.5	4.2	4199	2	S76412	hypothetical prote
37	113	4.2	2383	2	D64962	probable membrane
38	112.5	4.2	547	2	T41213	probable zinc fing
39	112.5	4.2	1014	1	NMCLSS	exo-alpha-sialidas
40	112.5	4.2	1324	2	S52863	DNA-binding protei
41	112.5	4.2	3013	2	AB0480	probable invasin Y
42	112	4.2	4753	1	A47437	LDL-receptor-relat
43	111.5	4.1	1104	2	S59310	probable membrane
44	110.5	4.1	448	2	AB3043	oxidoreductase Atu
45	110.5	4.1	468	2	B98243	hypothetical prote

ALIGNMENTS

RESULT 1
VHWWH2
structural protein 2 precursor - hepatitis E virus (strain Burma)
C;Species: hepatitis E virus
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: C40778
R;Tam, A.W.; Smith, M.M.; Guerra, M.E.; Huang, C.C.; Bradley, D.W.; Fry, K.E.; Reyes, G.P
Virology 185, 120-131, 1991
A;Title: Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length vi
A;Reference number: A40778; MUID:92024067; PMID:1926770
A;Accession: C40778
A;Molecule type: genomic RNA
A;Residues: 1-660 <TAM>
A;Cross-references: UNIPROT:P29326; GB:M73218; NID:g330023; PIDN:AAA45736.1; PID:g330026
A;Note: the authors translated the codon CGC for residue 2 as Ala
C;Superfamily: hepatitis E virus structural protein 2
C;Keywords: structural protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-660/Product: structural protein 2 #status predicted <SP2>

Query Match 100.0%; Score 2694; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 6.7e-180;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
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Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
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Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531
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Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
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Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 2
B44212
structural protein 2 precursor - hepatitis E virus (strain Mexico)
C;Species: hepatitis E virus
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: B44212
R;Huang, C.C.; Nguyen, D.; Fernandez, J.; Yun, K.Y.; Fry, K.E.; Bradley, D.W.; Tam, A.W.
Virology 191, 550-558, 1992
A;Title: Molecular cloning and sequencing of the Mexico isolate of hepatitis E virus (HE
A;Reference number: A44212; MUID:93079857; PMID:1448913
A;Accession: B44212
A;Molecule type: genomic RNA
A;Residues: 1-659 <HUA>
A;Cross-references: UNIPROT:Q03500; GB:M74506; NID:g330017; PIDN:AAA45732.1; PID:g330020
C;Superfamily: hepatitis E virus structural protein 2
C;Keywords: structural protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-659/Product: structural protein 2 #status predicted <SP2>

  Query Match             94.4%;  Score 2542.5;  DB 1;  Length 659;
  Best Local Similarity   94.1%;  Pred. No. 2.4e-169;
  Matches  494;  Conservative   13;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              |||||||| ||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||  ||||||||||||||   ||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||:|||||||||||||||||||:|||||||| |::|
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              ||:||| ||||| ||||||||| ||| |||||||||||||| ||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 635


RESULT 3
S55862
probable membrane protein YNL327w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N0320
C;Species: Saccharomyces cerevisiae
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55862; S63308; S51288
R;Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin, C.
Yeast 11, 567-572, 1995
A;Title: Sequencing analysis of a 15.4 kb fragment of yeast chromosome XIV identifies the
A;Reference number: S55859; MUID:95373280; PMID:7645347
A;Accession: S55862
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1041 <MAF>
A;Cross-references: UNIPROT:P42835; EMBL:Z46259; NID:g633655; PIDN:CAA86371.1; PID:g63365
R;Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin, C.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63287
A;Accession: S63308
A;Molecule type: DNA
A;Residues: 1-1041 <MAW>
A;Cross-references: EMBL:Z71603; NID:g1302444; PID:e239572; PID:g1302445; MIPS:YNL327w
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:EGT2
A;Cross-references: SGD:S0005271; MIPS:YNL327w
A;Map position: 14L
C;Keywords: transmembrane protein
F;4-20/Domain: transmembrane #status predicted <TM1>
F;1025-1041/Domain: transmembrane #status predicted <TM2>

  Query Match              5.0%;  Score 135.5;  DB 2;  Length 1041;
  Best Local Similarity   20.6%;  Pred. No. 0.28;
  Matches  125;  Conservative   82;  Mismatches  211;  Indels  189;  Gaps   27;

Qy         29 TSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEASNYAQYRVAR---ATIRYRP 85
              |:| :|  || |  :: :| :|        :|    |::::      |    :|: |
Db        405 TTPSSSLSATETYSIISSASISVTQASYIDNSTTTAVTQSTSTIAVSSAEKLSSTLSY-- 462

Qy         86 LVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQ 145
                    ||:|   | ||||: |  || | :   :|
Db        463 -----TSNVTISVSSATQHTTTPSYVS-NSTTLSSSSVL---------------------- 495

Qy        146 GWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPY---------TGALGLLDFALELE 196
              || :|         ||         |  :  || ||          |    :  ||: :
Db        496 --ESVISSPYLANTTVSG-------ASSASQSTNPPYVSNSTTSSATQLATIAPFAINIT 546

Qy        197 FRNLTPGNTNTRVSRYSSTARHRLRRG--------ADGTAELTTTAATRFMKDL------ 242
              :::   |||  |  |||    |  |         | |:  ||||  :  : ::
Db        547 GTSISSSITNT--SSVSSTT-SSLSSGPFVSNTAVASGSYILTTTTESAQLTEIGSLIPI 603

Qy        243 ----YFTSTNGVGEIGRG-------IALTLFNLADTLLGGLPTELISSA---------- 280
                  |:|:|  : |          || :: | :   :  : |   ::|
Db        604 STITTSTTTSGTDKTGSNKVASSTEIAQSIVNNSSLSVSTINTNAATAAANARNATFTHA 663

Qy        281 --GGQL---FYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQ 335
                | |   ::|  ::|:  :   |: |:  :  :|   ::      | :| |   |
Db        664 THSGSLQPSYHSSSLLSSTID--TKVTTATTSTSRDGSSSLAFTTGLNQSVVTGTD---- 717

Qy        336 HEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQ----STY------GSSTGPVYVSD 385
                        |  :||: : :    |   |||     ||        |:|    :
Db        718 -----------KSDTYSVISSTE----SAQVTEYDSLLPISTLKPTVVTGTSRNSTFSMV 762

Qy        386 SVTLVNVATG-----AQAVARSLDWTKVTLDGR--PLSTIQ------------------ 419
              | | :  ||       | :|  |    :|| |   |:||::
Db        763 SSTKLTEATATDKGDAYSVISSTQSAQVTEYGSMLPISTLETPTVIMSTDESGYFTLTTC 822

Qy        420 -------QYSKTFFVLPLRGKLSFWEAG--------TTKAGYPYNYNTTASDQLLVENAA 464
                    :|      :  | | : :   |         ||      |  :|:    : |
Db        823 TESGQATEYGSLIPISTLDGSVIYTFTGESVVVGYSTTVGAAQYAQHTSL---VPVSTIK 879

Qy        465 GHRVAIST-------YTTSLGAG---------PVSI---SAVAVLAPHSALALLEDTLDY 505
              | : ::||       |:|::||          |||    |  ::    | :|    |:|
Db        880 GSKTSLSTEESVVAGYSTTVGAAQYAQHTSLVPVSTIKGSKTSLSTEESVVAGYSTTVDS 939

Qy        506 PARA-HT 511
```

Db 940 AQYAEHT 946

RESULT 4
AB0821
probable exported protein STY2760 [imported] - Salmonella enterica subsp. enterica serov
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB0821
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0821
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2130 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02718.1; PID:g16503731; GSPDB:GN00176
C;Genetics:
A;Gene: STY2760

Query Match 4.8%; Score 129.5; DB 2; Length 2130;
Best Local Similarity 21.4%; Pred. No. 2.1;
Matches 108; Conservative 59; Mismatches 217; Indels 121; Gaps 21;

Qy 28 STSPLTSSVATGTNLVLYAAPLSPLLPLQ--DGTNTHIMATEASNYAQYRVARATIRYRP 85
Db 985 NTSVYTSCLAS-DNPVPAAITIEPVDPSQWYDGSGVHALKVKKGDTLQLKVTVKDASGKP 1043

Qy 86 LVPNAV------GGYAISISFWP-------QTTTTPTSVDMNSITSTDVRILVQPGIASE 132
Db 1044 -VPEAPFVLTRGDGYDRKGEKYTAQDGSDLQNIVTPVVIDGESLAWTTTKMGSQTGPDGT 1102

Qy 133 LVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFA 192
Db 1103 RIISVTRPD--THGTRTAITATLYENVAVSASI------DTIFTVVTSP--------DVS 1146

Qy 193 LELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAE--------------LTTTAATR 237
Db 1147 VARMWGHMTPSLTAADSAVYKRPLLYDELASKTGAAEYPEDNERWVVFYGPNTTKTVSPE 1206

Qy 238 FMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEP 297
Db 1207 ACSKGYFPSVEQL--------------DSLYSKYPNGAIK------------TAQGWP 1238

Qy 298 TVKLYTSVENAQQDKGIAIPHD---IDLGES--RVV--IQDYDNQHEQDRPTPSPAPSRP 350
Db 1239 IIRSYWSGTNAGTITPGAPPYDYYTVDLNDDAHRKVPNISDSDRQYQICAATPQPLAGR- 1297

Qy 351 FSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTL 410
Db 1298 --------ITLTSTLATDSDIQAVKAKN-----SDSIPL--VITTTDAAGNPVPYTPFSL 1342

Qy 411 DGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYN------TTASDQLLVENAA 464
Db 1343 I-RDAGTARNTSYTF-----TGSTNMMLAPPTGSAQQFYYNGYTIYGATGAD-------- 1388

Qy 465 GHRVAISTYTTSLGAGPVSISAVAV 489
Db 1389 --GTAVLTLTQAAGPGVKNVITAAL 1411

RESULT 5
S67571
hypothetical protein YDL038c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein D2726
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C;Accession: S67571
R;Paulin, L.; Saren, A.M.; Laamanen, P.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67560
A;Accession: S67571
A;Molecule type: DNA
A;Residues: 1-583 <PAU>
A;Cross-references: UNIPROT:Q99175; EMBL:Z74087; NID:g1431021; PID:e252991; PID:g1431023;
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YDL038c
A;Cross-references: SGD:S0002196
A;Map position: 4L
C;Superfamily: pig submaxillary mucin

Query Match 4.7%; Score 127; DB 2; Length 583;
Best Local Similarity 20.6%; Pred. No. 0.47;
Matches 106; Conservative 82; Mismatches 241; Indels 86; Gaps 17;

Qy 28 STSPLTSS-VATGTNLVLYAAPLSPLLPLQD---GTNTHIMATEASNYAQYRVARATIRY 83
Db 79 SIDPTSSSDVITSTVQTTSIEPTTSLVSSNDITTSTSLNISVVISTSTDSTSLIESTTTV 138

Qy 84 RPLVPNAVGG-YAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIAS---ELVIPSER 139
Db 139 GPHASSSVAGMYRTRSSDEVTTSTDPTS-------SSDVATSADPTSSSAVTTLVDPTTS 191

Qy 140 LHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFALELEFRN 199
Db 192 V---------VISTSVDQTSSSDVATSVDPTTSVISSTSADPTTSA------------DS 230

Qy 200 LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIAL 259
Db 231 TTSTVQTTSVDPTSSVVSSAPVDPASSVVSLTSSYPTSSSTVTISANSNGSATLA----- 285

Qy 260 TLFNLADTLLGGLPTELISSAGGQLFYSRP--------VVSANGEPTVKLYTSVE-NAQQ 310
Db 286 -----AQTTSIDPVSSIVSSSGATTIISSASIDPASSVVSSTSSEPTSFIVSSTSVYSTR 340

Qy 311 DKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYD 370
Db 341 PSGPTTSTDLATFSDTIILRVSTTSTSQDTQTVSSSLTDMVSSTGSADLSVSSIQRSQVD 400

Qy 371 QSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTK------------VTLDGRPLSTI 418
Db 401 PSTFAVSNSPVYPTASTG--STSTGIPIASESLSLSRQQGISATSSSSIVTLTPVDSASS 458

Qy 419 QQYSKTFFVLP----------LRGKLSFWEA-GTTKAGYP----YNYNTTASDQLLV-EN 462
Db 459 SRSSATSIIKPNMPVSSNDSKTQSSVSVVDAFQSTKSSYPSITSADPTTLASENGLVGSS 518

Qy 463 AAGHRVAIS-TYTTSLGAGPVSISAVAVLAPHSAL 496
Db 519 SSAHPITLDRTYASAHASVTDIVSRVTDSTRHTTL 553

RESULT 6
S25370
MSB2 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein G4017; protein YGR014w
C;Species: Saccharomyces cerevisiae
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S25370; S64305
R;Bender, A.; Pringle, J.R.
Yeast 8, 315-323, 1992
A;Title: A Ser/Thr-rich multicopy suppressor of a cdc24 bud emergence defect.
A;Reference number: S25370; MUID:92383951; PMID:1514328
A;Accession: S25370
A;Molecule type: DNA
A;Residues: 1-1306 <BEN>
A;Cross-references: UNIPROT:P32334; GB:M77354; NID:g171993; PIDN:AAA34798.1; PID:g171994
R;Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996

A;Reference number: S64071
A;Accession: S64305
A;Molecule type: DNA
A;Residues: 1-1306 <RIE>
A;Cross-references: EMBL:Z72799; NID:g1322977; PID:g1322978; MIPS:YGR014w
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:MSB2
A;Cross-references: SGD:S0003246; MIPS:YGR014w
A;Map position: 7R
C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase
C;Keywords: transmembrane protein
F;3-19/Domain: transmembrane #status predicted <TM1>
F;1189-1205/Domain: transmembrane #status predicted <TM2>

Query Match 4.7%; Score 125.5; DB 2; Length 1306;
Best Local Similarity 19.9%; Pred. No. 1.9;
Matches 110; Conservative 91; Mismatches 212; Indels 141; Gaps 24;

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Qy         27 LSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEASNYAQYRVARATIRYRP- 85
Db        441 LDSSSLASSSASSSDLTDYGVSSTASIPLLSASE------QASTSSSFSVVSPSVSFVPS 494

Qy         86 ---------LVPNAV-----------GG-----------YAISISFWPQTTTTPTSVDM 113
Db        495 QSSSDVASTSAPSVVSSSFSYTSLQAGGSSMTNPSSSTIVYSSSTGSSEESAASTASATL 554

Qy        114 NSITSTDV--RILVQPGIASELVIPSERLH---------------YRNQGW--------- 147
Db        555 SGSSSTYMAGNLQSQPPSTSSLLSESQATSTSAVLASSSVSTTSPYTTAGGASTEASSLI 614

Qy        148 --RSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTG-----ALGLLDFALELEFRNL 200
Db        615 SSTSAETSQVSYSQSTTALQTSSFASSSTTEGSETSSQGFSTSSVLVQMPSSISSEF--- 671

Qy        201 TPGNTNTRVSRYSSTARHR------LRRGADGTAELTTTAAT-RFMKDL---YFTSTNGV 250
Db        672 SPSQTTTQMNSASSSSQYTISSTGILSQVSDTSVSYTTSSSSVSQVSDTPVSYTTSSSSV 731

Qy        251 GEIG-RGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQ 309
Db        732 SQVSDTPVSYTTSSSSVSQVSDTPVSYTTSSSS--------VSQVSDTPVSYTTSSSSVS 783

Qy        310 QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAE- 368
Db        784 QVSDTSVPST----SSRSSV-------SQVSDTPVPSTSSRSSVSQTSSSLQPTTTSSQR 832

Qy        369 YDQSTYGSSTGPVYVSDSVTLVNVATGAQAVA-RSLDWTKVTLDGRPLSTIQQYSKTFFV 427
Db        833 FTISTHGALSESSSVSQQASEITSSINATASEYHSIQTTAAT----------QSTT--- 878

Qy        428 LPLRGKLSFWEAGTTKAGYPYNYNTT-------ASDQLLVENAAG-HRVAIST-YTTSLG 478
Db        879 ------LSFTDANSSSASAPLEVATSTPTPSSKASSLLLTPSTSSLSQVATNTNVQTSL- 931

Qy        479 AGPVSISAVAVLAP 492
Db        932 ----TTESTTVLEP 941
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RESULT 7
S74915
extracellular nuclease - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein sll0656
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74915
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis s.

A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74915
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1879 <KAN>
A;Cross-references: UNIPROT:P72938; EMBL:D90902; GB:AB001339; NID:g1652027; PIDN:BAA1695
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: nucH
A;Start codon: GTG

Query Match 4.7%; Score 125.5; DB 2; Length 1879;
Best Local Similarity 20.6%; Pred. No. 3.3;
Matches 118; Conservative 72; Mismatches 196; Indels 187; Gaps 26;

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Qy         28 STSPLTSSVATGTNLVLYAAPLSPLLPLQD--------GTNT-HIMATEASNYAQYRVAR 78
Db        466 NAAPVTVSVANGVNNLLENANTTSAIKLGNIIIGDDSLGTNTLSLSGADASNF------- 518

Qy         79 ATIRYRPLVPNAV-------------GGYAISISFWPQTT-TTPTSVDMNSITSTDVRIL 124
Db        519 ------EIVGNGLFLKAGTVLDFSTQSSYEVTIAVDDATLGNTP-----DAITTFTLDIT 567

Qy        125 VQPGIASELVIPSERLHYRNQGWRSVETSGVAE--EEATSGLVMLCIHGSLVN----SYT 178
Db        568 NTAGI-SDLIISEV------APWSSGNSSVGADWFEVTNTGANAIDITGWKVDDDSASFA 620

Qy        179 NTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRF 238
Db        621 NASALAGV-----------TNIAPGQSVVFV---------------DGDAN-TITA---- 649

Qy        239 MKDLYFTSTNGVG-EIGR---------GIALTLFNLADTLLGGLPTELISSAGGQLFYSR 288
Db        650 FIDLWFGGTAPAGLAIGTYGGPGLGTGGDAINLFDATGSLITG---------------- 692

Qy        289 PVVSANGEPTVKLYTSVENAQQDKGIAIPHD---------IDLGE--------------- 324
Db        693 --VTFGSSPSTSPFSTFDNALGNPSVANLSTVGSNGAFSVIDAGEGVILNGSPGAIAGSV 750

Qy        325 ---SRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYG-SSTGP 380
Db        751 SSNTTVGIAATGATGSENGPTPG-----EFTILRTGD----TSTALDVTYSISGDAANGT 801

Qy        381 VYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAG 440
Db        802 DYAAIDPTTVTIPAGQSQVKISIN---------PIDDVIIESTESIVITLTDTANYDVAT 852

Qy        441 TTKAG--------YPYNYNTTASDQLLVENAAGHRVAISTYTTS-------------LGA 479
Db        853 SASSATVNIEDNDTPITVSRLQITEFMYSGADGEFIEFTNIDTSSVDMTGWSFSDSGRVA 912

Qy        480 GPVSISAVAVLAPHSALALLEDTLDYPARAHTF 512
Db        913 GSVDLSAFGVVQPGESVILTE------ADAETF 939
```

RESULT 8
E82750
hemagglutinin-like secreted protein XF0889 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82750
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82750
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3282 <SIM>
A;Cross-references: UNIPROT:Q9PEY9; GB:AE003928; GB:AE003849; NID:g9105798; PIDN:AAF8369
A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0889

Query Match 4.6%; Score 125; DB 2; Length 3282;
Best Local Similarity 21.6%; Pred. No. 8;
Matches 130; Conservative 63; Mismatches 212; Indels 196; Gaps 26;

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Qy          1 AVAPAHDTP------PVP-----------------DVDSRGAILRRQYNLSTSPLTSSV 36
              :| || |||      |:|                  |:|:|| :     :     |
Db        439 SVPPATDTPPSTGTMPIPSHPQTAPVLAAGRLTLENDIDNRGGHITAGGAIDAILTTLDN 498

Qy         37 ATGTNLVLYAAPLSPL-LPLQDGTNTH---IMATEA-------SNYAQYRVARATIRYRP 85
                ||      | |: | |  |   | |   :||||       :| |       |:
Db        499 RDGT------AALNRLTLQGQRLDNQHGILTLATEATIHTHTLNNAAGQLHVNGTLDLTA 552

Qy         86 LVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQ 145
                 |   |: ::    ||: |  |  |:   ||  :         |  | : :  |
Db        553 QHLNNASGHLLTTG--PQSATL-TIADLLDNTSGTL------ASAGSLTLTAATL----- 598

Qy        146 GWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFALELEFRNLTPGNT 205
                       : | | |          ::: | | : | |   |          ||   |
Db        599 ------------DTTDGTVQSGQGPLHMDAATLTAHRGTLTSQD--------TLTLTGT 637

Qy        206 NTRVSRYSSTAR--------------------HRLRRGA-------------DGTAELT 231
              :| :|  ::||:                    | |:  |             :|| :|
Db        638 HTDLSHATTTAQQITLHTGDLTTAGGHLTAYGTHTLQLEARTRLDNTGGTIATNGTLDLH 697

Qy        232 TTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELI----SSAGGQLFYS 287
                | |        |: |:|   |      |  || | |  ||   || |      :: || |  :
Db        698 TAALDNTGGTLHSTAT---GPNRLDITDTLTNTAGHLLLNGPTTLTTGTWTNTGGHLQIT 754

Qy        288 RPVV-------------SANGEPTVKLYTSVENAQQDKGIAIPHD-IDLGESRVVIQDY 332
                |              :| |   :::  :: |  || |:    | : |  : ::
Db        755 GPATLHATTLDNRGGILHTATGPLDLRITGTLNN--QDNGLLTTTDALTLTAASLL---- 808

Qy        333 DNQH-EQDRPTPSPAP-----SRPFSVLRANDVLWL----------SLTAAEYDQSTYGS 376
               |||   |   |:          :|:   |||          :|||::    | |
Db        809 -NQHGTLDAAGPAHLTLTGLLDNTAGLLQTAHTLWLTSAGLTNRSGTLTASQLTLDTQGH 867

Qy        377 S-----------------TGPV-------------YVSDSVTLVNVATGAQAVARSLD 404
              :                 :||:               : : || |   ||   | :||
Db        868 TLDNTRGRLGTTTGNLTLHSGPLDNTAGLLQTAAALTIDTGAATLTNRDGGALLAATALD 927

Qy        405 WTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAA 464
               |  ||| |   ||  : |          |          | ||:  :  |   |  : |
Db        928 LTTATLDNRG-GTIDSQTAT--------HLHTTTLDNTTAGHISSSGTLQIDGTTLTNTG 978

Qy        465 G 465
              |
Db        979 G 979
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RESULT 9
E82589
hemagglutinin-like secreted protein XF2196 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82589
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82589
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3442 <SIM>
A;Cross-references: UNIPROT:Q9PBE8; GB:AE004032; GB:AE003849; NID:g9107324; PIDN:AAF8499
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2196

Query Match 4.6%; Score 125; DB 2; Length 3442;
Best Local Similarity 21.6%; Pred. No. 8.5;
Matches 130; Conservative 63; Mismatches 212; Indels 196; Gaps 26;

```
Qy          1 AVAPAHDTP------PVP-----------------DVDSRGAILRRQYNLSTSPLTSSV 36
              :| || |||      |:|                  |:|:|| :     :     |
Db        439 SVPPATDTPPSTGTMPIPSHPQTAPVLAAGRLTLENDIDNRGGHITAGGAIDAILTTLDN 498

Qy         37 ATGTNLVLYAAPLSPL-LPLQDGTNTH---IMATEA-------SNYAQYRVARATIRYRP 85
                ||      | |: | |  |   | |   :||||       :| |       |:
Db        499 RDGT------AALNRLTLQGQRLDNQHGILTLATEATIHTHTLNNAAGQLHVNGTLDLTA 552

Qy         86 LVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQ 145
                 |   |: ::    ||: |  |  |:   ||  :         |  | : :  |
Db        553 QHLNNASGHLLTTG--PQSATL-TIADLLDNTSGTL------ASAGSLTLTAATL----- 598

Qy        146 GWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFALELEFRNLTPGNT 205
                       : | | |          ::: | | : | |   |          ||   |
Db        599 ------------DTTDGTVQSGQGPLHMDAATLTAHRGTLTSQD--------TLTLTGT 637

Qy        206 NTRVSRYSSTAR--------------------HRLRRGA-------------DGTAELT 231
              :| :|  ::||:                    | |:  |             :|| :|
Db        638 HTDLSHATTTAQQITLHTGDLTTAGGHLTAYGTHTLQLEARTRLDNTGGTIATNGTLDLH 697

Qy        232 TTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELI----SSAGGQLFYS 287
                | |        |: |:|   |      |  || | |  ||   || |      :: || |  :
Db        698 TAALDNTGGTLHSTAT---GPNRLDITDTLTNTAGHLLLNGPTTLTTGTWTNTGGHLQIT 754

Qy        288 RPVV-------------SANGEPTVKLYTSVENAQQDKGIAIPHD-IDLGESRVVIQDY 332
                |              :| |   :::  :: |  || |:    | : |  : ::
Db        755 GPATLHATTLDNRGGILHTATGPLDLRITGTLNN--QDNGLLTTTDALTLTAASLL---- 808

Qy        333 DNQH-EQDRPTPSPAP-----SRPFSVLRANDVLWL----------SLTAAEYDQSTYGS 376
               |||   |   |:          :|:   |||          :|||::    | |
Db        809 -NQHGTLDAAGPAHLTLTGLLDNTAGLLQTAHTLWLTSAGLTNRSGTLTASQLTLDTQGH 867

Qy        377 S-----------------TGPV-------------YVSDSVTLVNVATGAQAVARSLD 404
              :                 :||:               : : || |   ||   | :||
Db        868 TLDNTRGRLGTTTGNLTLHSGPLDNTAGLLQTAAALTIDTGAATLTNRDGGALLAATALD 927

Qy        405 WTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAA 464
               |  ||| |   ||  : |          |          | ||:  :  |   |  : |
Db        928 LTTATLDNRG-GTIDSQTAT--------HLHTTTLDNTTAGHISSSGTLQIDGTTLTNTG 978

Qy        465 G 465
              |
```

```
Db        979 G 979


RESULT 10
B82519
hemagglutinin-like secreted protein XF2775 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82519
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: B82519
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3455 <SIM>
A;Cross-references: UNIPROT:Q9P9U6; GB:AE004082; GB:AE003849; NID:g9108003; PIDN:AAF8556
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2775

  Query Match             4.6%;  Score 125;  DB 2;  Length 3455;
  Best Local Similarity   21.6%;  Pred. No. 8.6;
  Matches  130;  Conservative   63;  Mismatches  212;  Indels  196;  Gaps   26;

Qy          1 AVAPAHDTP------PVP-----------------DVDSRGAILRRQYNLSTSPLTSSV 36
              :| || |||      |:|                |:|:||  :     :        |
Db        439 SVPPATDTPPSTGTMPIPSHPQTAPVLAAGRLTLENDIDNRGGHITAGGAIDAILTTLDN 498

Qy         37 ATGTNLVLYAAPLSPL-LPLQDGTNTH---IMATEA-------SNYAQYRVARATIRYRP 85
                ||       | |: | |  |    | |    :||||       :| |         |:
Db        499 RDGT------AALNRLTLQGQRLDNQHGILTLATEATIHTHTLNNAAGQLHVNGTLDLTA 552

Qy         86 LVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQ 145
                |   |: ::    ||: |  |  |:   ||  :         |  | : :  |
Db        553 QHLNNASGHLLTTG--PQSATL-TIADLLDNTSGTL------ASAGSLTLTAATL----- 598

Qy        146 GWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFALELEFRNLTPGNT 205
                      : | | |          ::: | | : | |   |             ||   |
Db        599 -------------DTTDGTVQSGQGPLHMDAATLTAHRGTLTSQD--------TLTLTGT 637

Qy        206 NTRVSRYSSTAR---------------------HRLRRGA-------------DGTAELT 231
              :| :|  ::||:                     | |:  |             :|| :|
Db        638 HTDLSHATTTAQQITLHTGDLTTAGGHLTAYGTHTLQLEARTRLDNTGGTIATNGTLDLH 697

Qy        232 TTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELI----SSAGGQLFYS 287
              | |        |: |:|    |      |  || | |  ||   || |      :: || |  :
Db        698 TAALDNTGGTLHSTAT---GPNRLDITDTLTNTAGHLLLNGPTTLTTGTWTNTGGHLQIT 754

Qy        288 RPVV--------------SANGEPTVKLYTSVENAQQDKGIAIPHD-IDLGESRVVIQDY 332
              |                :| |   :::  :: | || |:    | : |  : ::
Db        755 GPATLHATTLDNRGGILHTATGPLDLRITGTLNN--QDNGLLTTTDALTLTAASLL---- 808

Qy        333 DNQH-EQDRPTPSPAP-----SRPFSVLRANDVLWL----------SLTAAEYDQSTYGS 376
               |||    |   |:             :|:    |||          :|||::    | |
Db        809 -NQHGTLDAAGPAHLTLTGLLDNTAGLLQTAHTLWLTSAGLTNRSGTLTASQLTLDTQGH 867
```

```
Qy        377 S-----------------TGPV-------------YVSDSVTLVNVATGAQAVARSLD 404
              :                 :||:                : : || |   ||   | :||
Db        868 TLDNTRGRLGTTTGNLTLHSGPLDNTAGLLQTAAALTIDTGAATLTNRDGGALLAATALD 927

Qy        405 WTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAA 464
               |  ||| |   ||  : |          |       | ||:  :  |   |   : |
Db        928 LTTATLDNRG-GTIDSQTAT--------HLHTTTLDNTTAGHISSSGTLQIDGTTLTNTG 978

Qy        465 G 465
              |
Db        979 G 979


RESULT 11
T45025
mucin MUC5B, tracheobronchial [imported] - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45025
R;Desseyn, J.L.; Guyonnet-Duperat, V.; Porchet, N.; Aubert, J.P.; Laine, A.
J. Biol. Chem. 272, 3168-3178, 1997
A;Title: Human mucin gene MUC5B, the 10.7 kb large central exon encodes various alternate
A;Reference number: Z22899; MUID:97166151; PMID:9013550
A;Accession: T45025
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3570 <DES>
A;Cross-references: EMBL:Z72496; NID:g1834502; PIDN:CAA96577.1; PID:g1834503
A;Experimental source: placenta
C;Genetics:
A;Gene: MUC5B

  Query Match             4.6%;  Score 124.5;  DB 2;  Length 3570;
  Best Local Similarity   19.8%;  Pred. No. 9.8;
  Matches  112;  Conservative   56;  Mismatches  252;  Indels  147;  Gaps   19;

Qy          8 TPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAP-LSPLLPLQDGTNTHIMAT 66
              | | | |             ||| |:  || :      ::|  :  ||:   | |   ||
Db       2892 TAPPPKV------------LTSPATTPTATSSKATSSSSPRTATTLPVLTSTATKSTAT 2938

Qy         67 EASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSI---------- 116
                :                |:  : :|    :    |: ||||  :  |::|
Db       2939 SVT--------------PIPSSTLG----TTGTLPEQTTTPVAT-MSTIHPSSTPETTH 2978

Qy        117 TSTDVRILVQPGIASELVIPSERLHYRNQGWRSVE----------TSGVAEEEATSGLVM 166
              ||| :           |    ||          |   |              |   |  :| |
Db       2979 TSTVLTTKATTRATSSTSTPSST---PGTTWILTELTTAATTTAGTGPTATPSSTPGTTW 3035

Qy        167 LCIHGSLVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADG 226
              :     |  : | |  ||:   |        :   | | |  :  |||      :   |
Db       3036 ILT--ELTTTATTTASTGSTATLSSTPGTTWILTEPSTTATVTAPPGSTATASSTQATAG 3093

Qy        227 TAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFY 286
              |  ::||| |  :     ||:          | | |  |  |  |    |   :      |
Db       3094 TPHVSTTATTPTV-----TSSKATPSSSPGTATALPALRSTATTPTATSFTAIPSSSLGT 3148

Qy        287 SRPVVSANGEPTVKLYTSVENAQQDK-----------------GIAIPHDIDLGESRVV 328
              :   :|     ||  : |:  ::  :                 :| |
Db       3149 TWTRLSQTTTPTATMSTATPSSTPETVHTSTVLTTTATTTGATGSVATPSSTP------- 3201

Qy        329 IQDYDNQHEQDRP---------TPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTG 379
                      |          ||| :|    :       :|:| |        |  ::|
Db       3202 ----GTAHTTKVPTTTTTGFTATPSSSPGTALT-----PPVWISTT-------TTPTTTT 3245

Qy        380 PVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEA 439
              |     :||  ::  |    || | |  |:                        | ::   :
Db       3246 PTTSGSTVTPSSI-PGTTHTARVLTTTTTTV------------------ATGSMATPSS 3285

Qy        440 GTTKAGYPYNYNTTASDQLLVENAAGH---------RVAISTYTTSLGAGPVSISAVAVL 490
               |  :| | :  |||:        | |                |     ||:   | :|:|
Db       3286 STQTSGTPPSLTTTAT----TITATGSTTNPSSTPGTTPIPPVLTSMATTPAATSSKATS 3341

Qy        491 APHSALALLEDTLDYPARAHTFDDFCP 517
```

```
Db       3342 SSSPRTATTLPVLTSTATKSTATSFTP 3368


RESULT 12
E86719
hypothetical protein yhgD [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86719
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: E86719
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1180 <STO>
A;Cross-references: UNIPROT:Q9CHH4; GB:AE005176; PID:g12723674; PIDN:AAK04855.1; GSPDB:G
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: yhgD

  Query Match             4.5%;  Score 122;  DB 2;  Length 1180;
  Best Local Similarity   19.8%;  Pred. No. 2.9;
  Matches  124;  Conservative   76;  Mismatches  205;  Indels  220;  Gaps   31;

Qy         26 NLSTSPLT-----SSVATGTNLVLYAAPLSPLLP----LQDGTNTHIMATE---ASNYAQ 73
              ||:  | |      :||::||           |:|       | :|:   ||   :|||| 
Db         49 NLAFQPKTEKAQAASVSSGT-----------LVPGNTSYDTGGHTY-SGTEFANSSNYAL 96

Qy         74 YRVARATIRYRPLVPNAVGGYAI-----SISFWPQTT--TPTSVDMNSITS-TD----- 120
              |  |     :  || :     :     |:|    ||  |  ::: ::| :| ||     
Db         97 YGKAVVASNWINLVSSTANSVGLGIFNGSVSAISATTGPTLKSTIKVDSGSSLTDFTKSG 156

Qy        121 --VRILVQPGIASELVIPSE--------------------RLHYRN------------ 144
                : :::     ::|   ::                   |  | |            
Db        157 DAIGVILTGASKAQLAANAQSSQATNDGLGIRGLPNTVFLGRDLYSNLSNVSTGSLTGID 216

Qy        145 -----QGW----------RSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLL 189
                   ||           |: ::||  :       |     :  : |:   | ||     
Db        217 GSATVNGWTDGPGVVMAIRNTDSSGTLQAANYPSLGSAAPYSPVTNTQNGTAYT------ 270

Qy        190 DFALELEFR-----------------NLTPGNTNTRVSRYSSTARHRLRRGADGTAELTT 232
               || :  :                  ||  |||  : |:|                ||  
Db        271 -FATDTSYALGVASPITSSVQEPITVTWTPDATNTASTGYTS-----------GTLTFNL 318

Qy        233 TAATRFMKDLYFTSTNGV--------GEIGRGIALTLFNLADTLLGGLPTELISSAGGQL 284
                |          |::||         |  |      |  || ::|  |     :   ||  
Db        319 IAQ---------TTSNGALIGASAVNGGTGGYTLTTHTNLQNSLTVG----FVGGTGGN- 364

Qy        285 FYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPS 344
               |     || ||          ::  ::  : : |                :| |     : |  
Db        365 -YGNLSVSLNG-------ATITGSKGTEPVPI--------------NYLN-----KVTGQ 397

Qy        345 PAPSRPFSVLRA--NDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARS 402
               | ||    | :  | || :  :|||          |||  |   : :  :     || || : :
Db        398 PIPSMAQSSITANVNDTIGAALTAP--------SSTSPDNNTYTYVVPAAPTGYQANSAT 449

Qy        403 LDWTKVTLDGRPLSTIQQYSKT---FFV------------LPLRGKLSF-W--EAGTTKA 444
                  |    |  | ||    : |    | |             | :  :. | |   :||| | 
Db        450 ---TTTVLAANPASTTNTSATTVSNFIVGTTNPNALNVSYTPSQQTVLFNWAKASGTTLA 506

Qy        445 GYP----YNYNTTASDQLLVENAAGHRVAISTYTTSL------------GAGPVSISAV 487
                |    |           :: :|   :   :|:| |:|             |  ::|  
Db        507 NLPNQIAYGATGITDASVVTDNPFSNTTLLSSYATALSNAVPTGYNITQISNGTTTVSGA 566

Qy        488 AVLAPHSALALLEDTLDYPARAHTF 512
                | :|      |:  :  :|:    
Db        567 TTAATLAAFTSQNPTVGATSTLNTY 591


RESULT 13
```

```
B85547
probable RTX family exoprotein [imported] - Escherichia coli (strain O157:H7, substrain E
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85547
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85547
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5188 <STO>
A;Cross-references: UNIPROT:Q8X4H5; GB:AE005174; NID:g12513368; PIDN:AAG54838.1; GSPDB:GN
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z0615

  Query Match             4.5%;  Score 122;  DB 2;  Length 5188;
  Best Local Similarity   21.8%;  Pred. No. 25;
  Matches  114;  Conservative   68;  Mismatches  208;  Indels  134;  Gaps   24;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||| : :|    || :     :  ||: |  || : :|  :                :  |
Db       2535 AVAISINTVASDDVINAA---EKGTNLTLSGSTSGIESGQTVT-----------VTFGGK 2580

Qy         61 THIMATEASNYAQYRVARATIRYRP--------LVPNAVGGYAISISFWPQTTTTPTSVD 112
              |:  :  |:       |  | :   |                | :| |  | :   :    : || :
Db       2581 TYTASVAANGSWSVNVPAADLATLPEGAANVQASVSSASGNSASATHAYSVDASAPT-LT 2639

Qy        113 MNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGS 172
              :|:| | |:    : |  | | |                 || :  | |    | : ::|:
Db       2640 INTIASDDILNAAEAG--SPLTI----------------SGTSTAE-TGQTVTVTLNGA 2679

Qy        173 LVNSYTNTPY----------TGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRR 222
                 :|| |             | ||| |: :     |  |    :    :| | |  
Db       2680 ---TYTGTVQADGSWSVSVPTSALGALNAS------NYTVSATVNDKAGNPGSASHNL-- 2728

Qy        223 GADGTA---ELTTTAATRFMKD------LYFTSTNGVGEIGRGIALTLFNLADTLLGGLP 273
               | ||    : | |    : |       |  : |:  || |  ::: |
Db       2729 AVDTTAPVLTINTVAGDDIINDAEHAQALVISGTSSGGEXGDVVSVVL------------ 2776

Qy        274 TELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIP-HDID-LGESRVVIQD 331
                                 ||    | ||:  :|  :  : :|  |:  ||      |
Db       2777 --------------------NG----KTYTTTLDASGNWSVGVPAADVTALGSGAQTI-- 2810

Qy        332 YDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAE---------YDQSTYGSSTGPVY 382
                    ||   |   ||  :|  :  |: ::  | :             | :  :|| |
Db       2811 --TASVSDRAGNSDDASRTVTVSLSAPVISINTIAGDDVINATEKGSDLALSGTSDQPAG 2868

Qy        383 VSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ--YSKTFFVLPLRGKLSF---- 436
               : :||| |     :      | :|: ||:    :| : :  || |  |    :| |  
Db       2869 TAITVTL-NGQNYSATTDASGNWS-VTVPASAVSALGEATYSVTASVTNAQGNSSTASHN 2926

Qy        437 WEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
               :  |   |     |  |:| ::  :  ||    ||   |   ||
Db       2927 VQVNTALPG--ITINPVATDDIINASEAGSAQTISGQVTGAAAG 2968


RESULT 14
F90696
hypothetical protein ECs0542 [imported] - Escherichia coli (strain O157:H7, substrain RIM
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F90696
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90696
A;Status: preliminary
```

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A;Molecule type: DNA
A;Residues: 1-5291 <HAY>
A;Cross-references: UNIPROT:Q8X2T1; GB:BA000007; PIDN:BAB33965.1; PID:g13360000; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0542

  Query Match             4.5%;  Score 122;  DB 2;  Length 5291;
  Best Local Similarity   21.8%;  Pred. No. 26;
  Matches  114;  Conservative   68;  Mismatches  208;  Indels  134;  Gaps   24;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||| : :|    || :      :  ||: |  || : :|  :           :  |
Db       2535 AVAISINTVASDDVINAA---EKGTNLTLSGSTSGIESGQTVT----------VTFGGK 2580

Qy         61 THIMATEASNYAQYRVARATIRYRP--------LVPNAVGGYAISISFWPQTTTTPTSVD 112
              |:  :  |:       |  | :  |          | :| |  | :   :    : || :
Db       2581 TYTASVAANGSWSVNVPAADLATLPEGAANVQASVSSASGNSASATHAYSVDASAPT-LT 2639

Qy        113 MNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGS 172
              :|:| | |:    : |  | | |                 || :  | |   | : ::|:
Db       2640 INTIASDDILNAAEAG--SPLTI----------------SGTSTAE-TGQTVTVTLNGA 2679

Qy        173 LVNSYTNTPY----------TGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRR 222
               :|| |              | ||| |: :      | |   |    :   :| | |
Db       2680 ---TYTGTVQADGSWSVSVPTSALGALNAS------NYTVSATVNDKAGNPGSASHNL-- 2728

Qy        223 GADGTA---ELTTTAATRFMKD------LYFTSTNGVGEIGRGIALTLFNLADTLLGGLP 273
               | ||    : | |    : |       |  : |:  || |  ::: |
Db       2729 AVDTTAPVLTINTVAGDDIINDAEHAQALVISGTSSGGEAGDVVSVVL------------ 2776

Qy        274 TELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIP-HDID-LGESRVVIQD 331
                          ||    | ||:  :|  :  : :|  |:  ||     |
Db       2777 -------------------NG----KTYTTTLDASGNWSVGVPAADVTALGSGAQTI-- 2810

Qy        332 YDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAE---------YDQSTYGSSTGPVY 382
                    ||   |   ||  :|  :  |: ::  | :           |  :  |:|  |
Db       2811 --TASVSDRAGNSDDASRTVTVSLSAPVISINTIAGDDVINATEKGSDLALSGTSDQPAG 2868

Qy        383 VSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ--YSKTFFVLPLRGKLSF---- 436
               : :||| |    :     | :|: ||:    :| : :  || |  |   :|  |
Db       2869 TAITVTL-NGQNYSATTDASGNWS-VTVPASAVSALGEATYSVTASVTNAQGNSSTASHN 2926

Qy        437 WEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
               :  |   |      |  |:| ::  : ||    ||   |   ||
Db       2927 VQVNTALPG--ITINPVATDDIINASEAGSAQTISGQVTGAAAG 2968


RESULT 15
A47001
transcription factor Oct-1 - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Sep-1999
C;Accession: A47001; A31754
R;Sturm, R.A.; Cassady, J.L.; Das, G.; Romo, A.; Evans, G.A.
Genomics 16, 333-341, 1993
A;Title: Chromosomal structure and expression of the human OTF1 locus encoding the oct-1
A;Reference number: A47001; MUID:93300505; PMID:8314572
A;Accession: A47001
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-766 <STU>
A;Note: the sequence in GenBank entry HSOCT1, release 111.0, begins with Met-24
R;Sturm, R.A.; Das, G.; Herr, W.
Genes Dev. 2, 1582-1599, 1988
A;Title: The ubiquitous octamer-binding protein Oct-1 contains a POU domain with a homeo
A;Reference number: A31754; MUID:89107993; PMID:2905684
A;Accession: A31754
A;Molecule type: mRNA
A;Residues: 'P',8-400,'R',402-766 <ST2>
A;Cross-references: GB:X13403; NID:g35126; PIDN:CAA31767.1; PID:g35127
C;Genetics:
A;Gene: GDB:POU2F1; OTF1; OCT1
A;Cross-references: GDB:120254; OMIM:164175
A;Map position: 1q22-1q23
C;Superfamily: transcription factor Oct-1; homeobox homology; POU domain homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;310-377/Domain: POU domain homology <POU>
F;403-459/Domain: homeobox homology <HOX>

  Query Match             4.5%;  Score 121.5;  DB 1;  Length 766;
  Best Local Similarity   25.7%;  Pred. No. 1.7;
  Matches   78;  Conservative   40;  Mismatches  136;  Indels   49;  Gaps   13;

Qy         28 STSPL-------TSSVATGTNLVLYAA----PLSPLLPLQDGTNTHIMATEASNYAQYRV 76
              |:||:       || |||  :||  :|     :||:|||     |::  |  |:
Db       469 SSSPIKAIFPSPTSLVATTPSLVTSSAATTLTVSPVLPLTSAAVTNLSVTGTSDTTSNNT 528

Qy         77 ARATIRYRPLVPNAVGGYAISISFWPQ---TTTTPTSVDMNSITSTDVRILVQPGIASEL 133
              |   |   |   :||   ::| |  |    :|:  :|    | | |    |  |   |::
Db       529 A-TVISTAPPASSAVTSPSLSPS--PSASASTSEASSASETSTTQTTSTPLSSPLGTSQV 585

Qy        134 VIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFAL 193
              :: :  |    |   :    | |:  | : |  :     |  |        | | |
Db       586 MVTASGL----QTAAAAALQGAAQLPANASLAAMAAAAGLNPSLMAPSQFAAGGAL---- 637

Qy        194 ELEFRNLTPGNTNTRVS---RYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGV 250
               :| ||  :  :|     :||         : |:  :|:  ||    :| | :  |
Db       638 ----LSLNPGTLSGALSPALMSNSTLATIQALASGGSLPITSLDAT---GNLVFANAGGA 690

Qy        251 GEIGRGIALTLF----NLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVE 306
               |   :   ||    ||  :||   |  |:|:|     | || | :          || |
Db       691 PNI---VTAPLFLNPQNL--SLLTSNPVSLVSAAAASAGNSAPVASLHATS-----TSAE 740

Qy        307 NAQ 309
               : |
Db       741 SIQ 743


Search completed: July 14, 2005, 15:51:42
Job time : 10.0802 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 14, 2005, 01:31:43 ; Search time 38.3019 Seconds
(without alignments)
7019.016 Million cell updates/sec

Title: US-09-769-066-27
Perfect score: 2694
Sequence: 1 AVAPAHDTPPVPDVDSRGAI.....PARAHTFDDFCPECRPLGLQ 525

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2694	100.0	660	1	VST2_HEVBU	P29326 hepatitis e
2	2687	99.7	660	2	Q9E8G5	Q9e8g5 hepatitis e
3	2683	99.6	660	2	Q9W7W9	Q9w7w9 hepatitis e
4	2683	99.6	660	2	Q9WQA0	Q9wqa0 hepatitis e
5	2681	99.5	660	1	VST2_HEVPA	P33426 hepatitis e
6	2681	99.5	660	2	Q77EC8	Q77ec8 hepatitis e
7	2681	99.5	660	2	Q89468	Q89468 hepatitis e
8	2677	99.4	660	2	Q69419	Q69419 hepatitis e
9	2676	99.3	660	2	Q81871	Q81871 hepatitis e
10	2675	99.3	660	2	O91855	O91855 hepatitis e
11	2674	99.3	660	2	O91856	O91856 hepatitis e
12	2669	99.1	660	2	Q81878	Q81878 hepatitis e
13	2666	99.0	660	2	Q69411	Q69411 hepatitis e
14	2666	99.0	660	2	Q6XXV0	Q6xxv0 hepatitis e
15	2660	98.7	660	2	Q9WLL4	Q9wll4 hepatitis e
16	2656	98.6	660	2	Q68985	Q68985 hepatitis e
17	2655	98.6	659	2	Q8JT32	Q8jt32 hepatitis e
18	2653	98.5	660	1	VST2_HEVMY	Q04611 hepatitis e
19	2586	96.0	660	2	Q80IY5	Q80iy5 hepatitis e
20	2582	95.8	660	2	Q8JJM8	Q8jjm8 hepatitis e
21	2581	95.8	660	2	O36613	O36613 swine hepat
22	2581	95.8	660	2	Q6J8F7	Q6j8f7 hepatitis e
23	2580	95.8	660	2	Q8JJM4	Q8jjm4 hepatitis e
24	2578	95.7	660	2	Q8AZM3	Q8azm3 hepatitis e
25	2578	95.7	660	2	Q9YLQ9	Q9ylq9 hepatitis e
26	2575	95.6	660	2	Q6J8G3	Q6j8g3 hepatitis e
27	2575	95.6	660	2	Q80IR7	Q80ir7 hepatitis e
28	2574	95.5	660	2	Q8V729	Q8v729 swine hepat
29	2573	95.5	550	2	Q8JVV3	Q8jvv3 hepatitis e
30	2573	95.5	671	2	Q8JJM1	Q8jjm1 hepatitis e
31	2573	95.5	674	2	Q8JJN6	Q8jjn6 hepatitis e
32	2572	95.5	660	2	Q911I4	Q911i4 hepatitis e
33	2571	95.4	674	2	Q8JJN2	Q8jjn2 hepatitis e
34	2571	95.4	674	2	Q6BD83	Q6bd83 hepatitis e
35	2571	95.4	674	2	Q7TGF1	Q7tgf1 hepatitis e
36	2570	95.4	674	2	Q6BD78	Q6bd78 hepatitis e
37	2570	95.4	674	2	Q806D7	Q806d7 hepatitis e
38	2570	95.4	674	2	Q806E0	Q806e0 swine hepat
39	2570	95.4	674	2	Q80IR5	Q80ir5 hepatitis e
40	2568	95.3	660	2	Q9YLR2	Q9ylr2 hepatitis e
41	2567	95.3	660	2	Q8BB05	Q8bb05 swine hepat
42	2567	95.3	674	2	Q6PMR3	Q6pmr3 swine hepat
43	2543	94.4	672	2	Q9IVZ8	Q9ivz8 hepatitis e
44	2542.5	94.4	659	1	VST2_HEVME	Q03500 hepatitis e
45	2484	92.2	605	2	Q9YWL0	Q9ywl0 hepatitis e

ALIGNMENTS

RESULT 1
VST2_HEVBU
ID VST2_HEVBU STANDARD; PRT; 660 AA.
AC P29326;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Structural protein 2 precursor.
GN ORFNames=ORF2;
OS Hepatitis E virus (strain Burma) (HEV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=31767;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92024067; PubMed=1926770;
RA Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
RA Fry K.E., Reyes G.R.;
RT "Hepatitis E virus (HEV): molecular cloning and sequencing of the
RT full-length viral genome.";
RL Virology 185:120-131(1991).
CC -!- FUNCTION: Contains a high basic amino acid content suggesting that
CC it may be involved in the encapsidation of the genomic RNA by
CC effectively neutralizing the negatively charged RNA.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; M73218; AAA45736.1; -.
DR PIR; C40778; VHWWH2.
DR InterPro; IPR004261; SP2.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF03014; SP2; 1.
KW Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 660 Structural protein 2.
SQ SEQUENCE 660 AA; 70978 MW; 5832A013CCC4A61C CRC64;

Query Match 100.0%; Score 2694; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 1.5e-181;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231
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Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 2
Q9E8G5
ID Q9E8G5 PRELIMINARY; PRT; 660 AA.
AC Q9E8G5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Structural protein.
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Abb-2B;
RX MEDLINE=20271579; PubMed=10813471;
RA van Cuyck-Gandre H., Zhang H.Y., Tsarev S.A., Warren R.L.,
RA Caudill J.D., Snellings N.J., Begot L., Innis B.L., Longer C.F.;
RT "Phylogenetically distinct hepatitis E viruses in Pakistan.";
RL Am. J. Trop. Med. Hyg. 62:187-189(2000).
DR EMBL; AF185822; AAG16766.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70903 MW; 1F506BE3CFB3BACE CRC64;

Query Match 99.7%; Score 2687; DB 2; Length 660;
Best Local Similarity 99.8%; Pred. No. 4.7e-181;
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 3
Q9W7W9
ID Q9W7W9 PRELIMINARY; PRT; 660 AA.
AC Q9W7W9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Structural protein 2 (Structural viral protein).
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HEV-Morocco;
RX MEDLINE=99107414; PubMed=9892396;
RX DOI=10.1002/(SICI)1096-9071(199902)57:2<126::AID-JMV7>3.3.CO;2-F;
RA Meng J., Cong M., Dai X., Pillot J., Purdy M.A., Fields H.A.,
RA Khudyakov Y.E.;
RT "Primary structure of open reading frame 2 and 3 of the hepatitis E
RT virus isolated from Morocco.";
RL J. Med. Virol. 57:126-133(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen G., Meng J.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF065061; AAD10627.1; -.
DR EMBL; AY230202; AAO72992.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70943 MW; 9719D30CCD932950 CRC64;

Query Match 99.6%; Score 2683; DB 2; Length 660;
Best Local Similarity 99.6%; Pred. No. 8.9e-181;
Matches 523; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291
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Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK, 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 4
Q9WQA0
ID   Q9WQA0      PRELIMINARY;      PRT;   660 AA.
AC   Q9WQA0;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   ORF-2.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99350000; PubMed=10423137;
RA   Arankalle V.A., Paranjape S., Emerson S.U., Purcell R.H.,
RA   Walimbe A.M.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from India (1976-
RT   1993).";
RL   J. Gen. Virol. 80:1691-1700(1999).
DR   EMBL; AF124407; AAD45493.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71040 MW;  03B72DDF0AB7B521 CRC64;

  Query Match             99.6%;  Score 2683;  DB 2;  Length 660;
  Best Local Similarity   99.6%;  Pred. No. 8.9e-181;
  Matches  523;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              ||||||||| |||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVFAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 5
VST2_HEVPA
ID   VST2_HEVPA     STANDARD;      PRT;   660 AA.
AC   P33426;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   Structural protein 2 precursor.
GN   ORFNames=ORF2;
OS   Hepatitis E virus (strain Pakistan) (HEV).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=33774;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92115700; PubMed=1731327;
RA   Tsarev S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J.,
RA   Malik I.A., Iqbal M., Purcell R.H.;
RT   "Characterization of a prototype strain of hepatitis E virus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).
CC   -!- FUNCTION: Contains a high basic amino acid content suggesting that
CC       it may be involved in the encapsidation of the genomic RNA by
CC       effectively neutralizing the negatively charged RNA.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M80581; AAA45727.1; -.
DR   InterPro; IPR004261; SP2.
DR   InterPro; IPR008975; Viral_cap_coat.
DR   Pfam; PF03014; SP2; 1.
KW   Signal.
FT   SIGNAL       1     22       By similarity.
FT   CHAIN       23    660       Structural protein 2.
SQ   SEQUENCE   660 AA;  70980 MW;  8085BC53CFB46FD3 CRC64;

  Query Match             99.5%;  Score 2681;  DB 1;  Length 660;
  Best Local Similarity   99.4%;  Pred. No. 1.2e-180;
  Matches  522;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
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Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525

Db        592 PVSISAVAVLAPHSVLALLEDTMDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 6
Q77EC8
ID   Q77EC8      PRELIMINARY;      PRT;   660 AA.
AC   Q77EC8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Capsid protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sar-55;
RX   MEDLINE=21625046; PubMed=11742081; DOI=10.1073/pnas.251555098;
RA   Emerson S.U., Zhang M., Meng X.-J., Nguyen H., St Claire M.,
RA   Govindarajan S., Huang Y.K., Purcell R.H.;
RT   "Recombinant hepatitis E virus genomes infectious for primates:
RT   importance of capping and discovery of a cis-reactive element.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:15270-15275(2001).
DR   EMBL; AF444003; AAL50059.1; -.
DR   EMBL; AF444002; AAL50056.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70979 MW;  8085BC53CFB46FD3 CRC64;

  Query Match           99.5%;  Score 2681;  DB 2;  Length 660;
  Best Local Similarity   99.4%;  Pred. No. 1.2e-180;
  Matches  522;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180

Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525

Db        592 PVSISAVAVLAPHSVLALLEDTMDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 7
Q89468
ID   Q89468      PRELIMINARY;      PRT;   660 AA.
AC   Q89468;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Unnamed protein product (ORFs 1-3).
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yin S.R., Purcell R.H., Emerson S.U.;
RL   Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K52-87;
RX   MEDLINE=95176571; PubMed=7871758;
RA   Yin S., Purcell R.H., Emerson S.U.;
RT   "A new Chinese isolate of hepatitis E virus: comparison with strains
RT   recovered from different geographical regions.";
RL   Virus Genes 9:23-32(1994).
DR   EMBL; L25547; AAA91080.1; -.
DR   EMBL; L25595; AAA65490.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70979 MW;  DC68116DCD639175 CRC64;

  Query Match           99.5%;  Score 2681;  DB 2;  Length 660;
  Best Local Similarity   99.4%;  Pred. No. 1.2e-180;
  Matches  522;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180

Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
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Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||| |||||||||||:|||||||||||||||||||||
Db        592 PVSISAVAVLTPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQ 636


RESULT 8
Q69419
ID   Q69419      PRELIMINARY;      PRT;   660 AA.
AC   Q69419;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ORF1, ORF2 & ORF3.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   von Brunn A., Seebach J., Thyagarajan S.P., Mohanavalli B., Menon T.,
RA   Froesner G.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X99441; CAA67804.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70960 MW;  DAC3DF95F91689F8 CRC64;

  Query Match             99.4%;  Score 2677;  DB 2;  Length 660;
  Best Local Similarity   99.4%;  Pred. No. 2.4e-180;
  Matches  522;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              || ||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        412 LYRSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSALRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 9
Q81871
ID   Q81871      PRELIMINARY;      PRT;   660 AA.
AC   Q81871;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   ORF 2 precursor.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92024067; PubMed=1926770;
RA   Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
RA   Fry K.E., Reyes G.R.;
RT   "Hepatitis E virus (HEV): molecular cloning and sequencing of the
RT   full-length viral genome.";
RL   Virology 185:120-131(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92115700; PubMed=1731327;
RA   Tsarev S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J.,
RA   Malik I.A., Iqbal M., Purcell R.H.;
RT   "Characterization of a prototype strain of hepatitis E virus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92261377; PubMed=1584074;
RA   Uchida T., Suzuki K., Hayashi N., Iida F., Hara T., Oo S.S., Wang C.,
RA   Shikata T., Ichikawa M., Rikihisa T., Mizuno K., Win K.M.;
RT   "Hepatitis E virus: cDNA cloning and expression.";
RL   Microbiol. Immunol. 36:67-79(1992).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92335008; PubMed=1630924;
RA   Aye T.T., Uchida T., Ma M.Z., Iida F., Shikata T., Zhuang H.,
RA   Win K.M.;
RT   "Complete nucleotide sequence of a hepatitis E virus isolated from the
RT   Xinjiang epidemic (1986-1988) of China.";
RL   Nucleic Acids Res. 20:3512-3512(1992).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92271462; PubMed=1589964;
RA   Fry K.E., Tam A.W., Smith M.W., Kim J.P., Luk K.-C., Young L.M.,
RA   Piatak M., Feldman R.A., Yun K.Y., Purdy M.A., McCaustland K.A.,
RA   Bradley D.W., Reyes G.R.;
RT   "Hepatitis E virus (HEV): strain variation in the nonstructural gene
RT   region encoding consensus motifs for an RNA-dependent RNA polymerase
RT   and an ATP/GTP binding site.";
RL   Virus Genes 6:173-185(1992).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93348763; PubMed=8346669; DOI=10.1016/0168-1702(93)90024-H;
RA   Bi S-L., Purdy M.A., McCaustland K.A., Margolis H.S., Bradley D.W.;
RT   "The sequence of hepatitis E virus isolated directly from a single
RT   source during an outbreak in China.";
RL   Virus Res. 28:233-247(1993).
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DR   EMBL; L08816; AAA03191.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
KW   Signal.
FT   SIGNAL        1     19       Potential.
SQ   SEQUENCE   660 AA;  70979 MW;  B58F23955FDD6614 CRC64;

  Query Match             99.3%;  Score 2676;  DB 2;  Length 660;
  Best Local Similarity   99.2%;  Pred. No. 2.8e-180;
  Matches  521;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASEHVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTTQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||:|||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQ 636


RESULT 10
O91855
ID   O91855      PRELIMINARY;      PRT;   660 AA.
AC   O91855;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Structural protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=93-Egypt;
RX   MEDLINE=99105430; PubMed=9890424;
RX   DOI=10.1002/(SICI)1096-9071(199901)57:1<68::AID-JMV10>3.0.CO;2-E;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
RL   J. Med. Virol. 57:68-74(1999).
DR   EMBL; AF051351; AAC35761.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71039 MW;  044FF5EA7C492791 CRC64;

  Query Match             99.3%;  Score 2675;  DB 2;  Length 660;
  Best Local Similarity   99.0%;  Pred. No. 3.3e-180;
  Matches  520;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||:|||||:||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTSSDQLLIENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 11
O91856
ID   O91856      PRELIMINARY;      PRT;   660 AA.
AC   O91856;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Structural protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=94-Egypt;
RX   MEDLINE=99105430; PubMed=9890424;
RX   DOI=10.1002/(SICI)1096-9071(199901)57:1<68::AID-JMV10>3.0.CO;2-E;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
RL   J. Med. Virol. 57:68-74(1999).
DR   EMBL; AF051352; AAC35764.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71025 MW;  16C560FA16941F2A CRC64;

  Query Match             99.3%;  Score 2674;  DB 2;  Length 660;
  Best Local Similarity   99.0%;  Pred. No. 3.9e-180;
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  Matches  520;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              ||||||||||||||||||||||||||||||||||||||:||| ||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLIENATGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 12
Q81878
ID   Q81878      PRELIMINARY;      PRT;   660 AA.
AC   Q81878;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Complete genome sequence.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Uchida T.;
RL   Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; D11093; BAA01867.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70937 MW;  5412313F1A2EF4A9 CRC64;

  Query Match           99.1%;  Score 2669;  DB 2;  Length 660;
  Best Local Similarity   98.9%;  Pred. No. 8.7e-180;
  Matches  519;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYGISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGTDGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YCKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||:||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQ 636


RESULT 13
Q69411
ID   Q69411      PRELIMINARY;      PRT;   660 AA.
AC   Q69411;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Structural protein.
GN   Name=ORF2;
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Donati M.C., Fagan E.A., Harrison T.J.;
RT   "Sequence analysis of full length HEV clones derived directly from
RT   human liver in fulminant hepatitis E.";
RL   (In) Rizzetto M., Purcell R.H., Gerin J.L., Verme G (eds.);
RL   VIRAL HEPATITIS AND LIVER DISEASE, pp.313-316, Edizioni Minerva
RL   Medica, Torino (1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Harrison T.J.;
RL   Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X98292; CAA66937.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71024 MW;  F37E3FEFF7A4EAD1 CRC64;

  Query Match           99.0%;  Score 2666;  DB 2;  Length 660;
  Best Local Similarity   98.7%;  Pred. No. 1.4e-179;
  Matches  518;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSPVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
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                ||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGLPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
                ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALEFEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
                ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
                ||:||||||||||||||||:||||||||||||||||||||||
Db        592 PVAISAVAVLAPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQ 636


RESULT 14
Q6XXV0
ID   Q6XXV0      PRELIMINARY;      PRT;   660 AA.
AC   Q6XXV0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Structural protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RX   MEDLINE=98071272; PubMed=9407381;
RX   DOI=10.1002/(SICI)1096-9071(199712)53:4<340::AID-JMV5>3.0.CO;2-7;
RA   van Cuyck-Gandre H., Zhang H.Y., Tsarev S.A., Clements N.J.,
RA   Cohen S.J., Caudill J.D., Buisson Y., Coursaget P., Warren R.L.,
RA   Longer C.F.;
RT   "Characterization of hepatitis E virus (HEV) from Algeria and Chad by
RT   partial genome sequence.";
RL   J. Med. Virol. 53:340-347(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RX   MEDLINE=99105430; PubMed=9890424;
RX   DOI=10.1002/(SICI)1096-9071(199901)57:1<68::AID-JMV10>3.0.CO;2-E;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
RL   J. Med. Virol. 57:68-74(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RX   MEDLINE=22987819; PubMed=14625096; DOI=10.1016/S0928-8244(03)00241-4;
RA   van Cuyck H., Juge F., Roques P.;
RT   "Phylogenetic analysis of the first complete hepatitis E virus (HEV)
RT   genome from Africa.";
RL   FEMS Immunol. Med. Microbiol. 39:133-139(2003).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RA   Van Cuyck-Gandre H., Zhang H.Y., Tsarev S.A., Clements N.J.,
RA   Cohen S.J., Caudill J.D., Buisson Y., Coursaget P., Warren R.L.,
RA   Longer C.F.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RA   van Cuyck H., Roberston D., Juge F., Roques P., Lemey P.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY204877; AAB61825.2; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70949 MW;  EA56732D458D0AB1 CRC64;

  Query Match             99.0%;  Score 2666;  DB 2;  Length 660;
  Best Local Similarity   98.9%;  Pred. No. 1.4e-179;
  Matches  519;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
                ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVSDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
                |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
                |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
                ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
                ||||||||||||||||||||||||||||||||||||:|| ||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLIENVAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
                ||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 15
Q9WLL4
ID   Q9WLL4      PRELIMINARY;      PRT;   660 AA.
AC   Q9WLL4;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Capsid protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
```

```
RP   SEQUENCE FROM N.A.
RC   STRAIN=TK15/92;
RX   MEDLINE=99049628; PubMed=9833882; DOI=10.1016/S0168-1702(98)00079-3;
RA   Gouvea V., Snellings N., Popek M.J., Longer C.F., Innis B.L.;
RT   "Hepatitis E virus: complete genome sequence and phylogenetic analysis
RT   of a Nepali isolate.";
RL   Virus Res. 57:21-26(1998).
DR   EMBL; AF051830; AAC97188.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70798 MW;  A04C0185ACC085DB CRC64;

  Query Match             98.7%;  Score 2660;  DB 2;  Length 660;
  Best Local Similarity   99.0%;  Pred. No. 3.8e-179;
  Matches  520;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60
              ||||||||||||||| |||||| ||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTPPVPDVGSRGAILCRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARAAIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASGQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


Search completed: July 14, 2005, 15:50:32
Job time : 39.3019 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 14, 2005, 00:29:03 ; Search time 43.4198 Seconds
(without alignments)
4676.418 Million cell updates/sec

Title: US-09-769-066-28
Perfect score: 2701
Sequence: 1 AVAPAHDTSPVPDVDSRGAI.....PGRAHTFDDFCPECRALGLQ 525

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2701	100.0	525	2	AAR96104	Aar96104 Hepatitis
2	2701	100.0	540	2	AAR96102	Aar96102 Hepatitis
3	2701	100.0	549	2	AAR96092	Aar96092 Hepatitis
4	2701	100.0	660	2	AAR96090	Aar96090 Hepatitis
5	2674.5	99.0	659	2	AAR38787	Aar38787 HEV ORF2
6	2674.5	99.0	659	2	AAW35827	Aaw35827 Hepatitis
7	2674.5	99.0	659	2	AAW93387	Aaw93387 Human HEV
8	2671.5	98.9	659	2	AAR39308	Aar39308 Mexico st
9	2638.5	97.7	659	5	ABJ04808	Abj04808 Hepatitis
10	2579	95.5	549	2	AAW76367	Aaw76367 Hepatitis
11	2579	95.5	660	2	AAR70323	Aar70323 Hepatitis
12	2579	95.5	660	2	AAW76369	Aaw76369 Hepatitis
13	2575	95.3	660	2	AAR91814	Aar91814 Hepatitis
14	2575	95.3	660	2	AAW93386	Aaw93386 Human HEV
15	2575	95.3	660	2	AAW93388	Aaw93388 Human HEV
16	2575	95.3	660	5	ABB81670	Abb81670 Hepatitis
17	2575	95.3	660	6	ADA50060	Ada50060 Hepatitis
18	2575	95.3	660	7	ADB97807	Adb97807 HEV ORF2
19	2569	95.1	525	2	AAR96103	Aar96103 Hepatitis
20	2569	95.1	540	2	AAR96101	Aar96101 Hepatitis
21	2569	95.1	549	2	AAR96091	Aar96091 Hepatitis
22	2569	95.1	660	2	AAR38785	Aar38785 HEV ORF2
23	2569	95.1	660	2	AAR39306	Aar39306 Burma str
24	2569	95.1	660	2	AAR96089	Aar96089 Hepatitis
25	2569	95.1	660	2	AAW35826	Aaw35826 Hepatitis
26	2569	95.1	660	2	AAW80197	Aaw80197 Protein e
27	2569	95.1	660	2	AAW93389	Aaw93389 Human HEV
28	2569	95.1	660	2	AAW93390	Aaw93390 Human HEV
29	2569	95.1	660	3	AAB24120	Aab24120 Hepatitis
30	2569	95.1	660	4	AAB62523	Aab62523 HEV-Burma
31	2569	95.1	660	5	AAO15699	Aao15699 Hepatitis
32	2569	95.1	660	7	ADD24376	Add24376 Hepatitis
33	2568	95.1	660	2	AAW93392	Aaw93392 Human HEV
34	2566	95.0	660	2	AAR51265	Aar51265 HEV strai
35	2566	95.0	660	2	AAW81520	Aaw81520 Hepatitis
36	2564	94.9	660	5	ABJ04811	Abj04811 Hepatitis
37	2563	94.9	660	2	AAW93391	Aaw93391 Human HEV
38	2562	94.9	660	2	AAW71210	Aaw71210 Protein e
39	2560	94.8	660	4	AAE12980	Aae12980 Hepatitis
40	2560	94.8	660	5	ABJ04820	Abj04820 Hepatitis
41	2560	94.8	660	5	ABJ04807	Abj04807 Hepatitis
42	2560	94.8	660	5	ABJ04809	Abj04809 Hepatitis
43	2560	94.8	660	5	ABJ04819	Abj04819 Hepatitis
44	2557	94.7	660	5	ABJ04822	Abj04822 Hepatitis
45	2556	94.6	660	7	ADE06700	Ade06700 Hepatitis

ALIGNMENTS

RESULT 1
AAR96104
ID AAR96104 standard; protein; 525 AA.
XX
AC AAR96104;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Mexico strain) recombinant 62K antigen.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid.
XX
OS Hepatitis E virus; Mexico strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Claim 8; Page 97-98; 125pp; English.
XX
CC DNA (AAT27110) coding for the 62K antigen (AAR96092) of hepatitis E virus
CC (HEV) Mexico strain capsid protein was cloned into baculovirus expression
CC vector pBluBacIII and recombinant 62K was expressed in Sf9 insect cells.
CC High levels of expression were obtd. and the recombinant 62K was obtd. in
CC over 95% purity. However, C-terminal processing resulted in the deletion
CC of 9 or 23 amino acids from 62K, giving 2 related polypeptide species
CC (AAR96102 and AAR96104). Similar results were obtd. with HEV Burma 62K
CC antigen (see also AAR96101 and AAR96103). Recombinant 62K represents an
CC improved antigen, in comparison to bacterial expressed proteins, for use
CC in HEV diagnostic assays, and also has excellent immunogenic properties.
CC (Updated on 16-OCT-2003 to standardise OS field)

```
XX
SQ   Sequence 525 AA;

  Query Match            100.0%;  Score 2701;  DB 2;  Length 525;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-225;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525


RESULT 2
AAR96102
ID   AAR96102 standard; protein; 540 AA.
XX
AC   AAR96102;
XX
DT   16-OCT-2003  (revised)
DT   06-AUG-1996  (first entry)
XX
DE   Hepatitis E virus (Mexico strain) recombinant 62K antigen.
XX
KW   HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW   diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW   capsid.
XX
OS   Hepatitis E virus; Mexico strain.
XX
PN   WO9612807-A2.
XX
PD   02-MAY-1996.
XX
PF   23-OCT-1995;   95WO-US013703.
XX
PR   24-OCT-1994;   94US-00327952.
PR   13-OCT-1995;   95US-00542634.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fuerst TR,  Mcatee CP,  Yarbough PO,  Zhang Y;
XX
DR   WPI; 1996-230608/23.
XX
PT   Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT   diagnostic reagents for determining HEV infection and in vaccines.
XX
PS   Claim 6; Page 93-95; 125pp; English.
XX
CC   DNA (AAT27110) coding for the 62K antigen (AAR96092) of hepatitis E virus
CC   (HEV) Mexico strain capsid protein was cloned into baculovirus expression
CC   vector pBluBacIII and recombinant 62K was expressed in Sf9 insect cells.
CC   High levels of expression were obtd. and the recombinant 62K was obtd. in
CC   over 95% purity. However, C-terminal processing resulted in the deletion
CC   of 9 or 23 amino acids from 62K, giving 2 related polypeptide species
CC   (AAR96102 and AAR96104). Similar results were obtd. with HEV Burma 62K
CC   antigen (see also AAR96101 and AAR96103). Recombinant 62K represents an
CC   improved antigen, in comparison to bacterial expressed proteins, for use
CC   in HEV diagnostic assays, and also has excellent immunogenic properties.
CC   (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 540 AA;

  Query Match            100.0%;  Score 2701;  DB 2;  Length 540;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-225;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525


RESULT 3
AAR96092
ID   AAR96092 standard; protein; 549 AA.
XX
AC   AAR96092;
XX
DT   16-OCT-2003  (revised)
DT   06-AUG-1996  (first entry)
XX
DE   Hepatitis E virus (Mexico strain) 62K antigen.
```

```
XX
KW   HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW   diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW   capsid.
XX
OS   Hepatitis E virus; Mexico strain.
XX
PN   WO9612807-A2.
XX
PD   02-MAY-1996.
XX
PF   23-OCT-1995;   95WO-US013703.
XX
PR   24-OCT-1994;   94US-00327952.
PR   13-OCT-1995;   95US-00542634.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fuerst TR,  Mcatee CP,  Yarbough PO,  Zhang Y;
XX
DR   WPI; 1996-230608/23.
DR   N-PSDB; AAT27110.
XX
PT   Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT   diagnostic reagents for determining HEV infection and in vaccines.
XX
PS   Claim 4; Page 84-86; 125pp; English.
XX
CC   62K antigen (AAR96092) comprises the C-terminal 549 amino acids of
CC   hepatitis E virus (HEV) Mexico strain capsid protein (see also AAR96090).
CC   It is obtd. by PCR amplification of HEV Mexico ORF-2 (AAT27108),
CC   insertion of amplified DNA (AAT27110) into vector pGEX and expression in
CC   E. coli cells. Expression of full-length ORF-2 in Sf9 insect cells using
CC   a baculovirus system also results in prodn. of 62K antigen (see also
CC   AAR96102 and AAR96104). 62K represents an improved antigen, in comparison
CC   to bacterial expressed proteins, for use in HEV diagnostic assays, and
CC   also has excellent immunogenic properties. (Updated on 16-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 549 AA;

  Query Match             100.0%;  Score 2701;  DB 2;  Length 549;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-225;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525


RESULT 4
AAR96090
ID   AAR96090 standard; protein; 660 AA.
XX
AC   AAR96090;
XX
DT   16-OCT-2003  (revised)
DT   06-AUG-1996  (first entry)
XX
DE   Hepatitis E virus (Mexico strain) capsid protein.
XX
KW   HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW   diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW   capsid.
XX
OS   Hepatitis E virus; Mexico strain.
XX
PN   WO9612807-A2.
XX
PD   02-MAY-1996.
XX
PF   23-OCT-1995;   95WO-US013703.
XX
PR   24-OCT-1994;   94US-00327952.
PR   13-OCT-1995;   95US-00542634.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fuerst TR,  Mcatee CP,  Yarbough PO,  Zhang Y;
XX
DR   WPI; 1996-230608/23.
DR   N-PSDB; AAT27108.
XX
PT   Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT   diagnostic reagents for determining HEV infection and in vaccines.
XX
PS   Disclosure; Page 80-82; 125pp; English.
XX
CC   The putative capsid protein (AAR96090) of hepatitis E virus (HEV) Mexico
CC   strain is encoded by ORF-2 (AAT27108) of the virus. PCR amplification of
CC   ORF-2 allows prodn. of capsid protein or of C-terminal regions of the
CC   capsid protein (see also AAR96092, AAR96094 and AAR96096) and expression
CC   in Spodoptera frugiperda Sf9 insect cells using a baculovirus vector
CC   provides recombinant C-terminal regions (see also AAR96102 and AAR96104)
CC   useful as diagnostic reagents and in vaccines. The HEV Burma strain
CC   capsid protein (AAR96089) may similarly be used. (Updated on 16-OCT-2003
CC   to standardise OS field)
XX
SQ   Sequence 660 AA;

  Query Match             100.0%;  Score 2701;  DB 2;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 2e-225;
  Matches  525;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        592 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 636
```

RESULT 5
AAR38787
ID AAR38787 standard; protein; 659 AA.
XX
AC AAR38787;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 11-JAN-1994 (first entry)
XX
DE HEV ORF2 protein.
XX
KW Enterically transmitted non-A non-B hepatitis; ET-NANB; vaccine.
XX
OS Hepatitis E virus; Mexico strain.
XX
FH Key Location/Qualifiers
FT Peptide 225. .659
FT /label= C2
FT Peptide 333. .659
FT /label= SG3
FT Peptide 612. .659
FT /label= 406.3-2
XX
PN WO9314116-A1.
XX
PD 22-JUL-1993.
XX
PF 15-JAN-1993; 93WO-US000459.
XX
PR 17-JAN-1992; 92US-00822335.
PR 01-MAY-1992; 92US-00876941.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
PA (USSH) US SEC DEPT HEALTH.
XX
PI Reyes GR, Bradley DW, Tam AW, Carl M;
XX
DR WPI; 1993-243144/30.
DR N-PSDB; AAQ47130.
XX
PT New immunogenic hepatitis E virus (HEV) peptide(s) - are from the ORF1,
PT ORF2 and ORF3 regions of HEV, useful as a vaccine against HEV infection.
XX
PS Disclosure; Fig 8; 48pp; English.
XX
CC Immunogenic hepatitis E virus (HEV) peptides are selected from the ORF1,
CC ORF2 and ORF3 regions of HEV. The peptides can be used in vaccines to
CC prevent infection by HEV. The antibodies can neutralise and block HEV
CC infection and can be used to prevent or treat HEV infection. The peptides
CC and antibodies can also be used as diagnostic reagents. (Updated on 25-
CC MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 659 AA;

```
  Query Match            99.0%;  Score 2674.5;  DB 2;  Length 659;
  Best Local Similarity  99.4%;  Pred. No. 4e-223;
  Matches  522;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 635
```

RESULT 6
AAW35827
ID AAW35827 standard; protein; 659 AA.
XX
AC AAW35827;
XX
DT 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 26-FEB-1998 (first entry)
XX
DE Hepatitis E virus Mexico strain protein from ORF2.
XX
KW Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
KW diagnosis; HEV.
XX
OS Hepatitis E virus; - Mexico strain.
XX
PN US5686239-A.
XX
PD 11-NOV-1997.
XX
PF 09-MAY-1994; 94US-00240049.

```
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   17-JAN-1992;   92US-00822335.
PR   20-APR-1992;   92US-00870985.
PR   01-MAY-1992;   92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Tam AW,  Reyes GR,  Yarbough PO;
XX
DR   WPI; 1997-558132/51.
DR   N-PSDB; AAT96960.
XX
PT   Diagnosis of hepatitis E virus Burma and Mexico strain infection - by
PT   immunoassay with hepatitis E virus peptide antigens.
XX
PS   Disclosure; Col 43-46; 36pp; English.
XX
CC   A method has been developed for detecting hepatitis E virus (HEV)
CC   antibodies (Ab). The method comprises: (a) reacting a serum sample with a
CC   HEV peptide antigen; and (b) examining the peptide for the presence of
CC   bound Ab, where the presence of bound Ab indicates the presence of HEV
CC   Ab. The present sequence represents the protein from the open reading
CC   frame, ORF2, from HEV Mexico strain. The method can be used to diagnose
CC   infection with the enterically transmitted non-A/non-B viral hepatitis
CC   agent HEV, specifically the HEV Burma and Mexico strains. (Updated on 25-
CC   MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to standardise OS
CC   field)
XX
SQ   Sequence 659 AA;

  Query Match             99.0%;  Score 2674.5;  DB 2;  Length 659;
  Best Local Similarity   99.4%;  Pred. No. 4e-223;
  Matches  522;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 635


RESULT 7
AAW93387
ID   AAW93387 standard; protein; 659 AA.
XX
AC   AAW93387;
XX
DT   11-JUN-1999  (first entry)
XX
DE   Human HEV ORF 2 protein from strain Mexico.
XX
KW   Swine hepatitis E virus; HEV; cross-reaction; antibody; human; therapy;
KW   vaccine; immunise; infection; detection; diagnosis; prevention.
XX
OS   Hepatitis E virus.
XX
PN   WO9904029-A2.
XX
PD   28-JAN-1999.
XX
PF   17-JUL-1998;   98WO-US014665.
XX
PR   18-JUL-1997;   97US-0053069P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Meng X,  Emerson SU,  Purcell RH;
XX
DR   WPI; 1999-132270/11.
XX
PT   New isolated swine hepatitis E virus - used to develop products for the
PT   diagnosis, prevention and treatment of hepatitis E virus infection in
PT   mammals, particularly humans.
XX
PS   Example 1; Fig 3A; 70pp; English.
XX
CC   This invention describes a swine hepatitis E virus (HEV) and its natural
CC   mutants which are capable of cross-reacting with antibodies reactive with
CC   a human HEV strain or natural mutants. The HEV and the proteins can be
CC   used in vaccines for immunising against HEV infection. The swine HEV can
CC   be used in humans to prevent possible infection by human HEV. The swine
CC   HEV can also be used as a therapeutic treatment for infection by other
CC   strains of HEV. The swine HEV can also be used for the production of
CC   antibodies which can be used in therapy, detection and diagnosis. The
CC   products can also be used for determining the susceptibility of cells or
CC   organs to infection with swine HEV. The swine HEV is particularly useful
CC   for the development of agents for the prevention, treatment and detection
CC   of human HEV because it is not a human virus and thus can be handled both
CC   experimentally and clinically without fear of severe infection and/or
CC   contamination
XX
SQ   Sequence 659 AA;

  Query Match             99.0%;  Score 2674.5;  DB 2;  Length 659;
  Best Local Similarity   99.4%;  Pred. No. 4e-223;
  Matches  522;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
```

```
                ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
                |||||||||||||||||||||||||||||||||||||||||||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 635
```

RESULT 8
AAR39308
ID AAR39308 standard; protein; 659 AA.
XX
AC AAR39308;
XX
DT 25-MAR-2003 (revised)
DT 14-FEB-1994 (first entry)
XX
DE Mexico strain HEV ORF2 puative virus capsid protein.
XX
KW Hepatitis E virus; vaccine; neutralising antibodies; infection; block;
KW open reading frame; antibodies.
XX
OS Hepatitis E virus.
XX
PN WO9314208-A2.
XX
PD 22-JUL-1993.
XX
PF 19-JAN-1993; 93WO-US000475.
XX
PR 17-JAN-1992; 92US-00822335.
PR 20-APR-1992; 92US-00870985.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Reyes GR, Bradley DW, Twu J, Purdy MA, Tam AW, Krawczynski KZ;
XX
DR WPI; 1993-243223/30.
DR N-PSDB; AAQ46814.
XX
PT Antigen and antibody vaccines against hepatitis E virus infection -
PT contain peptide(s) derived from capsid protein C-terminal or antibodies
PT against protein.
XX
PS Disclosure; Fig 7; 43pp; English.
XX
CC The sequence is that of the putative virus capsid protein encoded by
CC Mexico strain hepatitis E virus (HEV) open reading frame ORF2. This
CC protein or peptide fragments of it may be used in a vaccine composition
CC for immunising an individual against HEV. Antibodies raised against these
CC peptides can also be used in such vaccines. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 659 AA;

Query Match 98.9%; Score 2671.5; DB 2; Length 659;
Best Local Similarity 99.2%; Pred. No. 7.4e-223;
Matches 521; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

```
Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKLTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 635
```

RESULT 9
ABJ04808
ID ABJ04808 standard; protein; 659 AA.
XX
AC ABJ04808;
XX
DT 07-NOV-2002 (first entry)
XX
DE Hepatitis E virus Mexico strain ORF2 capsid gene.
XX
KW Avian hepatitis E virus; vaccine; hepatitis E; ORF2; zoonosis; virucide;
KW avian hepatitis-splenomegaly syndrome; HEV; HS syndrome.
XX
OS Hepatitis E virus.
XX
PN WO200253712-A2.
XX
PD 11-JUL-2002.
XX
PF 04-JAN-2002; 2002WO-US000215.
XX
PR 05-JAN-2001; 2001US-0259846P.
PR 31-DEC-2001; 2001US-00029840.
XX
PA (VIRG) VIRGINIA TECH INTELLECTUAL PROPERTIES.
XX
PI Meng X, Haqshenas G, Huang F;
XX
DR WPI; 2002-548085/58.
XX
PT Novel isolated avian hepatitis E virus useful in a vaccine for protecting
PT an avian or mammalian species from viral infection or hepatitis-
PT splenomegaly syndrome caused by the avian or mammalian hepatitis E virus.

```
XX
PS   Example 11; Fig 5; 95pp; English.
XX
CC   The present invention relates to an isolated avian hepatitis E virus
CC   having the nucleic acid sequence shown in ABT05872. Vaccines against the
CC   virus are also described, and can be used for protecting an avian or
CC   mammalian species from viral infection or hepatitis-splenomegaly syndrome
CC   caused by the avian or mammalian HEV. The present sequence is a hepatitis
CC   E virus protein described in the exemplification of the invention
XX
SQ   Sequence 659 AA;

  Query Match             97.7%;  Score 2638.5;  DB 5;  Length 659;
  Best Local Similarity   97.9%;  Pred. No. 5.4e-220;
  Matches  514;  Conservative    3;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||| |||||||||||||||    |||||||||||||||| |
Db        292 PYTGALGLLDFALELEFRMLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFHK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              |||||| |||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGTNGVGEIGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWTKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| ||||||||||||||||||||||||||||||||
Db        591 PVSISAVAVLAPHSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 635


RESULT 10
AAW76367
ID   AAW76367 standard; protein; 549 AA.
XX
AC   AAW76367;
XX
DT   03-DEC-1998  (first entry)
XX
DE   Hepatitis E virus hollow particle protein ORF2.
XX
KW   Hollow particle protein; virus; antibody; detection; immunoassay;
KW   infection.
XX
OS   Hepatitis virus.
XX
FH   Key             Location/Qualifiers
FT   Protein         1. .549
FT                   /label= ORF2
FT                   /note= "partial sequence"
XX
PN   JP10234383-A.
XX
PD   08-SEP-1998.
XX
PF   28-FEB-1997;   97JP-00062445.
XX
PR   28-FEB-1997;   97JP-00062445.
XX
PA   (DENK-) DENKA SEIKEN KK.
PA   (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR   WPI; 1998-535037/46.
DR   N-PSDB; AAV61686.
XX
PT   Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids
PT   encoding it - useful for more accurate detection of HEV in samples, using
PT   immuno-assays and nucleic acid hybridisation.
XX
PS   Claim 1; Page 15-17; 29pp; Japanese.
XX
CC   This sequence represents a Hepatitis E viral hollow particle protein
CC   described as ORF2. This polypeptide can be used to raise antibodies to
CC   detect HEV infection in samples, e.g. by immuno-assay based techniques,
CC   and the nucleic acid can be used for the same in nucleic acid
CC   hybridisation assays. The polypeptide and nucleic acid allow more
CC   accurate detection of HEV than previously possible
XX
SQ   Sequence 549 AA;

  Query Match             95.5%;  Score 2579;  DB 2;  Length 549;
  Best Local Similarity   94.9%;  Pred. No. 6.2e-215;
  Matches  498;  Conservative   13;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| ||||||||||||||||||||||||||||:||||||||||:| ||||||||
Db          1 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 60

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        181 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        241 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||:||||||||||||||||||||||||||||||||||||||
Db        301 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||:|||||||||||||||||||||||||:|||||||| |::|
Db        361 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 420

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 480

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| ||||||||| ||| ||||||||||||| ||||
Db        481 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 525


RESULT 11
AAR70323
ID   AAR70323 standard; protein; 660 AA.
```

```
XX
AC   AAR70323;
XX
DT   25-MAR-2003  (revised)
DT   28-SEP-1995  (first entry)
XX
DE   Hepatitis E virus ORF2 protein.
XX
KW   HEV; ORF2; antigen; vaccine; immunogen.
XX
OS   Hepatitis E virus.
XX
PN   WO9508632-A1.
XX
PD   30-MAR-1995.
XX
PF   23-SEP-1994;   94WO-AU000572.
XX
PR   24-SEP-1993;   93AU-00001423.
PR   15-DEC-1993;   93AU-00002964.
XX
PA   (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX
PI   Anderson DA,  Locarnini SA,  Torresi J,  Li F,  Hui Z;
XX
DR   WPI; 1995-139601/18.
DR   N-PSDB; AAQ86592.
XX
PT   Antigens of hepatitis E virus (HEV) - selectively immuno:reactive to
PT   convalescent and/or acute phase circulating antibodies to HEV.
XX
PS   Disclosure; Page 39-41; 78pp; English.
XX
CC   RNA from an HEV strain isolated in the Xinjiang region of China was
CC   subjected to RT-PCR to obtain fragments corresp. to ORF2 (given in
CC   AAQ86592) and ORF3 (AAQ86593) that encoded antigenic proteins (AAR70323-
CC   24, respectively). DNA fragments were manipulated into pGEX vectors for
CC   production of GST fusion proteins in E. coli. Applications include HEV
CC   infection diagnosis, therapy and vaccine development. (Updated on 25-MAR-
CC   2003 to correct PN field.)
XX
SQ   Sequence 660 AA;

  Query Match             95.5%;  Score 2579;  DB 2;  Length 660;
  Best Local Similarity   94.9%;  Pred. No. 8.1e-215;
  Matches  498;  Conservative   13;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:|||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||:||||||||||||||||||||:||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| |||||||||| ||| ||||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQ 636


RESULT 12
AAW76369
ID   AAW76369 standard; protein; 660 AA.
XX
AC   AAW76369;
XX
DT   03-DEC-1998  (first entry)
XX
DE   Hepatitis E virus hollow particle protein #2.
XX
KW   Hollow particle protein; virus; antibody; detection; immunoassay;
KW   infection.
XX
OS   Hepatitis virus.
XX
PN   JP10234383-A.
XX
PD   08-SEP-1998.
XX
PF   28-FEB-1997;   97JP-00062445.
XX
PR   28-FEB-1997;   97JP-00062445.
XX
PA   (DENK-) DENKA SEIKEN KK.
PA   (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR   WPI; 1998-535037/46.
DR   N-PSDB; AAV61688.
XX
PT   Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids
PT   encoding it - useful for more accurate detection of HEV in samples, using
PT   immuno-assays and nucleic acid hybridisation.
XX
PS   Claim 13; Page 24-26; 29pp; Japanese.
XX
CC   This sequence represents a Hepatitis E viral hollow particle protein.
CC   This polypeptide can be used to raise antibodies to detect HEV infection
CC   in samples, e.g. by immuno-assay based techniques, and the nucleic acid
CC   can be used for the same in nucleic acid hybridisation assays. The
CC   polypeptides and nucleic acids allow more accurate detection of HEV than
CC   previously possible
XX
SQ   Sequence 660 AA;

  Query Match             95.5%;  Score 2579;  DB 2;  Length 660;
  Best Local Similarity   94.9%;  Pred. No. 8.1e-215;
  Matches  498;  Conservative   13;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:|||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
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Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:|||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              |||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| ||||||||| ||| |||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 13
AAR91814
ID   AAR91814 standard; protein; 660 AA.
XX
AC   AAR91814;
XX
DT   26-NOV-1996  (first entry)
XX
DE   Hepatitis E virus strain SAR-55 ORF-2.
XX
KW   Hepatitis E virus; HEV; SAR-55 strain; enteric transmission;
KW   structural region; antigen; detection; antibody; vaccine; immunisation;
KW   infection.
XX
OS   Hepatitis E virus.
XX
PN   WO9610580-A2.
XX
PD   11-APR-1996.
XX
PF   03-OCT-1995;   95WO-US013102.
XX
PR   03-OCT-1994;   94US-00316765.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Tsarev SA,  Emerson SU,  Purcell RH;
XX
DR   WPI; 1996-209320/21.
DR   N-PSDB; AAT27394.
XX
PT   Isolated and purified hepatitis E virus strain SAR-55 DNA - encodes
PT   antigenic protein useful in diagnosis, prophylaxis and treatment of
PT   hepatitis E virus infection.
XX
PS   Claim 6; Page 13-15; 121pp; English.
XX
CC   The present sequence is the protein prod. of ORF-2 from the hepatitis E
CC   virus (HEV) strain SAR-55, which was implicated in an enterically
CC   transmitted non-A, non-B hepatitis in Pakistan. The protein encoded by
CC   the structural region of the virus (i.e. ORF-2), which is capable of
CC   forming HEV like particles, is useful for the detection of HEV antibodies
CC   (pref. IgG or IgM) in blood, plasma, sera, cerebrospinal fluid, tissue,
CC   urine or pleural fluid. The protein, and anti-HEV antibodies generated
CC   using the protein, can also be used in vaccines for immunising an animal
CC   against HEV infection. The protein is identified as a band of greater
CC   than 50 kD following SDS-PAGE of cell lysates of insect cells infected
CC   with a HEV ORF-2 contg. baculovirus, i.e. the claimed recombinant
CC   expression vectors pPIC9-1779, -1780 and -1781
XX
SQ   Sequence 660 AA;

  Query Match          95.3%;  Score 2575;  DB 2;  Length 660;
  Best Local Similarity   94.7%;  Pred. No. 1.8e-214;
  Matches  497;  Conservative   13;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
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Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
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Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:|||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              |||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| | ||||||| ||| |||||||||||| ||||
Db        592 PVSISAVAVLAPHSVLALLEDTMDYPARAHTFDDFCPECRPLGLQ 636


RESULT 14
AAW93386
ID   AAW93386 standard; protein; 660 AA.
XX
AC   AAW93386;
XX
DT   11-JUN-1999  (first entry)
XX
DE   Human HEV ORF 2 protein from strain Sar55.
XX
KW   Swine hepatitis E virus; HEV; cross-reaction; antibody; human; therapy;
KW   vaccine; immunise; infection; detection; diagnosis; prevention.
XX
OS   Hepatitis E virus.
XX
PN   WO9904029-A2.
XX
PD   28-JAN-1999.
XX
PF   17-JUL-1998;   98WO-US014665.
XX
PR   18-JUL-1997;   97US-0053069P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Meng X,  Emerson SU,  Purcell RH;
XX
DR   WPI; 1999-132270/11.
XX
PT   New isolated swine hepatitis E virus - used to develop products for the
```

```
PT   diagnosis, prevention and treatment of hepatitis E virus infection in
PT   mammals, particularly humans.
XX
PS   Example 1; Fig 3A; 70pp; English.
XX
CC   This invention describes a swine hepatitis E virus (HEV) and its natural
CC   mutants which are capable of cross-reacting with antibodies reactive with
CC   a human HEV strain or natural mutants. The HEV and the proteins can be
CC   used in vaccines for immunising against HEV infection. The swine HEV can
CC   be used in humans to prevent possible infection by human HEV. The swine
CC   HEV can also be used as a therapeutic treatment for infection by other
CC   strains of HEV. The swine HEV can also be used for the production of
CC   antibodies which can be used in therapy, detection and diagnosis. The
CC   products can also be used for determining the susceptibility of cells or
CC   organs to infection with swine HEV. The swine HEV is particularly useful
CC   for the development of agents for the prevention, treatment and detection
CC   of human HEV because it is not a human virus and thus can be handled both
CC   experimentally and clinically without fear of severe infection and/or
CC   contamination
XX
SQ   Sequence 660 AA;

  Query Match             95.3%;  Score 2575;  DB 2;  Length 660;
  Best Local Similarity   94.7%;  Pred. No. 1.8e-214;
  Matches  497;  Conservative   13;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:|||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| | ||||||| ||| |||||||||||| ||||
Db        592 PVSISAVAVLAPHSVLALLEDTMDYPARAHTFDDFCPECRPLGLQ 636


RESULT 15
AAW93388
ID   AAW93388 standard; protein; 660 AA.
XX
AC   AAW93388;
XX
DT   11-JUN-1999  (first entry)
XX
DE   Human HEV ORF 2 protein from strain KS2-87.
XX
KW   Swine hepatitis E virus; HEV; cross-reaction; antibody; human; therapy;
KW   vaccine; immunise; infection; detection; diagnosis; prevention.
XX
OS   Hepatitis E virus.
XX
PN   WO9904029-A2.
XX
PD   28-JAN-1999.
XX
PF   17-JUL-1998;   98WO-US014665.
XX
PR   18-JUL-1997;   97US-0053069P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Meng X,  Emerson SU,  Purcell RH;
XX
DR   WPI; 1999-132270/11.
XX
PT   New isolated swine hepatitis E virus - used to develop products for the
PT   diagnosis, prevention and treatment of hepatitis E virus infection in
PT   mammals, particularly humans.
XX
PS   Example 1; Fig 3A; 70pp; English.
XX
CC   This invention describes a swine hepatitis E virus (HEV) and its natural
CC   mutants which are capable of cross-reacting with antibodies reactive with
CC   a human HEV strain or natural mutants. The HEV and the proteins can be
CC   used in vaccines for immunising against HEV infection. The swine HEV can
CC   be used in humans to prevent possible infection by human HEV. The swine
CC   HEV can also be used as a therapeutic treatment for infection by other
CC   strains of HEV. The swine HEV can also be used for the production of
CC   antibodies which can be used in therapy, detection and diagnosis. The
CC   products can also be used for determining the susceptibility of cells or
CC   organs to infection with swine HEV. The swine HEV is particularly useful
CC   for the development of agents for the prevention, treatment and detection
CC   of human HEV because it is not a human virus and thus can be handled both
CC   experimentally and clinically without fear of severe infection and/or
CC   contamination
XX
SQ   Sequence 660 AA;

  Query Match             95.3%;  Score 2575;  DB 2;  Length 660;
  Best Local Similarity   94.7%;  Pred. No. 1.8e-214;
  Matches  497;  Conservative   13;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:|||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531
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Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
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Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
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Db        592 PVSISAVAVLTPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQ 636
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Search completed: July 14, 2005, 15:46:32
Job time : 44.4198 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 14, 2005, 02:26:53 ; Search time 9.08019 Seconds
(without alignments)
5563.078 Million cell updates/sec

Title: US-09-769-066-28
Perfect score: 2701
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2674.5	99.0	659	1	B44212	structural protein
2	2569	95.1	660	1	VHWWH2	structural protein
3	128.5	4.8	5188	2	B85547	probable RTX famil
4	128.5	4.8	5291	2	P90696	hypothetical prote
5	127	4.7	1367	1	S48478	glucan 1,4-alpha-g
6	125	4.6	3282	2	E82750	hemagglutinin-like
7	125	4.6	3442	2	E82589	hemagglutinin-like
8	125	4.6	3455	2	B82519	hemagglutinin-like
9	122.5	4.5	1077	2	H96007	probable acriflavi
10	121	4.5	725	2	A41258	a-agglutinin core
11	120	4.4	1041	2	S55862	probable membrane
12	118.5	4.4	547	2	T41213	probable zinc fing
13	118.5	4.4	2130	2	AB0821	probable exported
14	118	4.4	1104	2	S59310	probable membrane
15	116.5	4.3	583	2	S67571	hypothetical prote
16	116	4.3	351	1	VCVETC	coat protein - tur
17	116	4.3	1975	2	B81192	hemagglutinin/hemo
18	116	4.3	1995	2	G81044	hemagglutinin/hemo
19	115.5	4.3	2054	2	T46612	multi PDZ domain p
20	115	4.3	2015	2	B81989	hypothetical prote
21	115	4.3	3083	2	AH2493	hypothetical prote
22	113.5	4.2	1213	2	T51032	hypothetical prote
23	113.5	4.2	1483	2	C97012	probably celluloso
24	113	4.2	797	1	VGBEX1	glycoprotein X pre
25	113	4.2	1350	2	AF2005	RNA polymerase bet
26	112.5	4.2	1643	2	D71630	outer membrane pro
27	112	4.1	1180	2	E86719	hypothetical prote
28	112	4.1	1345	2	H90975	hypothetical prote
29	112	4.1	1377	2	I54632	tsh protein - Esch
30	112	4.1	2505	1	XYRTFA	enoyl-[acyl-carrie
31	112	4.1	2660	2	E85822	probable invasin Z
32	111.5	4.1	962	2	S03818	carboxymethylcellu
33	111.5	4.1	1374	2	AE3259	extracellular seri
34	111.5	4.1	3570	2	T45025	mucin MUC5B, trach
35	111	4.1	3972	2	S75251	hypothetical prote
36	110.5	4.1	1014	1	NMCLSS	exo-alpha-sialidas
37	110.5	4.1	1306	2	S25370	MSB2 protein - yea
38	110.5	4.1	1746	1	S19694	tenascin precursor
39	110.5	4.1	3624	2	AD0835	large repetitive p
40	110	4.1	1112	2	T32733	AMPA glutamate rec
41	110	4.1	1131	2	T41144	hypothetical serin
42	109.5	4.1	1016	2	H71460	probable outer mem
43	109.5	4.1	1802	2	S69703	HKR1 protein precu
44	109.5	4.1	4199	2	S76412	hypothetical prote
45	109	4.0	973	2	B86547	polymorphic outer

ALIGNMENTS

RESULT 1
B44212
structural protein 2 precursor - hepatitis E virus (strain Mexico)
C;Species: hepatitis E virus
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: B44212
R;Huang, C.C.; Nguyen, D.; Fernandez, J.; Yun, K.Y.; Fry, K.E.; Bradley, D.W.; Tam, A.W.,
Virology 191, 550-558, 1992
A;Title: Molecular cloning and sequencing of the Mexico isolate of hepatitis E virus (HEV
A;Reference number: A44212; MUID:93079857; PMID:1448913
A;Accession: B44212
A;Molecule type: genomic RNA
A;Residues: 1-659 <HUA>
A;Cross-references: UNIPROT:Q03500; GB:M74506; NID:g330017; PIDN:AAA45732.1; PID:g330020
C;Superfamily: hepatitis E virus structural protein 2
C;Keywords: structural protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-659/Product: structural protein 2 #status predicted <SP2>

Query Match 99.0%; Score 2674.5; DB 1; Length 659;
Best Local Similarity 99.4%; Pred. No. 4.4e-179;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
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Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
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Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
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Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPPSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPPSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
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Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
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Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 635


RESULT 2
VHWWH2
structural protein 2 precursor - hepatitis E virus (strain Burma)
C;Species: hepatitis E virus
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: C40778
R;Tam, A.W.; Smith, M.M.; Guerra, M.E.; Huang, C.C.; Bradley, D.W.; Fry, K.E.; Reyes, G.
Virology 185, 120-131, 1991
A;Title: Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length vi
A;Reference number: A40778; MUID:92024067; PMID:1926770
A;Accession: C40778
A;Molecule type: genomic RNA
A;Residues: 1-660 <TAM>
A;Cross-references: UNIPROT:P29326; GB:M73218; NID:g330023; PIDN:AAA45736.1; PID:g330026
A;Note: the authors translated the codon CGC for residue 2 as Ala
C;Superfamily: hepatitis E virus structural protein 2
C;Keywords: structural protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-660/Product: structural protein 2 #status predicted <SP2>

  Query Match             95.1%;  Score 2569;  DB 1;  Length 660;
  Best Local Similarity   94.7%;  Pred. No. 1.1e-171;
  Matches  497;  Conservative   13;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| ||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:||||||||||||||||||||:||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              |||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| |||||||||| ||| |||||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 3
B85547
probable RTX family exoprotein [imported] - Escherichia coli (strain O157:H7, substrain
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85547
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85547
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5188 <STO>
A;Cross-references: UNIPROT:Q8X4H5; GB:AE005174; NID:g12513368; PIDN:AAG54838.1; GSPDB:GN
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z0615

  Query Match             4.8%;  Score 128.5;  DB 2;  Length 5188;
  Best Local Similarity   21.2%;  Pred. No. 8.1;
  Matches  122;  Conservative   70;  Mismatches  242;  Indels  141;  Gaps   27;

Qy         11 VPDVDSRGAILRRQYNLSTS--PLTSSVASGTNLVLYAAPLNPPLPLQDG-----TNTHI 63
              | |          | ::|    :| :  || | :| |     || :  |     |   :
Db       2215 VTDAGGNSGSATHQVTVNTGLPTITFNAISGDN-ILNADEKGQPLTISGGSTGLATGAQV 2273

Qy         64 MAT-EASNYAQYRVARA----TIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITS 118
                |    ||:    |      |:    |       | :| |          ||   |:  |
Db       2274 TVTLNGHNYSATTDASGNWTLTVPVSDLAALGQANYTVSAS--------ATSAAGNT-AS 2324

Qy        119 TDVRILVQPGIASELV--IPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNS 176
              :   :||  |:    :  :  : :    :          |||    |    | : : |   |:
Db       2325 SQANLLVDSGLPDVTINTVAGDDIINAAEAGADQTISGVVTRAAAGDTVTVTLGG---NT 2381

Qy        177 YTNTPYTG------------ALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRG 223
              || |  :              |||  |  :     ::|  | ||
Db       2382 YTATVQSNLSWSVSVPTADLQALGNGDLTIT---ASVTNANGNT---------------- 2422

Qy        224 ADGTAELTTTAATRFMKDLHFTGLNGVGEVGRGIALTLLNLADTL-LGGLPTELISSAGG 282
                || ::|  |    ::     | : |  :  | || :   :  |  | : |  |:|
Db       2423 GSGTRDITIDANLPGLRVDTVAGDDIVNSIEHGQALVITGGSSGLNAGAVLTVTINSVA- 2481

Qy        283 QLFYSRPVVSANGEPTVKLYTSVENAQQDKGVAIP-HDIDLGDSRVVIQDYDNQHEQDRP 341
                                |::   |      | ||  ::    :  :  : | |   : |
Db       2482 -------------------YSATVQADGSWSVGIPAANVSAWPAGPLTVEVDGQSSANNP 2522

Qy        342 TPSPAPSRPFSV-----------LRANDVLWLSLTAAEYDQS-TYGSSTGPVYISDSVTL 389
                : | ||:|          : ::||    : |||   : |   ||  :    :||:
Db       2523 V---SVSHPFTVDLTAVAISINTVASDDV----INAAEKGTNLTLSGSTSGIESGQTVTV 2575

Qy        390 V-NVATGAQAVARSLDWSKVTLDGRPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPY 448
                |   :|| :  || | :    | |: : :       ::  :|     :  | : |
Db       2576 TFGGKTYTASVAANGSWS-VNVPAADLATLPEGAAN-----VQASVSSASGNSASATHAY 2629

Qy        449 N---------YNTTASDQILIENAAGHRVAIS-TYTTRLG-----------AGPV-AIS 485
              :           || ||| ||     ||  : || | |   |              | | |
Db       2630 SVDASAPTLTINTIASDDILNAAEAGSPLTISGTSTAETGQTVTVTLNGATYTGTVQADG 2689

Qy        486 AAAVLAPRSAL-----------ALLEDTFDYPGRA 509
              : :|  | |||           | : |   || |
Db       2690 SWSVSVPTSALGALNASNYTVSATVNDKAGNPGSA 2724


RESULT 4
F90696
hypothetical protein ECs0542 [imported] - Escherichia coli (strain O157:H7, substrain RIM
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F90696
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90696
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5291 <HAY>
A;Cross-references: UNIPROT:Q8X2T1; GB:BA000007; PIDN:BAB33965.1; PID:g13360000; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0542

  Query Match             4.8%;  Score 128.5;  DB 2;  Length 5291;
  Best Local Similarity   21.2%;  Pred. No. 8.4;
  Matches  122;  Conservative   70;  Mismatches  242;  Indels  141;  Gaps   27;

Qy         11 VPDVDSRGAILRRQYNLSTS--PLTSSVASGTNLVLYAAPLNPPLPLQDG-----TNTHI 63
              | |           |  ::|    :| :  || | :| |     || :  |     |   :
Db       2215 VTDAGGNSGSATHQVTVNTGLPTITFNAISGDN-ILNADEKGQPLTISGGSTGLATGAQV 2273

Qy         64 MAT-EASNYAQYRVARA----TIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITS 118
                |    ||:    |      |:    |       | :| |          ||   |:  |
Db       2274 TVTLNGHNYSATTDASGNWTLTVPVSDLAALGQANYTVSAS--------ATSAAGNT-AS 2324

Qy        119 TDVRILVQPGIASELV--IPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNS 176
              :   :||  |:    :  :  : :    :       |||    |    | : : |   |:
Db       2325 SQANLLVDSGLPDVTINTVAGDDIINAAEAGADQTISGVVTRAAAGDTVTVTLGG---NT 2381

Qy        177 YTNTPYTG-------------ALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRG 223
              || | :               ||| |  :     ::|  | ||
Db       2382 YTATVQSNLSWSVSVPTADLQALGNGDLTIT---ASVTNANGNT---------------- 2422

Qy        224 ADGTAELTTTAATRFMKDLHFTGLNGVGEVGRGIALTLLNLADTL-LGGLPTELISSAGG 282
               || ::|  |    ::    | : |  :  | || :   :   |  | : |  |:|
Db       2423 GSGTRDITIDANLPGLRVDTVAGDDIVNSIEHGQALVITGGSSGLNAGAVLTVTINSVA- 2481

Qy        283 QLFYSRPVVSANGEPTVKLYTSVENAQQDKGVAIP-HDIDLGDSRVVIQDYDNQHEQDRP 341
                            |::  |     | ||  ::    :  :  : | |   : |
Db       2482 -------------------YSATVQADGSWSVGIPAANVSAWPAGPLTVEVDGQSSANNP 2522

Qy        342 TPSPAPSRPFSV-----------LRANDVLWLSLTAAEYDQS-TYGSSTGPVYISDSVTL 389
              : | ||:|           : ::||    : |||   : |   ||  :    :||:
Db       2523 V---SVSHPFTVDLTAVAISINTVASDDV----INAAEKGTNLTLSGSTSGIESGQTVTV 2575

Qy        390 V-NVATGAQAVARSLDWSKVTLDGRPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPY 448
               |   :|| :  || | :   | |: : :      ::  :|     :  | : |
Db       2576 TFGGKTYTASVAANGSWS-VNVPAADLATLPEGAAN-----VQASVSSASGNSASATHAY 2629

Qy        449 N---------YNTTASDQILIENAAGHRVAIS-TYTTRLG------------AGPV-AIS 485
              :           || ||| ||    ||  : || | |   |             | | |
Db       2630 SVDASAPTLTINTIASDDILNAAEAGSPLTISGTSTAETGQTVTVTLNGATYTGTVQADG 2689

Qy        486 AAAVLAPRSAL-----------ALLEDTFDYPGRA 509
              : :|  | |||           | : |    || |
Db       2690 SWSVSVPTSALGALNASNYTVSATVNDKAGNPGSA 2724


RESULT 5
S48478
glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae)
N;Alternate names: extracellular glucoamylase; mucin-like protein MUC1; protein YIR019c
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S48478; A26877; B26877; S27281; JC6123
R;Rowley, K.
submitted to the EMBL Data Library, October 1994
A;Reference number: S48478
A;Accession: S48478
A;Molecule type: DNA
A;Residues: 1-1367 <ROW>
A;Cross-references: UNIPROT:P08640; GB:Z47047; EMBL:Z38061; NID:g603997; PID:g763364; GS
R;Yamashita, I.; Nakamura, M.; Fukui, S.
J. Bacteriol. 169, 2142-2149, 1987
A;Title: Gene fusion is a possible mechanism underlying the evolution of STA1.
A;Reference number: A91831; MUID:87194600; PMID:3106330
A;Accession: A26877
A;Molecule type: DNA
A;Residues: 1-242 <YAM>
A;Cross-references: EMBL:M16164; NID:g172522; PIDN:AAA35014.1; PID:g172525
A;Accession: B26877
A;Molecule type: DNA
A;Residues: 762-1331 <YA2>
A;Cross-references: EMBL:M16165; NID:g172523; PIDN:AAA35015.1; PID:g172526
R;Pardo, J.M.; Ianez, E.; Zalacain, M.; Claros, M.G.; Jimenez, A.
FEBS Lett. 239, 179-184, 1988
A;Title: Similar short elements in the 5' regions of the STA2 and SGA genes from Saccharc
A;Reference number: S27281; MUID:89031230; PMID:3141213
A;Accession: S27281
A;Molecule type: DNA
A;Residues: 1-31 <PAR>
A;Cross-references: EMBL:X13857; NID:g4551; PIDN:CAA32069.1; PID:g4552
R;Lambrechts, M.G.; Bauer, F.F.; Marmur, J.; Pretorius, I.S.
Proc. Natl. Acad. Sci. U.S.A. 93, 8419-8424, 1996
A;Title: Muc1, a mucin-like protein that is regulated by Mss10, is critical for pseudohyp
A;Reference number: JC6123; MUID:96323237; PMID:8710886
A;Accession: JC6123
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1367 <LAM>
A;Cross-references: GB:U30626; NID:g1304386; PIDN:AAC49609.1; PID:g1304387
C;Genetics:
A;Gene: SGD:MUC1; STA2; MAL5; DEX2; SGD:S0001458
A;Cross-references: MIPS:YIR019c; SGD:S0001458
A;Map position: 9R
C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase h
C;Keywords: glycosidase; hydrolase; polysaccharide degradation; transmembrane protein
F;5-21/Domain: transmembrane #status predicted <TM1>
F;1350-1366/Domain: transmembrane #status predicted <TM2>

  Query Match             4.7%;  Score 127;  DB 1;  Length 1367;
  Best Local Similarity   20.0%;  Pred. No. 1.5;
  Matches  121;  Conservative   69;  Mismatches  258;  Indels  156;  Gaps   23;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              :|||     | |               |:| :|||  | |         : |:|    :
Db        805 SVAPV----PTPS-------------SSSNITSSAPSSTPFSSSTESSSVPVPTPSSST 846

Qy         61 TH------IMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDM- 113
               |          :|  |: |       ::       |:::   : : ||   || ||:|
Db        847 TESSSAPVSSSTTESSVAPVPTPSSSSNITSSAPSSIPFSSTTESFSTGTTVTPSSSKYP 906

Qy        114 -----NSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLC 168
                  |::||    :|     : :  ||              ::|    | |||    |
Db        907 GSQTETSVSSTTETTIVPTKTTTSVTTPSTTTITTTVCSTGTNSAG----ETTSG----C 958

Qy        169 IHGSPVNSYTNTPYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADG-- 226
                ||     |  | |                 ::|| :|  |  :   ||  :       |
Db        959 ---SPKTVTTTVPTTTT-----------TSVTTSSTTTITTTVCSTGTNSAGETTSGCS 1003

Qy        227 -------------------------TAELTTTAATRFMKDLHFTGLNGVGE-----VGR 255
                                      |  :||  :|  :   : |      ||      | :
Db       1004 PKTITTTVPCSTSPSETASESTTTSPTTPVTTVVSTTVVTTEYSTSTKPGGEITTTFVTK 1063

Qy        256 GIALTLLNL------ADTLLGGLPTEL--------ISSAG--------GQLFYSRPVVSA 293
              | | |          |:    || :          :|||          :  : | :
Db       1064 NIPTTYLTTIAPTPSVTTVTNFTPTTITTTVCSTGTNSAGETTSGCSPKTVTTTVPCSTG 1123

Qy        294 NGEPTVKLYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSV 353
              || | :  | | |          |          :       |  :         : ||| | |
Db       1124 TGEYTTEATTLVTTAVTTTVVTTESSTGTNSAGKTTTGYTTKSVPTTYVTTLAPSAP--V 1181

Qy        354 LRANDVLWLSLTAAEYDQST--YGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLD 411
              | : :  ::|  |    :|    | :|    :  : |:|: |:  :  | |       |
Db       1182 TPATNAVPTTITTTECSAATNAAGETTS---VCSAKTIVSSASAGENTAPSATTPVTT-- 1236

Qy        412 GRPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGY-----PYNYNTTASDQILIENAAGH 466
                :||         |:     :    || |  ||      |  | ||     ||  : |
Db       1237 --AIPTT--------VITTESSVGTNSAGETTTGYTTKSIPTTYITT-----LIPGSNGA 1281

Qy        467 R-----------VAISTYTTRLGAGPVAISAAAVLAPRSALALLED-------TFDYPGR 508
```

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Db       1282 KNYETVATATNPISIKT-TSQLATTASASSVAPVVTSPSLTGPLQSASGSAVATYSVPSI 1340

Qy        509 AHTF 512
Db       1341 SSTY 1344
```

RESULT 6
E82750
hemagglutinin-like secreted protein XF0889 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82750
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82750
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3282 <SIM>
A;Cross-references: UNIPROT:Q9PEY9; GB:AE003928; GB:AE003849; NID:g9105798; PIDN:AAF8369
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0889

Query Match 4.6%; Score 125; DB 2; Length 3282;
Best Local Similarity 21.2%; Pred. No. 7.3;
Matches 128; Conservative 63; Mismatches 212; Indels 200; Gaps 27;

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Qy          1 AVAPAHD------TSPVP-----------------DVDSRGAILRRQYNLSTSPLTSSV 36
Db        439 SVPPATDTPPSTGTMPIPSHPQTAPVLAAGRLTLENDIDNRGGHITAGGAIDAILTTLDN 498

Qy         37 ASGTNLVLYAAPLNPPLPLQDG--TNTH---IMATEA-------SNYAQYRVARATIRYR 84
Db        499 RDGT------AALN-RLTLQGQRLDNQHGILTLATEATIHTHTLNNAAGQLHVNGTLDLT 551

Qy         85 PLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRN 144
Db        552 AQHLNNASGHLLTTG--PQSATL-TIADLLDNTSGTL------ASAGSLTLTAATL---- 598

Qy        145 QGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTTCN 204
Db        599 --------------DTTDGTVQSGQGPLHMDAATLTAHRGTLTSQD--------TLTLTG 636

Qy        205 TNTRVSRYSSTARHRLRRGADGTAELTT-------------------------TAATRF 238
Db        637 THTDLSHATTTAQQITLH----TGDLTTAGGHLTAYGTHTLQLEARTRLDNTGGTIATNG 692

Qy        239 MKDLHFTGLNGVGEVGRGIAL---------TLLNLADTLLGGLPTELI----SSAGGQLF 285
Db        693 TLDLHTAALDNTGGTLHSTATGPNRLDITDTLTNTAGHLLLNGPTTLTTGTWTNTGGHLQ 752

Qy        286 YSRPVV--------------SANGEPTVKLYTSVENAQQDKGVAIPHD-IDLGDSRVVIQ 330
Db        753 ITGPATLHATTLDNRGGILHTATGPLDLRITGTLNN--QDNGLLTTTDALTLTAASLL-- 808

Qy        331 DYDNQH-EQDRPTPSPAP-----SRPFSVLRANDVLWL----------SLTAAEYDQST- 373
Db        809 ---NQHGTLDAAGPAHLTLTGLLDNTAGLLQTAHTLWLTSAGLTNRSGTLTASQLTLDTQ 865

Qy        374 ----------YGSSTGPVYI--------------------SDSVTLVNVATGAQAVARS 402
Db        866 GHTLDNTRGRLGTTTGNLTLHSGPLDNTAGLLQTAAALTIDTGAATLTNRDGGALLAATA 925

Qy        403 LDWSKVTLDGRPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIEN 462
Db        926 LDLTTATLDNRG-GTIDSQTAT--------HLHTTTLDNTTAGHISSSGTLQIDGTTLTN 976

Qy        463 AAG 465
Db        977 TGG 979
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RESULT 7
E82589
hemagglutinin-like secreted protein XF2196 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82589
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82589
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3442 <SIM>
A;Cross-references: UNIPROT:Q9PBE8; GB:AE004032; GB:AE003849; NID:g9107324; PIDN:AAF8499
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2196

Query Match 4.6%; Score 125; DB 2; Length 3442;
Best Local Similarity 21.2%; Pred. No. 7.9;
Matches 128; Conservative 63; Mismatches 212; Indels 200; Gaps 27;

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Qy          1 AVAPAHD------TSPVP-----------------DVDSRGAILRRQYNLSTSPLTSSV 36
Db        439 SVPPATDTPPSTGTMPIPSHPQTAPVLAAGRLTLENDIDNRGGHITAGGAIDAILTTLDN 498

Qy         37 ASGTNLVLYAAPLNPPLPLQDG--TNTH---IMATEA-------SNYAQYRVARATIRYR 84
Db        499 RDGT------AALN-RLTLQGQRLDNQHGILTLATEATIHTHTLNNAAGQLHVNGTLDLT 551

Qy         85 PLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRN 144
Db        552 AQHLNNASGHLLTTG--PQSATL-TIADLLDNTSGTL------ASAGSLTLTAATL---- 598

Qy        145 QGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTTCN 204
Db        599 --------------DTTDGTVQSGQGPLHMDAATLTAHRGTLTSQD--------TLTLTG 636

Qy        205 TNTRVSRYSSTARHRLRRGADGTAELTT-------------------------TAATRF 238
```

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Db        637 THTDLSHATTTAQQITLH----TGDLTTAGGHLTAYGTHTLQLEARTRLDNTGGTIATNG 692

Qy        239 MKDLHFTGLNGVGEVGRGIAL---------TLLNLADTLLGGLPTELI----SSAGGQLF 285

Db        693 TLDLHTAALDNTGGTLHSTATGPNRLDITDTLTNTAGHLLLNGPTTLTTGTWTNTGGHLQ 752

Qy        286 YSRPVV--------------SANGEPTVKLYTSVENAQQDKGVAIPHD-IDLGDSRVVIQ 330

Db        753 ITGPATLHATTLDNRGGILHTATGPLDLRITGTLNN--QDNGLLTTTDALTLTAASLL-- 808

Qy        331 DYDNQH-EQDRPTPSPAP-----SRPFSVLRANDVLWL----------SLTAAEYDQST- 373

Db        809 ---NQHGTLDAAGPAHLTLTGLLDNTAGLLQTAHTLWLTSAGLTNRSGTLTASQLTLDTQ 865

Qy        374 ----------YGSSTGPVYI--------------------SDSVTLVNVATGAQAVARS 402

Db        866 GHTLDNTRGRLGTTTGNLTLHSGPLDNTAGLLQTAAALTIDTGAATLTNRDGGALLAATA 925

Qy        403 LDWSKVTLDGRPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIEN 462

Db        926 LDLTTATLDNRG-GTIDSQTAT--------HLHTTTLDNTTAGHISSSGTLQIDGTTLTN 976

Qy        463 AAG 465

Db        977 TGG 979
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RESULT 8
B82519
hemagglutinin-like secreted protein XF2775 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82519
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: B82519
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3455 <SIM>
A;Cross-references: UNIPROT:Q9P9U6; GB:AE004082; GB:AE003849; NID:g9108003; PIDN:AAF8556
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2775

  Query Match   4.6%; Score 125; DB 2; Length 3455;
  Best Local Similarity   21.2%; Pred. No. 7.9;
  Matches 128; Conservative   63; Mismatches 212; Indels 200; Gaps   27;

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Qy          1 AVAPAHD------TSPVP-----------------DVDSRGAILRRQYNLSTSPLTSSV 36

Db        439 SVPPATDTPPSTGTMPIPSHPQTAPVLAAGRLTLENDIDNRGGHITAGGAIDAILTTLDN 498

Qy         37 ASGTNLVLYAAPLNPPLPLQDG--TNTH---IMATEA-------SNYAQYRVARATIRYR 84

Db        499 RDGT------AALN-RLTLQGQRLDNQHGILTLATEATIHTHTLNNAAGQLHVNGTLDLT 551

Qy         85 PLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRN 144

Db        552 AQHLNNASGHLLTTG--PQSATL-TIADLLDNTSGTL------ASAGSLTLTAATL---- 598

Qy        145 QGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTTCN 204

Db        599 -------------DTTDGTVQSGQGPLHMDAATLTAHRGTLTSQD--------TLTLTG 636

Qy        205 TNTRVSRYSSTARHRLRRGADGTAELTT-------------------------TAATRF 238

Db        637 THTDLSHATTTAQQITLH----TGDLTTAGGHLTAYGTHTLQLEARTRLDNTGGTIATNG 692

Qy        239 MKDLHFTGLNGVGEVGRGIAL---------TLLNLADTLLGGLPTELI----SSAGGQLF 285

Db        693 TLDLHTAALDNTGGTLHSTATGPNRLDITDTLTNTAGHLLLNGPTTLTTGTWTNTGGHLQ 752

Qy        286 YSRPVV--------------SANGEPTVKLYTSVENAQQDKGVAIPHD-IDLGDSRVVIQ 330

Db        753 ITGPATLHATTLDNRGGILHTATGPLDLRITGTLNN--QDNGLLTTTDALTLTAASLL-- 808

Qy        331 DYDNQH-EQDRPTPSPAP-----SRPFSVLRANDVLWL----------SLTAAEYDQST- 373

Db        809 ---NQHGTLDAAGPAHLTLTGLLDNTAGLLQTAHTLWLTSAGLTNRSGTLTASQLTLDTQ 865

Qy        374 ----------YGSSTGPVYI--------------------SDSVTLVNVATGAQAVARS 402

Db        866 GHTLDNTRGRLGTTTGNLTLHSGPLDNTAGLLQTAAALTIDTGAATLTNRDGGALLAATA 925

Qy        403 LDWSKVTLDGRPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIEN 462

Db        926 LDLTTATLDNRG-GTIDSQTAT--------HLHTTTLDNTTAGHISSSGTLQIDGTTLTN 976

Qy        463 AAG 465

Db        977 TGG 979
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RESULT 9
H96007
probable acriflavin resistence protein [imported] - Sinorhizobium meliloti (strain 1021)
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: H96007
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernanc
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endos
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: H96007
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1077 <KUR>
A;Cross-references: UNIPROT:Q92U15; GB:AL591985; PIDN:CAC49728.1; PID:g15141215; GSPDB:GN
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: acrF; SMb21498
A;Genome: plasmid
C;Superfamily: acriflavin resistance protein

  Query Match   4.5%; Score 122.5; DB 2; Length 1077;
  Best Local Similarity   19.4%; Pred. No. 2.2;
  Matches 109; Conservative   79; Mismatches 212; Indels 161; Gaps   23;

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Qy         10 PVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTNTHIMATEAS 69
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                ||  | :   ||   ::|:|  | : | :   :|  |  :   :       |  : | :|:
Db        375 PVALVGTFAVILAMGFSLNTVSLLALVLAIGIVVDDAIVVVENVERVMEENPGMSAAQAA 434

Qy         70 NYAQYRVARATIRYRPLVPNAVGGYAISISFWP-------QTTTTPTSVDMNSITSTDVR 122
               |   :  | :   :: :      : ::| |       |       || |  : |
Db        435 RLAMGEITGAIVAITLVLLSVF----VPVAFIPGLSGQLFQQFAVAVSVSM--VISAINA 488

Qy        123 ILVQPGIASELVIPSERLHYRNQGWRS----------VETSGVAEEEATSGLVMLCIH-G 171
               : : | : : |: |          || |           :|      |  |:::| :  |
Db        489 LTLSPALCAILLKPHHGPKRGILGWISRGIDRTRNGYAHVAGSIARRAIIGVILLAVAIG 548

Qy        172 SPVNSYTNTPYTGALGLLD---FALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTA 228
               :   :  | || |   |   |  |:      : |   | |  |    :  | :| |
Db        549 ASGWLFRIVP-TGFLPSEDQGAFFAEIRLPEGASFNRTDAVVREVET----MLGGIEGVA 603

Qy        229 ELTTTAATRFMKDL---------------------------------------------- 242
               :||     |:  :
Db        604 NVTTVTGYSFLDGIAKSSSAFAIVTMKPFAERQDESASVNAAIGTVMAKGAAIRNAQVFA 663

Qy        243 -HFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGE----P 297
               :  : |:|  | |    ||:|     | | || ::||| :      |:||      |
Db        664 FNLPPIIGLG-TGSGFEYQLLDLQ----GRSPAELAATAGGLM------VAANQNPQLGP 712

Qy        298 TVKLYTSVE-----NAQQDKGVAIPHDIDLGDSRVVIQD-----YDNQHEQDRPTPSPAP 347
               |   |::       |  :|:  |:   : : |   :|      | |
Db        713 TFSTYSASSPQLYLNLDRDRLQAL--GVSVSDLFATLQGTLGSYYVND------------ 758

Qy        348 SRPFSVLRANDVLW-LSLTAAEYDQSTYG--------SSTGPVYISDSVTLVNVATGAQA 398
                 |::   :   | ::: ||| |:            :: | :    ||  |:   | |:
Db        759 ---FNLFGRS---WKVTMQAAEADRDAVDDISRLHVRNAAGDMVPVASVARVDYIVGPQS 812

Qy        399 VARSLDWSKVTLDGRPLP---------TVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPYN 449
               : |  ::  :||:|:|  |           :|| |                | |   || :
Db        813 IVRYNNYRSITLNGQPAPGISSGQALAAMEQVS----------------AATLPPGYSFE 856

Qy        450 YNTTASDQILIENAAGHRVAI 470
               :  ||  ::    |||    |
Db        857 WTGTALQEL---EAAGQTTVI 874


RESULT 10
A41258
a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: a-agglutinin attachment protein AGA1; protein N3431; protein YNR044w
C;Species: Saccharomyces cerevisiae
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C;Accession: A41258; S63375; S17031
R;Roy, A.; Lu, C.F.; Marykwas, D.L.; Lipke, P.N.; Kurjan, J.
Mol. Cell. Biol. 11, 4196-4206, 1991
A;Title: The AGA1 product is involved in cell surface attachment of the Saccharomyces ce
A;Reference number: A41258; MUID:91304412; PMID:2072914
A;Accession: A41258
A;Molecule type: DNA
A;Residues: 1-725 <ROY>
A;Cross-references: UNIPROT:P32323; GB:M60590; NID:g170963; PIDN:AAA34382.1; PID:g170964
R;Pohl, T.M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63346
A;Accession: S63375
A;Molecule type: DNA
A;Residues: 1-725 <POH>
A;Cross-references: EMBL:Z71659; NID:g1302551; PIDN:CAA96325.1; PID:e239834; PID:g130255
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:AGA1
A;Cross-references: SGD:S0005327; MIPS:YNR044w
A;Map position: 14R
C;Keywords: glycoprotein; transmembrane protein
F;8-24/Domain: transmembrane #status predicted <TM1>
F;708-724/Domain: transmembrane #status predicted <TM2>

  Query Match             4.5%;  Score 121;  DB 2;  Length 725;
  Best Local Similarity   19.3%;  Pred. No. 1.6;
  Matches  106;  Conservative   84;  Mismatches  187;  Indels  172;  Gaps   22;

Qy          8 TSPVPDVDSRGAILRRQYNLSTSP-LTSSVASGTNLVLYAAPLNPPLPLQDGTNTHIMAT 66
              |||      |  :     |: |||| ||||              :| |     ::| | :|
Db        275 TSPSSKSTSASSTSTSSYSTSTSPSLTSS-------------SPTLASTSPSSTSISST 320

Qy         67 EASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTT------TTPTSVDMNSITSTD 120
                 : :               : :::   : |:| :  :|      :| ::|   |:||:
Db        321 FTDSTSS------------LGSSIASSSTSVSLYSPSTPVYSVPSTSSNVATPSMTSST 367

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVET-------------SGV----------A 156
              |   |    :|| :  |           |: |                |||          :
Db        368 VETTVSSQSSSEYITKS----------SISTTIPSFSMSTYFTTVSGVTTMYTTWCPYS 416

Qy        157 EEEATSGLVML----------CIHGSPVNSYTNTPYTGALGLLDFALELEFRNL-TTCNT 205
              |  || |  :          | | | : | | :       |:  :::  :|: |: :|
Db        417 SESETSTLTSMHETVTTDATVCTHESCMPSQTTS-------LITSSIKMSTKNVATSVST 469

Qy        206 NTRVSRY-------SSTARHRLRRGADGTAELTTTAATRFMKDL---------HFTGLNG 249
              :|  | |       :| :   ::  :  :    ||:   ::  :          | ||
Db        470 STVESSYACSTCAETSHSYSSVQTASSSSVTQQTTSTKSWVSSMTTSDEDFNKHATGKYH 529

Qy        250 VGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSA-------NGEPTVKLY 302
              |   |      | :: | |    : :|  |         |  |:|:       : : |: |:
Db        530 VTSSGTSTISTSVSEA-TSTSSIDSE--SQEQSSHLLSTSVLSSSSLSATLSSDSTILLF 586

Qy        303 TSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWL 362
              :|| :            : :  | |      :  |  :|| | |
Db        587 SSVSS------------LSVEQSPVTTLQISSTSEILQPTSSTA---------------- 618

Qy        363 SLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQYS 422
                    :|  :||       |::  :::| : :|  ::: | :|     |||
Db        619 --------IATISAST------SSLSATSISTPSTSVESTIESSSLT------PTVSSIF 658

Qy        423 KTFFVLP--LRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
               :    |  |:  ::  |  ||      |      |  : |    |      |  |||  |
Db        659 LSSSSAPSSLQTSVTTTEVSTTSISIQYQ----TSSMVTISQYMG-----SGSQTRLPLG 709

Qy        481 PVAISAAAV 489
               :  :  ||
Db        710 KLVFAIMAV 718


RESULT 11
S55862
probable membrane protein YNL327w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N0320
C;Species: Saccharomyces cerevisiae
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55862; S63308; S51288
R;Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin, C.
Yeast 11, 567-572, 1995
A;Title: Sequencing analysis of a 15.4 kb fragment of yeast chromosome XIV identifies the
A;Reference number: S55859; MUID:95373280; PMID:7645347
A;Accession: S55862
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1041 <MAF>
A;Cross-references: UNIPROT:P42835; EMBL:Z46259; NID:g633655; PIDN:CAA86371.1; PID:g63365
R;Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin, C.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63287
A;Accession: S63308
A;Molecule type: DNA
A;Residues: 1-1041 <MAW>
A;Cross-references: EMBL:Z71603; NID:g1302444; PID:e239572; PID:g1302445; MIPS:YNL327w
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:EGT2
A;Cross-references: SGD:S0005271; MIPS:YNL327w
A;Map position: 14L
C;Keywords: transmembrane protein
F;4-20/Domain: transmembrane #status predicted <TM1>
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F;1025-1041/Domain: transmembrane #status predicted <TM2>

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Qy         29 TSPLTSSVASGTNLVLYAAPLNPPLPLQDGTNTHIMATEASNYAQYRVAR---ATIRYRP 85
Db        405 TTPSSSLSATETYSIISSASISVTQASYIDNSTTTAVTQSTSTIAVSSAEKLSSTLSY-- 462

Qy         86 LVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQ 145
Db        463 -----TSNVTISVSSATQHTTTPSYVS-NSTTLSSSSVL---------------------- 495

Qy        146 GWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTPY---------TGALGLLDFALELE 196
Db        496 --ESVISSPYLANTTVSG-------ASSASQSTNPPYVSNSTTSSATQLATIAPFAINIT 546

Qy        197 FRNLTTCNTNTRVSRYSSTARHRLRRG--------ADGTAELTTTAATRFMKDL------ 242
Db        547 GTSISSSITNT--SSVSSTT-SSLSSGPFVSNTAVASGSYILTTTTESAQLTEIGSLIPI 603

Qy        243 ----HFTGLNGVGEVGRG-------IALTLLNLADTLLGGLPTELISSA---------- 280
Db        604 STITTSTTTSGTDKTGSNKVASSTEIAQSIVNNSSLSVSTINTNAATAAANARNATFTHA 663

Qy        281 --GGQL---FYSRPVVSANGEPTVKLYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQ 335
Db        664 THSGGSLQPSYHSSSLLSSTID--TKVTTATTSTSRDGSSSLAFTTGLNQSVVTGTD---- 717

Qy        336 HEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQ----STY------GSSTGPVYISD 385
Db        718 -----------KSDTYSVISSTE----SAQVTEYDSLLPISTLKPTVVTGTSRNSTFSMV 762

Qy        386 SVTLVNVATG-----AQAVARSLDWSKVTLDGRPLP--TVE------------------- 419
Db        763 SSTKLTEATATDKGDAYSVISSTQSAQVTEYGSMLPISTLETPTVIMSTDESGYFTLTTC 822

Qy        420 -------QYSKTFFVLPLRGKLSFWEAG--------TTKAGYPYNYNTTASDQILIENAA 464
Db        823 TESGQATEYGSLIPISTLDGSVIYTFTGESVVVGYSTTVGAAQYAQHTSL---VPVSTIK 879

Qy        465 GHRVAIST-------YTTRLGAGPVA-----ISAAAVLAPRSALALLE----------DT 502
Db        880 GSKTSLSTEESVVAGYSTTVGAAQYAQHTSLVPVSTIKGSKTSLSTEESVVAGYSTTVDS 939

Qy        503 FDYPGRAH--------------TFDDFCPECRAL 522
Db        940 AQYAEHTNLVAIDTLKTSTFQKATATEVCVTCTAL 974


RESULT 12
T41213
probable zinc finger protein SPCC1906.05 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 20-Oct-2000 #sequence_revision 08-Dec-2000 #text_change 09-Jul-2004
C;Accession: T41213; T41109
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z21969
A;Accession: T41213
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-379 <LYN1>
A;Cross-references: UNIPROT:O74463; EMBL:AL031538; NID:g3581923; PIDN:CAA20774.1; PID:g3
A;Experimental source: strain 972h-; cosmid c1906
A;Accession: T41109
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 320-547 <LYN2>
A;Cross-references: EMBL:AL031540; NID:g3581876; PIDN:CAA20775.1; PID:g3581877; GSPDB:GN
A;Experimental source: strain 972h-; cosmid c1739
C;Genetics:
A;Gene: SPDB:SPCC1906.05; SPDB:SPCC1739.01
A;Map position: 3

  Query Match             4.4%;  Score 118.5;  DB 2;  Length 547;
  Best Local Similarity   21.8%;  Pred. No. 1.6;
  Matches  109;  Conservative   66;  Mismatches  187;  Indels  139;  Gaps   21;

Qy         45 YAAPLNPPLPLQDGTNTHIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQT 104
Db         92 HALPGNTNLP--NGTSTNTMASMAANGGASSVA----------SKQMGANQISPSLSSKT 139

Qy        105 TTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVE---------TSGV 155
Db        140 MKNPAD-KANNTTATDVR----GNTATSPYFPFSRSPGRHSGNSTINGMMTTPNFLSSGV 194

Qy        156 AE------EEATSGLVMLCIHGSPV--------------NSYTNTPYTGALGLLDFALE 194
Db        195 NSRSVDEFNNSSSGFPS-SLNGIPIASPPLATSPTSFSLASSASSTNLGGSKGLL----- 248

Qy        195 LEFRNLTTCNT-----------NTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLH 243
Db        249 --FQQMTSENNRDYFSRRPTLLNTYGNRCSSTDT------LSSLSRLTSQDPLKASLPLQ 300

Qy        244 FTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYT 303
Db        301 SPPL--APKTGVSLSRPRLTL-DQSLGNL------SLGSGINQRRQVPRSNS--YAGAFP 349

Qy        304 SVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLS 363
Db        350 SVVSASLPTKVDLNHQMDVSD-----------EEQRFLSTPLGSFDESILGSSPINRLS 397

Qy        364 LTAAEYDQS----------------------TYGSSTGPVYISDSVTLVNVATGAQ--- 397
Db        398 SSFKQYTSSLKSPGLSTRTSSTMNSLNSSRFGAYFSKSRYVEGSGSMSTTPLATSVNNSY 457

Qy        398 ------AVARSLDWSKVTLDG-RPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNY 450
Db        458 KLPSGFSVREEAVFSSPTTEGSRPVSLARLKSEPIF-------RSDTASPETIAG----L 506

Qy        451 NTTASDQILIENAAGHRVAIS 471
Db        507 GDTKNDPVVSTNNSVSRITVA 527


RESULT 13
AB0821
probable exported protein STY2760 [imported] - Salmonella enterica subsp. enterica serova
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB0821
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0821
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2130 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02718.1; PID:g16503731; GSPDB:GN00176
C;Genetics:
A;Gene: STY2760

  Query Match             4.4%;  Score 118.5;  DB 2;  Length 2130;
  Best Local Similarity   22.6%;  Pred. No. 11;
  Matches  114;  Conservative   55;  Mismatches  215;  Indels  121;  Gaps   24;

Qy         28 STSPLTSSVASGTNLVLYAAPLNPPLPLQ--DGTNTHIMATEASNYAQYRVARATIRYRP 85
Db        985 NTSVYTSCLAS-DNPVPAAITIEPVDPSQWYDGSGVHALKVKKGDTLQLKVTVKDASGKP 1043
```

```
Qy          86 LVPNAV------GGYAISISFWP-------QTTTTPTSVDMNSITSTDVRILVQPGIASE 132
               || |        ||      :       |   ||  :|  |:  |  ::  | |
Db        1044 -VPEAPFVLTRGDGYDRKGEKYTAQDGSDLQNIVTPVVIDGESLAWTTTKMGSQTGPDGT 1102

Qy         133 LVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFA 192
               :|   |      | |:  |: : |  | |  :        : :   :|       | :
Db        1103 RIISVTRPD--THGTRTAITATLYENVAVSASI------DTIFTVVTSP--------DVS 1146

Qy         193 LELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKD----LHFTGLN 248
               :   : ::|   |    :  |     :       |  |  : | |  : :|    : | | |
Db        1147 VARMWGHMTPSLTAADSAVYKRPLLY------DELA--SKTGAAEYPEDNERWVVFYGPN 1198

Qy         249 GVGEV-----GRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYT 303
               |      :|   ::  | |:|    |   |                :| | | :: |
Db        1199 TTKTVSPEACSKGYFPSVEQL-DSLYSKYPNGAIK------------TAQGWPIIRSYW 1244

Qy         304 SVENAQQDKGVAIPHD---IDLGDS--RVV--IQDYDNQHEQDRPTPSPAPSRPFSVLRA 356
               |  ||      | |:|   :|| |   | |  | | |::    || |   |
Db        1245 SGTNAGTITPGAPPYDYYTVDLNDDAHRKVPNISDSDRQYQICAATPQPLAGR------- 1297

Qy         357 NDVLWLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLP 416
                 :   | | : |     :       |||: ||   | |                 | :|
Db        1298 --ITLTSTLATDSDIQAVKAKN-----SDSIPLVITTTDAA-------------GNPVP 1336

Qy         417 -----------TVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAG 465
                        |   | ||      |  :   |  | :   : ||       |  | |
Db        1337 YTPFSLIRDAGTARNTSYTF-----TGSTNMMLAPPTGSAQQFYYN-----GYTIYGATG 1386

Qy         466 -HRVAISTYTTRLGAGPVAISAAAV 489
               |: | |   | |   :  ||:
Db        1387 ADGTAVLTLTQAAGPGVKNVITAAL 1411
```

RESULT 14
S59310
probable membrane protein YMR317w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YM9924.09
C;Species: Saccharomyces cerevisiae
C;Date: 29-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 19-Apr-2002
C;Accession: S59310
R;Churcher, C.M.
submitted to the EMBL Data Library, September 1995
A;Reference number: S59302
A;Accession: S59310
A;Molecule type: DNA
A;Residues: 1-1104 <CHU>
A;Cross-references: EMBL:Z54141; GSPDB:GN00013; MIPS:YMR317w
A;Experimental source: strain AB972
C;Genetics:
A;Gene: MIPS:YMR317w
A;Cross-references: SGD:S0004936
A;Map position: 13R

  Query Match 4.4%; Score 118; DB 2; Length 1104;
  Best Local Similarity 19.0%; Pred. No. 4.7;
  Matches 109; Conservative 92; Mismatches 214; Indels 160; Gaps 23;

```
Qy           7 DTSPVPDVDSRGAIL----------RRQYNLST-----------SPLTSSVA-----SGT 40
               | |  | : | |: :          :  :: ||           || :|:::     | |
Db         192 DVSSSPKISSSGSAVTSVGTTSDASKEVFSSSTSDVSSLLSSTSSPASSTISETLPFSST 251

Qy          41 NLVLYAAPLNPPLPLQDGTNTHIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISI-- 98
               | : ::|::   |    |:: : :  :|: :    : | :   :| :       |:
Db         252 ILSITSSPVSSEAP--SATSSSVSSEASSSTSSSVSSEAPLATSSVVSSEAPSSTSSVVS 309

Qy          99 SFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSE----------------RLH 141
               |  | :|::  | :::| ||: |    :  :|:  |: ||
Db         310 SEAPSSTSSSVSSEISSTTSSSVS--SEAPLATSSVVSSEAPSSTSSSVSSEAPSSTSSS 367

Qy         142 YRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLT 201
                 ::   | :|  :|  :|   ||      |  :|  ::    |:  |  |    | :
Db         368 VSSEAPSSTSSSVSSEISSTKSSVMSSEVSSATSSLVSSEAPSAISSL--ASSRLFSSKN 425
```

```
Qy         202 TCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLHFTGLNGVGEVGRGIALTL 261
               |  |:| |:  :|:    ||  ::     | |:   ::    || |           |
Db         426 TSVTSTLVATEASSVTSSLRPSSE------TLASNSIIESSLSTGYNST-------VSTT 472

Qy         262 LNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGVAIPHDID 321
               : | : ||      :||:  ::  |:              ||  ::   |   |
Db         473 TSAASSTLG----SKVSSSNSRMATSK-------------TSSTSSDLSKSSVI----- 509

Qy         322 LGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYD--QSTYGSSTG 379
               |:|  |     :       | || ||           :|  :|::|      |   ||:
Db         510 FGNSSTVT---TSPSASISLTASPLPS----------VWSDITSSEASSISSNLASSSA 555

Qy         380 P---------------------------VYISDSVTLVNVATGA------QAVARSLDW 405
               |                           :  |::    |:|| :      :| ||||
Db         556 PSDNNSTIASASLIVTKTKNSVVSSIVSSITSSETTNESNLATSSTSLLSNKATARSLST 615

Qy         406 SKVTLDGRPLPT---VEQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIEN 462
               |  |     :||       | |  : |          | : :      |:|    ::  :
Db         616 SNAT-SASNVPTGTFSSMSSHTSVITP----------GFSTSSASLAINST----VVSSS 660

Qy         463 AAGHRVAI-----STYTTRLGAGPVAISAAAVLAP 492
               ||:  :      :| |       |  :|:    ||
Db         661 LAGYSFSTPESSPTTSTLVTSEAPSTVSSMTTSAP 695
```

RESULT 15
S67571
hypothetical protein YDL038c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein D2726
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C;Accession: S67571
R;Paulin, L.; Saren, A.M.; Laamanen, P.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67560
A;Accession: S67571
A;Molecule type: DNA
A;Residues: 1-583 <PAU>
A;Cross-references: UNIPROT:Q99175; EMBL:Z74087; NID:g1431021; PID:e252991; PID:g1431023;
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YDL038c
A;Cross-references: SGD:S0002196
A;Map position: 4L
C;Superfamily: pig submaxillary mucin

  Query Match 4.3%; Score 116.5; DB 2; Length 583;
  Best Local Similarity 18.8%; Pred. No. 2.4;
  Matches 102; Conservative 91; Mismatches 227; Indels 123; Gaps 20;

```
Qy          28 STSPLTSSVASGTNLVLYAAPLNPPLPLQDGTNTHIMATEA----------SNYAQYRV 76
               |:| : :||   |:::  ::    |    | | : :  | |          :|   : |
Db          18 SSSDVATSVDPTTSVI--SSTSADPTTSADSTTSTVQTTSAGPSNNIGNSTLANSTTFAV 75

Qy          77 ARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIP 136
               :  :|   |   : |    :  :    ||:  :| |: : || :: :::     |  :|
Db          76 SSTSI--DPTSSSDVITSTVQTTSIEPTTSLVSSNDITTSTSLNISVVISTSTDSTSLIE 133

Qy         137 SERL----------HYRNQGWRSVETS---GVAEEEATSGLVMLCIHGSPVNSYTNT-- 180
               |            || :   | ||     : : |||         | :|   |
Db         134 STTTVGPHASSSVAGMYRTRSSDEVTTSTDPTSSSDVATS--------ADPTSSSAVTTL 185

Qy         181 --PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRF 238
                 | |    ::  :::    :    : :   |  |||:       || |    :| :|
Db         186 VDPTTSV--VISTSVDQTSSSDVATSVDPTTSVISSTS-------ADPTTSADSTTST-- 234

Qy         239 MKDLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPT----------------------- 274
                  : | ::    |      :   :   :|    ||
Db         235 ---VQTTSVDPTSSVVSSAPVDPASSVVSLTSSYPTSSSTVTISANSNGSATLAAQTTSI 291

Qy         275 ----ELISSAGGQLFYSRP--------VVSANGEPTVKLYTSVE-NAQQDKGVAIPHDID 321
                   ::||:|     |          | | : |||  : :|    : :  |     |:
```

```
Db        292 DPVSSIVSSSGATTIISSASIDPASSVVSSTSSEPTSFIVSSTSVYSTRPSGPTTSTDLA 351

Qy        322 LGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPV 381
              ::::         ||  | | : :   |   : |:   |:  :: | ||:  |  ||
Db        352 TFSDTIILRVSTTSTSQDTQTVSSSLTDMVSSTGSADLSVSSIQRSQVDPSTFAVSNSPV 411

Qy        382 YISDSVTLVNVATGAQAVARSLDWSK-----------VTLDGRPLPTVEQYSKTFFVLP 429
              | : |    : :||    : ||  |:            |||      :  : | |  : |
Db        412 YPTASTG--STSTGIPIASESLSLSRQQGISATSSSSIVTLTPVDSASSSRSSATSIIKP 469

Qy        430 ----------LRGKLSFWEA-GTTKAGYP----YNYNTTASDQILI-ENAAGHRVAIS-T 472
                       :  :|  :|  :||: ||     :  | ||:  |:  ::: | : :  |
Db        470 NMPVSSNDSKTQSSVSVVDAFQSTKSSYPSITSADPTTLASENGLVGSSSSAHPITLDRT 529

Qy        473 YTT 475
              | :
Db        530 YAS 532
```

Search completed: July 14, 2005, 15:51:44
Job time : 11.0802 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 14, 2005, 01:31:43 ; Search time 38.3019 Seconds
(without alignments)
7019.016 Million cell updates/sec

Title: US-09-769-066-28
Perfect score: 2701
Sequence: 1 AVAPAHDTSPVPDVDSRGAI.....PGRAHTFDDFCPECRALGLQ 525

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2674.5	99.0	659	1	VST2_HEVME	Q03500 hepatitis e
2	2579	95.5	660	2	Q9E8G5	Q9e8g5 hepatitis e
3	2575	95.3	660	1	VST2_HEVPA	P33426 hepatitis e
4	2575	95.3	660	2	Q77EC8	Q77ec8 hepatitis e
5	2575	95.3	660	2	Q89468	Q89468 hepatitis e
6	2575	95.3	660	2	Q9W7W9	Q9w7w9 hepatitis e
7	2575	95.3	660	2	Q9WQA0	Q9wqa0 hepatitis e
8	2569	95.1	660	1	VST2_HEVBU	P29326 hepatitis e
9	2569	95.1	660	2	O91855	O91855 hepatitis e
10	2569	95.1	660	2	Q69419	Q69419 hepatitis e
11	2568	95.1	660	2	O91856	O91856 hepatitis e
12	2568	95.1	660	2	Q69411	Q69411 hepatitis e
13	2563	94.9	660	2	Q81878	Q81878 hepatitis e
14	2560	94.8	660	2	Q6XXV0	Q6xxv0 hepatitis e
15	2559	94.7	660	2	Q80IY5	Q80iy5 hepatitis e
16	2556	94.6	660	2	Q8JJM8	Q8jjm8 hepatitis e
17	2555	94.6	660	2	Q81871	Q81871 hepatitis e
18	2554	94.6	660	2	Q8JJM4	Q8jjm4 hepatitis e
19	2553	94.5	660	2	O36613	O36613 swine hepat
20	2553	94.5	660	2	Q6J8F7	Q6j8f7 hepatitis e
21	2552	94.5	660	2	Q8V729	Q8v729 swine hepat
22	2552	94.5	660	2	Q8AZM3	Q8azm3 hepatitis e
23	2552	94.5	660	2	Q9WLL4	Q9wll4 hepatitis e
24	2552	94.5	660	2	Q9YLQ9	Q9ylq9 hepatitis e
25	2550	94.4	660	2	Q80IR7	Q80ir7 hepatitis e
26	2548	94.3	660	2	Q68985	Q68985 hepatitis e
27	2547	94.3	659	2	Q8JT32	Q8jt32 hepatitis e
28	2547	94.3	660	2	Q911I4	Q911i4 hepatitis e
29	2547	94.3	660	2	Q6J8G3	Q6j8g3 hepatitis e
30	2545	94.2	660	1	VST2_HEVMY	Q04611 hepatitis e
31	2543	94.2	660	2	Q8BB05	Q8bb05 swine hepat
32	2542	94.1	660	2	Q9YLR2	Q9ylr2 hepatitis e
33	2532	93.7	674	2	Q8JJN2	Q8jjn2 hepatitis e
34	2532	93.7	674	2	Q7TGF1	Q7tgf1 hepatitis e
35	2531	93.7	674	2	Q6BD78	Q6bd78 hepatitis e
36	2529	93.6	550	2	Q8JVV3	Q8jvv3 hepatitis e
37	2529	93.6	671	2	Q8JJM1	Q8jjm1 hepatitis e
38	2529	93.6	674	2	Q8JJN6	Q8jjn6 hepatitis e
39	2528	93.6	674	2	Q6BD83	Q6bd83 hepatitis e
40	2526	93.5	674	2	Q806D7	Q806d7 hepatitis e
41	2526	93.5	674	2	Q806E0	Q806e0 swine hepat
42	2526	93.5	674	2	Q80IR5	Q80ir5 hepatitis e
43	2525	93.5	674	2	Q6PMR3	Q6pmr3 swine hepat
44	2506	92.8	672	2	Q9IVZ8	Q9ivz8 hepatitis e
45	2395	88.7	605	2	Q9YWL0	Q9ywl0 hepatitis e

ALIGNMENTS

RESULT 1
VST2_HEVME
ID VST2_HEVME STANDARD; PRT; 659 AA.
AC Q03500;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Structural protein 2 precursor.
GN ORFNames=ORF2;
OS Hepatitis E virus (strain Mexico) (HEV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=31768;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93079857; PubMed=1448913;
RA Huang C.C., Nguyen D., Fernandez J., Yun K.Y., Fry K.E., Bradley D.W.,
RA Tam A.W., Reyes G.R.;
RT "Molecular cloning and sequencing of the Mexico isolate of hepatitis E
RT virus (HEV).";
RL Virology 191:550-558(1992).
CC -!- FUNCTION: Contains a high basic amino acid content suggesting that
CC it may be involved in the encapsidation of the genomic RNA by
CC effectively neutralizing the negatively charged RNA.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; M74506; AAA45732.1; -.
DR PIR; B44212; B44212.
DR InterPro; IPR004261; SP2.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF03014; SP2; 1.
KW Signal.
FT SIGNAL 1 22 By similarity.
FT CHAIN 23 659 Structural protein 2.
SQ SEQUENCE 659 AA; 70640 MW; CF75E75EFD8FBE2C CRC64;

Query Match 99.0%; Score 2674.5; DB 1; Length 659;
Best Local Similarity 99.4%; Pred. No. 6.1e-178;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```
Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231
```

```
Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHS-ARGADGTAELTTTAATRFMK 350

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 410

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 470

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 530

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 590

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||||||||||||||||||||||||||||||||||||||||||
Db        591 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 635
```

RESULT 2
Q9E8G5
ID Q9E8G5 PRELIMINARY; PRT; 660 AA.
AC Q9E8G5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Structural protein.
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Abb-2B;
RX MEDLINE=20271579; PubMed=10813471;
RA van Cuyck-Gandre H., Zhang H.Y., Tsarev S.A., Warren R.L.,
RA Caudill J.D., Snellings N.J., Begot L., Innis B.L., Longer C.F.;
RT "Phylogenetically distinct hepatitis E viruses in Pakistan.";
RL Am. J. Trop. Med. Hyg. 62:187-189(2000).
DR EMBL; AF185822; AAG16766.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70903 MW; 1F506BE3CFB3BACE CRC64;

Query Match 95.5%; Score 2579; DB 2; Length 660;
Best Local Similarity 94.9%; Pred. No. 2.8e-171;
Matches 498; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

```
Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||:|||||||||||||||||||||||||:|||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| ||||||||| ||| ||||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 3
VST2_HEVPA
ID VST2_HEVPA STANDARD; PRT; 660 AA.
AC P33426;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Structural protein 2 precursor.
GN ORFNames=ORF2;
OS Hepatitis E virus (strain Pakistan) (HEV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=33774;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92115700; PubMed=1731327;
RA Tsarev S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J.,
RA Malik I.A., Iqbal M., Purcell R.H.;
RT "Characterization of a prototype strain of hepatitis E virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).
CC -!- FUNCTION: Contains a high basic amino acid content suggesting that
CC it may be involved in the encapsidation of the genomic RNA by
CC effectively neutralizing the negatively charged RNA.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; M80581; AAA45727.1; -.
DR InterPro; IPR004261; SP2.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF03014; SP2; 1.
KW Signal.
FT SIGNAL 1 22 By similarity.
FT CHAIN 23 660 Structural protein 2.
SQ SEQUENCE 660 AA; 70980 MW; 8085BC53CFB46FD3 CRC64;

Query Match 95.3%; Score 2575; DB 1; Length 660;
Best Local Similarity 94.7%; Pred. No. 5.3e-171;
Matches 497; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171
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Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:||||||| ||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||:|||||||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| | ||||||| ||| ||||||||||||| ||||
Db        592 PVSISAVAVLAPHSVLALLEDTMDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 4
Q77EC8
ID Q77EC8 PRELIMINARY; PRT; 660 AA.
AC Q77EC8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Capsid protein.
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sar-55;
RX MEDLINE=21625046; PubMed=11742081; DOI=10.1073/pnas.251555098;
RA Emerson S.U., Zhang M., Meng X.-J., Nguyen H., St Claire M.,
RA Govindarajan S., Huang Y.K., Purcell R.H.;
RT "Recombinant hepatitis E virus genomes infectious for primates:
RT importance of capping and discovery of a cis-reactive element.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:15270-15275(2001).
DR EMBL; AF444003; AAL50059.1; -.
DR EMBL; AF444002; AAL50056.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70979 MW; 8085BC53CFB46FD3 CRC64;

Query Match 95.3%; Score 2575; DB 2; Length 660;
Best Local Similarity 94.7%; Pred. No. 5.3e-171;
Matches 497; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| ||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:||||||| ||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||:|||||||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| | ||||||| ||| ||||||||||||| ||||
Db        592 PVSISAVAVLAPHSVLALLEDTMDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 5
Q89468
ID Q89468 PRELIMINARY; PRT; 660 AA.
AC Q89468;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Unnamed protein product (ORFs 1-3).
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RA Yin S.R., Purcell R.H., Emerson S.U.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K52-87;
RX MEDLINE=95176571; PubMed=7871758;
RA Yin S., Purcell R.H., Emerson S.U.;
RT "A new Chinese isolate of hepatitis E virus: comparison with strains
RT recovered from different geographical regions.";
RL Virus Genes 9:23-32(1994).
DR EMBL; L25547; AAA91080.1; -.
DR EMBL; L25595; AAA65490.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70979 MW; DC68116DCD639175 CRC64;

Query Match 95.3%; Score 2575; DB 2; Length 660;
Best Local Similarity 94.7%; Pred. No. 5.3e-171;
Matches 497; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

```
Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| ||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
                 ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
                 ||:||  |||||:||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
                 |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
                 ||||||||||||||||||||:||||||||||||||||||:|||||||||  |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
                 ||||||||||||||||||||||||||||||||||||:|:|||||||||||||||  ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
                 ||:||| ||| | |||||||| ||| |||||||||||| ||||
Db        592 PVSISAVAVLTPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQ 636


RESULT 6
Q9W7W9
ID   Q9W7W9      PRELIMINARY;      PRT;   660 AA.
AC   Q9W7W9;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Structural protein 2 (Structural viral protein).
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HEV-Morocco;
RX   MEDLINE=99107414; PubMed=9892396;
RX   DOI=10.1002/(SICI)1096-9071(199902)57:2<126::AID-JMV7>3.3.CO;2-F;
RA   Meng J., Cong M., Dai X., Pillot J., Purdy M.A., Fields H.A.,
RA   Khudyakov Y.E.;
RT   "Primary structure of open reading frame 2 and 3 of the hepatitis E
RT   virus isolated from Morocco.";
RL   J. Med. Virol. 57:126-133(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Chen G., Meng J.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF065061; AAD10627.1; -.
DR   EMBL; AY230202; AAO72992.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70943 MW;  9719D30CCD932950 CRC64;

  Query Match             95.3%;  Score 2575;  DB 2;  Length 660;
  Best Local Similarity   94.7%;  Pred. No. 5.3e-171;
  Matches  497;  Conservative   14;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
                 |||||||| |||||||||||||||||||||||||||:|||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
                 ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
                 ||:|:  |||||:||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
                 |||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
                 ||||||||||||||||||||:||||||||||||||||||:|||||||||  |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
                 ||||||||||||||||||||||||||||||||||||:|:|||||||||||||||  ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
                 ||:||| ||||| |||||||| ||| |||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 7
Q9WQA0
ID   Q9WQA0      PRELIMINARY;      PRT;   660 AA.
AC   Q9WQA0;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   ORF-2.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99350000; PubMed=10423137;
RA   Arankalle V.A., Paranjape S., Emerson S.U., Purcell R.H.,
RA   Walimbe A.M.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from India (1976-
RT   1993).";
RL   J. Gen. Virol. 80:1691-1700(1999).
DR   EMBL; AF124407; AAD45493.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71040 MW;  03B72DDF0AB7B521 CRC64;

  Query Match             95.3%;  Score 2575;  DB 2;  Length 660;
  Best Local Similarity   94.7%;  Pred. No. 5.3e-171;
  Matches  497;  Conservative   13;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
                 |||||||| |||||||||||||||||||||||||||:|||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
                 ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
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Db        292 PYTGALGLLDFALELEPRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||:|||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||:|||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| || || ||||||||| ||| |||||||||||| ||||
Db        592 PVSISAVAVFAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 8
VST2_HEVBU
ID   VST2_HEVBU     STANDARD;      PRT;   660 AA.
AC   P29326;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   Structural protein 2 precursor.
GN   ORFNames=ORF2;
OS   Hepatitis E virus (strain Burma) (HEV).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=31767;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92024067; PubMed=1926770;
RA   Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
RA   Fry K.E., Reyes G.R.;
RT   "Hepatitis E virus (HEV): molecular cloning and sequencing of the
RT   full-length viral genome.";
RL   Virology 185:120-131(1991).
CC   -!- FUNCTION: Contains a high basic amino acid content suggesting that
CC       it may be involved in the encapsidation of the genomic RNA by
CC       effectively neutralizing the negatively charged RNA.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M73218; AAA45736.1; -.
DR   PIR; C40778; VHWWH2.
DR   InterPro; IPR004261; SP2.
DR   InterPro; IPR008975; Viral_cap_coat.
DR   Pfam; PF03014; SP2; 1.
KW   Signal.
FT   SIGNAL       1     19       Potential.
FT   CHAIN       20    660       Structural protein 2.
SQ   SEQUENCE   660 AA;  70978 MW;  5832A013CCC4A61C CRC64;

  Query Match             95.1%;  Score 2569;  DB 1;  Length 660;
  Best Local Similarity   94.7%;  Pred. No. 1.4e-170;
  Matches  497;  Conservative   13;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||:||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||:|||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||:|||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||:|:|||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| ||||||||| ||| |||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 9
O91855
ID   O91855      PRELIMINARY;      PRT;   660 AA.
AC   O91855;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Structural protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=93-Egypt;
RX   MEDLINE=99105430; PubMed=9890424;
RX   DOI=10.1002/(SICI)1096-9071(199901)57:1<68::AID-JMV10>3.0.CO;2-E;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
RL   J. Med. Virol. 57:68-74(1999).
DR   EMBL; AF051351; AAC35761.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71039 MW;  044FF5EA7C492791 CRC64;

  Query Match             95.1%;  Score 2569;  DB 2;  Length 660;
  Best Local Similarity   94.5%;  Pred. No. 1.4e-170;
  Matches  496;  Conservative   14;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||:||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231
```

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Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:|:  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||:||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||||||||:|||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||:|||:||||||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTSSDQLLIENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| |||||||| ||| ||||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 10
Q69419
ID Q69419 PRELIMINARY; PRT; 660 AA.
AC Q69419;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ORF1, ORF2 & ORF3.
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RA von Brunn A., Seebach J., Thyagarajan S.P., Mohanavalli B., Menon T.,
RA Froesner G.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; X99441; CAA67804.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 70960 MW; DAC3DF95F91689F8 CRC64;

Query Match 95.1%; Score 2569; DB 2; Length 660;
Best Local Similarity 94.5%; Pred. No. 1.4e-170;
Matches 496; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:|:  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||:||||||||||||||||||||||||||||||||||||||||
Db        412 LYRSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSALRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||||||||:|||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||:|||:||||||||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| |||||||| ||| ||||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636
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RESULT 11
O91856
ID O91856 PRELIMINARY; PRT; 660 AA.
AC O91856;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Structural protein.
OS Hepatitis E virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC Hepevirus.
OX NCBI_TaxID=12461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=94-Egypt;
RX MEDLINE=99105430; PubMed=9890424;
RX DOI=10.1002/(SICI)1096-9071(199901)57:1<68::AID-JMV10>3.0.CO;2-E;
RA Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RT "Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
RL J. Med. Virol. 57:68-74(1999).
DR EMBL; AF051352; AAC35764.1; -.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR004261; SP2.
DR Pfam; PF03014; SP2; 1.
SQ SEQUENCE 660 AA; 71025 MW; 16C560FA16941F2A CRC64;

Query Match 95.1%; Score 2568; DB 2; Length 660;
Best Local Similarity 94.5%; Pred. No. 1.6e-170;
Matches 496; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

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Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||||||:||||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:|:  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||||:|||||||:||||||||||||||||||||||||||||||||||||||||
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Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||||:||||||||||||||||||||||:|||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||:||||| |||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLIENATGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| ||||||||| ||| |||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 12
Q69411
ID   Q69411      PRELIMINARY;      PRT;   660 AA.
AC   Q69411;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Structural protein.
GN   Name=ORF2;
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Donati M.C., Fagan E.A., Harrison T.J.;
RT   "Sequence analysis of full length HEV clones derived directly from
RT   human liver in fulminant hepatitis E.";
RL   (In) Rizzetto M., Purcell R.H., Gerin J.L., Verme G (eds.);
RL   VIRAL HEPATITIS AND LIVER DISEASE, pp.313-316, Edizioni Minerva
RL   Medica, Torino (1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Harrison T.J.;
RL   Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X98292; CAA66937.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  71024 MW;  F37E3FEFF7A4EAD1 CRC64;

  Query Match           95.1%;  Score 2568;  DB 2;  Length 660;
  Best Local Similarity   94.7%;  Pred. No. 1.6e-170;
  Matches  497;  Conservative   11;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              |||||||| |||||||||||||||||||||||| ||:|||||||||:| ||||||||
Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSPVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGLPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||||||||| |||||| ||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALEFEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||:|||||||:||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||||||:||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||:||||| |||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              |||||| ||||| ||||||||| ||| |||||||||||| ||||
Db        592 PVAISAVAVLAPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQ 636


RESULT 13
Q81878
ID   Q81878      PRELIMINARY;      PRT;   660 AA.
AC   Q81878;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Complete genome sequence.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Uchida T.;
RL   Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; D11093; BAA01867.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70937 MW;  5412313F1A2EF4A9 CRC64;

  Query Match           94.9%;  Score 2563;  DB 2;  Length 660;
  Best Local Similarity   94.1%;  Pred. No. 3.7e-170;
  Matches  494;  Conservative   14;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
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Db        112 AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYGISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              |||||||:|||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGVLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGTDGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:||  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||:|||||||:||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              |||||||||||||||||||||:|||||||||||||||||||||||:||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
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Db        532 YCKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
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              ||:||| ||||| ||||||||| ||| |||||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTMDYPARAHTFDDFCPECRPLGLQ 636


RESULT 14
Q6XXV0
ID   Q6XXV0      PRELIMINARY;      PRT;   660 AA.
AC   Q6XXV0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Structural protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RX   MEDLINE=98071272; PubMed=9407381;
RX   DOI=10.1002/(SICI)1096-9071(199712)53:4<340::AID-JMV5>3.0.CO;2-7;
RA   van Cuyck-Gandre H., Zhang H.Y., Tsarev S.A., Clements N.J.,
RA   Cohen S.J., Caudill J.D., Buisson Y., Coursaget P., Warren R.L.,
RA   Longer C.F.;
RT   "Characterization of hepatitis E virus (HEV) from Algeria and Chad by
RT   partial genome sequence.";
RL   J. Med. Virol. 53:340-347(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RX   MEDLINE=99105430; PubMed=9890424;
RX   DOI=10.1002/(SICI)1096-9071(199901)57:1<68::AID-JMV10>3.0.CO;2-E;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RT   "Phylogenetic analysis of hepatitis E virus isolates from Egypt.";
RL   J. Med. Virol. 57:68-74(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RX   MEDLINE=22987819; PubMed=14625096; DOI=10.1016/S0928-8244(03)00241-4;
RA   van Cuyck H., Juge F., Roques P.;
RT   "Phylogenetic analysis of the first complete hepatitis E virus (HEV)
RT   genome from Africa.";
RL   FEMS Immunol. Med. Microbiol. 39:133-139(2003).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RA   Van Cuyck-Gandre H., Zhang H.Y., Tsarev S.A., Clements N.J.,
RA   Cohen S.J., Caudill J.D., Buisson Y., Coursaget P., Warren R.L.,
RA   Longer C.F.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RA   Tsarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K.,
RA   van Cuyck-Gandre H., Longer C.F., Innis B.L.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T3;
RA   van Cuyck H., Roberston D., Juge F., Roques P., Lemey P.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY204877; AAB61825.2; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70949 MW;  EA56732D458D0AB1 CRC64;

  Query Match             94.8%;  Score 2560;  DB 2;  Length 660;
  Best Local Similarity   94.3%;  Pred. No. 5.9e-170;
  Matches  495;  Conservative   13;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
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Db        112 AVAPAHDTPPVSDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
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Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
              ||:|:  |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db        352 DLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
              |||||||||||:|||||||||:||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
              ||||||||||||||||||||:|||||||||||||||||||||:||||||||| |::|
Db        472 WLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
              ||||||||||||||||||||||||||||||||||||||:|||| ||||||||||| ||||
Db        532 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLIENVAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
              ||:||| ||||| ||||||||| ||| |||||||||||||| ||||
Db        592 PVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQ 636


RESULT 15
Q80IY5
ID   Q80IY5      PRELIMINARY;      PRT;   660 AA.
AC   Q80IY5;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Structural protein.
OS   Hepatitis E virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
OC   Hepevirus.
OX   NCBI_TaxID=12461;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Osh 205;
RA   Robertson B.H., Lu L., Drobeniuc J., Favorov M., Usmanov R.,
RA   Kobylnilkov N., Balayan M.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF455784; AAO67359.1; -.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR004261; SP2.
DR   Pfam; PF03014; SP2; 1.
SQ   SEQUENCE   660 AA;  70881 MW;  AB83CAC3F181164E CRC64;

  Query Match             94.7%;  Score 2559;  DB 2;  Length 660;
  Best Local Similarity   94.1%;  Pred. No. 6.9e-170;
  Matches  494;  Conservative   13;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLPLQDGTN 60
              ||:|| ||:|||||||||||||||||||||||||||||||||||||| ||||||||
Db        112 AVSPAPDTAPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPLLPLQDGTN 171

Qy         61 THIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 120
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db        172 THIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTD 231

Qy        121 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 180
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 VRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNT 291

Qy        181 PYTGALGLLDFALELEFRNLTTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK 240
                |||||||||||||||||||||  |||||||||:|||||||||||||||||||||||||||||
Db        292 PYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMK 351

Qy        241 DLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 300
                ||||||  ||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        352 DLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK 411

Qy        301 LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 360
                |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db        412 LYTSVENAQQDKGIAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVL 471

Qy        361 WLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQ 420
                ||||||||||:|||||| |:|:||:|| |||||||||||||||||||||||||||| |::|
Db        472 WLSLTAAEYDQTTYGSSTNPMYVSDTVTFVNVATGAQAVARSLDWSKVTLDGRPLTTIQQ 531

Qy        421 YSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAG 480
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Db        532 YSKTFYVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTSLGAG 591

Qy        481 PVAISAAAVLAPRSALALLEDTFDYPGRAHTFDDFCPECRALGLQ 525
                ||::||  |||| |||| |||| ||| ||||||||||||| ||||
Db        592 PVSVSAVGVLAPHSALAALEDTIDYPARAHTFDDFCPECRNLGLQ 636
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Search completed: July 14, 2005, 15:50:33
Job time : 39.3019 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2005, 08:49:38 ; Search time 140 Seconds
(without alignments)
2.312 Million cell updates/sec

Title: US-09-769-066-15
Perfect score: 549
Sequence: 1 AVAPAHDTPPVPDVDSRGAI.....QSTVAELQRLKMKVGKTREL 549

Scoring table: UNITARY_AA
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 612 seqs, 294732 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 2000 summaries

Command line parameters:
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-DB=rge15.seq -SUFFIX=pto -OUT=foley066-15.rge -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=unitary_AA -TRANS=human40.cdi
-LIST=2000 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=612
-MODE=LOCAL -OUTFMT=pto -NORM=stat -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-NCPU=6 -NEG_SCORES=0 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : rge15.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	549	100.0	1647	1	AR170406	ACCESSION:AR170406
2	549	100.0	1983	1	I73139	ACCESSION:I73139
3	548	99.8	1647	1	E17105	ACCESSION:E17105
4	549	100.0	2049	1	AR002160	ACCESSION:AR002160
5	549	100.0	2049	1	AR170404	ACCESSION:AR170404
6	549	100.0	2049	1	AR232465	ACCESSION:AR232465
7	549	100.0	2094	1	AR002158	ACCESSION:AR002158
8	549	100.0	2094	1	AR232463	ACCESSION:AR232463
9	548	99.8	1983	1	E17107	ACCESSION:E17107
10	547	99.6	1686	1	AR278920	ACCESSION:AR278920
11	547	99.6	1983	1	AF124407	ACCESSION:AF124407
12	547	99.6	1984	1	AR278906	ACCESSION:AR278906
13	547	99.6	2173	1	AF065061	ACCESSION:AF065061
14	544	99.1	2104	1	AF051351	ACCESSION:AF051351
15	544	99.1	2106	1	AF051352	ACCESSION:AF051352
16	542	98.7	2082	1	HEU22532	ACCESSION:U22532
17	538	98.0	1658	1	AR278918	ACCESSION:AR278918
18	522	95.1	1649	1	HPEPPG	ACCESSION:D90274
19	518	94.4	1666	1	AB082545	ACCESSION:AB082545
20	506.5	92.3	1644	1	AR170407	ACCESSION:AR170407
21	506.5	92.3	1980	1	I73140	ACCESSION:I73140
22	487	88.7	1946	1	HEVBCN6	ACCESSION:AF058684
23	482.5	87.9	1643	1	E03815	ACCESSION:E03815
24	458	83.4	1497	1	AF151962	ACCESSION:AF151962
25	440	80.1	1402	1	AF151963	ACCESSION:AF151963
26	436	79.4	1311	1	AR002166	ACCESSION:AR002166
27	436	79.4	1311	1	AR232471	ACCESSION:AR232471
28	429	78.1	1309	1	AF141652	ACCESSION:AF141652
29	397.5	72.4	1308	1	AR002167	ACCESSION:AR002167
30	397.5	72.4	1308	1	AR232472	ACCESSION:AR232472
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33	327	59.6	984	1	AR170408	ACCESSION:AR170408
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36	322	58.7	1020	1	AX181847	ACCESSION:AX181847
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41	305	55.6	1026	1	AX181913	ACCESSION:AX181913
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44	304	55.4	981	1	AR002165	ACCESSION:AR002165
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50	276	50.3	860	1	AF516178	ACCESSION:AF516178
51	276	50.3	860	1	AF527942	ACCESSION:AF527942
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53	262	47.7	960	1	AX181806	ACCESSION:AX181806
54	262	47.7	960	1	BD077209	ACCESSION:BD077209
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56	255	46.4	919	1	AX181904	ACCESSION:AX181904
57	255	46.4	919	1	BD077293	ACCESSION:BD077293
58	247	45.0	745	1	HPEBCAP	ACCESSION:D10333
59	242	44.1	901	1	AX181871	ACCESSION:AX181871
60	242	44.1	901	1	BD077271	ACCESSION:BD077271
61	239	43.5	890	1	AX181903	ACCESSION:AX181903
62	239	43.5	890	1	BD077292	ACCESSION:BD077292
63	232	42.3	720	1	AY714267	ACCESSION:AY714267
64	232	42.3	720	1	AY714269	ACCESSION:AY714269
65	232	42.3	720	1	AY714270	ACCESSION:AY714270
66	232	42.3	720	1	AY714272	ACCESSION:AY714272
67	231	42.1	720	1	AY641398	ACCESSION:AY641398
68	231	42.1	720	1	AY714268	ACCESSION:AY714268
69	230	41.9	720	1	AY714271	ACCESSION:AY714271
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72	225	41.0	680	1	AF020607	ACCESSION:AF020607
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74	224	40.8	680	1	AF020604	ACCESSION:AF020604
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77	212	38.6	678	1	BD077228	ACCESSION:BD077228
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84	152	27.7	476	1	AF336294	ACCESSION:AF336294
85	152	27.7	476	1	AF336295	ACCESSION:AF336295
86	152	27.7	476	1	AF336296	ACCESSION:AF336296
87	152	27.7	476	1	AF336298	ACCESSION:AF336298
88	151	27.5	476	1	AF336297	ACCESSION:AF336297
89	151	27.5	476	1	AF336299	ACCESSION:AF336299
90	150	27.3	473	1	AF503511	ACCESSION:AF503511
91	150	27.3	473	1	AF503512	ACCESSION:AF503512
92	149	27.1	448	1	AF020492	ACCESSION:AF020492
93	149	27.1	448	1	AF020493	ACCESSION:AF020493
94	149	27.1	448	1	AF020494	ACCESSION:AF020494
95	149	27.1	448	1	AF020495	ACCESSION:AF020495
96	149	27.1	448	1	AF020497	ACCESSION:AF020497
97	149	27.1	453	1	HEU40046	ACCESSION:U40046
98	148	27.0	448	1	AF020496	ACCESSION:AF020496

99	148	27.0	476	1	AF336291	ACCESSION:AF336291
100	144	26.2	448	1	AF047864	ACCESSION:AF047864
101	141	25.7	451	1	AY370687	ACCESSION:AY370687
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434	112	20.4	348	1	HEE344187	ACCESSION:AJ344187
435	110	20.0	348	1	AY621097	ACCESSION:AY621097
436	110	20.0	348	1	AY621100	ACCESSION:AY621100
437	110	20.0	348	1	HEE344171	ACCESSION:AJ344171
438	110	20.0	359	1	AF172999	ACCESSION:AF172999
439	110	20.0	359	1	AF173000	ACCESSION:AF173000
440	110	20.0	359	1	AF173001	ACCESSION:AF173001
441	110	20.0	359	1	AF173230	ACCESSION:AF173230
442	110	20.0	359	1	AF173231	ACCESSION:AF173231
443	110	20.0	359	1	AF173232	ACCESSION:AF173232
444	109	19.9	346	1	AF117275	ACCESSION:AF117275
445	109	19.9	346	1	AF117278	ACCESSION:AF117278
446	109	19.9	346	1	AF117279	ACCESSION:AF117279
447	109	19.9	348	1	AY596309	ACCESSION:AY596309
448	109	19.9	348	1	AY596315	ACCESSION:AY596315
449	109	19.9	348	1	AY621098	ACCESSION:AY621098
450	109	19.9	348	1	AY621099	ACCESSION:AY621099
451	109	19.9	348	1	HEE344172	ACCESSION:AJ344172
452	109	19.9	348	1	HEE344179	ACCESSION:AJ344179
453	109	19.9	348	1	HEE344180	ACCESSION:AJ344180
454	109	19.9	348	1	HEE344183	ACCESSION:AJ344183
455	109	19.9	348	1	HEE344184	ACCESSION:AJ344184
456	109	19.9	348	1	HEE344192	ACCESSION:AJ344192
457	109	19.9	348	1	HEE344193	ACCESSION:AJ344193
458	109	19.9	348	1	HEE344194	ACCESSION:AJ344194
459	108	19.7	346	1	AF117276	ACCESSION:AF117276
460	108	19.7	346	1	AF117277	ACCESSION:AF117277
461	108	19.7	348	1	AY596308	ACCESSION:AY596308
462	108	19.7	348	1	AY596311	ACCESSION:AY596311
463	108	19.7	348	1	AY596312	ACCESSION:AY596312
464	108	19.7	348	1	AY596313	ACCESSION:AY596313
465	108	19.7	348	1	AY596317	ACCESSION:AY596317
466	108	19.7	348	1	AY596318	ACCESSION:AY596318
467	108	19.7	348	1	AY596319	ACCESSION:AY596319
468	108	19.7	348	1	AY596320	ACCESSION:AY596320
469	108	19.7	348	1	AY621096	ACCESSION:AY621096
470	108	19.7	348	1	HEE344185	ACCESSION:AJ344185
471	108	19.7	348	1	HEE344191	ACCESSION:AJ344191
472	107	19.5	346	1	AF117280	ACCESSION:AF117280
473	107	19.5	346	1	AF117281	ACCESSION:AF117281
474	107	19.5	348	1	AY596310	ACCESSION:AY596310
475	107	19.5	348	1	AY596314	ACCESSION:AY596314
476	107	19.5	348	1	AY596316	ACCESSION:AY596316
477	107	19.5	348	1	HEE344177	ACCESSION:AJ344177
478	107	19.5	348	1	HEE344181	ACCESSION:AJ344181
479	107	19.5	348	1	HEE344186	ACCESSION:AJ344186
480	107	19.5	348	1	HEE344188	ACCESSION:AJ344188
481	105	19.1	318	1	AF446094	ACCESSION:AF446094
482	104	18.9	317	1	AF446095	ACCESSION:AF446095
483	103	18.8	312	1	AF446093	ACCESSION:AF446093
484	99	18.0	304	1	AF093896	ACCESSION:AF093896
485	99	18.0	304	1	AF093897	ACCESSION:AF093897
486	99	18.0	304	1	AF093898	ACCESSION:AF093898
487	99	18.0	304	1	AF093900	ACCESSION:AF093900
488	99	18.0	304	1	AF093901	ACCESSION:AF093901
489	99	18.0	304	1	AF093902	ACCESSION:AF093902
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491	99	18.0	304	1	AF093904	ACCESSION:AF093904
492	99	18.0	304	1	AF093905	ACCESSION:AF093905
493	99	18.0	304	1	AF093906	ACCESSION:AF093906
494	99	18.0	304	1	AF093907	ACCESSION:AF093907
495	99	18.0	304	1	AF093908	ACCESSION:AF093908
496	99	18.0	304	1	AF093909	ACCESSION:AF093909
497	99	18.0	304	1	AF093910	ACCESSION:AF093910
498	98	17.9	304	1	AF093899	ACCESSION:AF093899
499	98	17.9	304	1	AF093911	ACCESSION:AF093911
500	98	17.9	304	1	AF302069	ACCESSION:AF302069
501	97	17.7	295	1	AF446092	ACCESSION:AF446092
502	97	17.7	296	1	AF105021	ACCESSION:AF105021
503	97	17.7	300	1	HEE428851	ACCESSION:AJ428851
504	95	17.3	300	1	AF466660	ACCESSION:AF466660
505	95	17.3	300	1	AF466661	ACCESSION:AF466661
506	95	17.3	300	1	AF466662	ACCESSION:AF466662
507	95	17.3	300	1	AF466663	ACCESSION:AF466663
508	95	17.3	300	1	AF466666	ACCESSION:AF466666
509	95	17.3	300	1	AF466667	ACCESSION:AF466667
510	95	17.3	301	1	AF466665	ACCESSION:AF466665
511	95	17.3	301	1	AF466668	ACCESSION:AF466668
512	95	17.3	301	1	AF466669	ACCESSION:AF466669
513	95	17.3	301	1	AF466670	ACCESSION:AF466670
514	95	17.3	301	1	AF466671	ACCESSION:AF466671
515	95	17.3	301	1	AF466672	ACCESSION:AF466672
516	95	17.3	301	1	AF466673	ACCESSION:AF466673
517	95	17.3	301	1	AF466674	ACCESSION:AF466674
518	95	17.3	301	1	AF466675	ACCESSION:AF466675
519	95	17.3	301	1	AF466677	ACCESSION:AF466677
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521	95	17.3	301	1	AF466679	ACCESSION:AF466679
522	95	17.3	301	1	AF466680	ACCESSION:AF466680
523	95	17.3	301	1	AF466681	ACCESSION:AF466681
524	95	17.3	301	1	AF466682	ACCESSION:AF466682
525	95	17.3	301	1	AF466683	ACCESSION:AF466683
526	95	17.3	301	1	AF466684	ACCESSION:AF466684
527	95	17.3	301	1	AF466685	ACCESSION:AF466685
528	95	17.3	304	1	AF195061	ACCESSION:AF195061
529	95	17.3	304	1	AF195062	ACCESSION:AF195062
530	95	17.3	304	1	AF296165	ACCESSION:AF296165
531	95	17.3	304	1	AF296166	ACCESSION:AF296166
532	95	17.3	304	1	AY032756	ACCESSION:AY032756
533	95	17.3	304	1	AY032757	ACCESSION:AY032757
534	95	17.3	304	1	AY032758	ACCESSION:AY032758
535	95	17.3	304	1	AY032759	ACCESSION:AY032759
536	95	17.3	304	1	AY362357	ACCESSION:AY362357

537	94	17.1	299	1	AF324501	ACCESSION:AF324501
538	94	17.1	299	1	AF324502	ACCESSION:AF324502
539	94	17.1	299	1	AF324503	ACCESSION:AF324503
540	94	17.1	300	1	AF466659	ACCESSION:AF466659
541	94	17.1	300	1	AF466664	ACCESSION:AF466664
542	94	17.1	301	1	AF466676	ACCESSION:AF466676
543	94	17.1	304	1	AF195063	ACCESSION:AF195063
544	94	17.1	304	1	AF296159	ACCESSION:AF296159
545	94	17.1	304	1	AF296160	ACCESSION:AF296160
546	94	17.1	304	1	AY052774	ACCESSION:AY052774
547	93	16.9	283	1	AY697426	ACCESSION:AY697426
548	93	16.9	299	1	AF324504	ACCESSION:AF324504
549	93	16.9	300	1	HEE428852	ACCESSION:AJ428852
550	93	16.9	301	1	AF134812	ACCESSION:AF134812
551	93	16.9	301	1	AF134917	ACCESSION:AF134917
552	93	16.9	302	1	AY621101	ACCESSION:AY621101
553	93	16.9	302	1	AY621102	ACCESSION:AY621102
554	93	16.9	304	1	AF302068	ACCESSION:AF302068
555	92	16.8	300	1	HEE428853	ACCESSION:AJ428853
556	92	16.8	300	1	HEE428854	ACCESSION:AJ428854
557	92	16.8	300	1	HEE428855	ACCESSION:AJ428855
558	92	16.8	301	1	AF103940	ACCESSION:AF103940
559	92	16.8	301	1	AF134916	ACCESSION:AF134916
560	92	16.8	304	1	AF296161	ACCESSION:AF296161
561	92	16.8	304	1	AF296162	ACCESSION:AF296162
562	92	16.8	304	1	AF296164	ACCESSION:AF296164
563	92	16.8	304	1	AF296167	ACCESSION:AF296167
564	91	16.6	300	1	HEE428856	ACCESSION:AJ428856
565	91	16.6	304	1	AF296163	ACCESSION:AF296163
566	88	16.0	266	1	AY697428	ACCESSION:AY697428
567	87	15.8	265	1	AY697427	ACCESSION:AY697427
568	84	15.3	255	1	AF228533	ACCESSION:AF228533
569	84	15.3	256	1	AF228529	ACCESSION:AF228529
570	84	15.3	256	1	AF228530	ACCESSION:AF228530
571	84	15.3	256	1	AF228534	ACCESSION:AF228534
572	84	15.3	256	1	AF228535	ACCESSION:AF228535
573	84	15.3	256	1	AF228537	ACCESSION:AF228537
574	83	15.1	250	1	AX181955	ACCESSION:AX181955
575	83	15.1	250	1	AX181956	ACCESSION:AX181956
576	83	15.1	250	1	AX181957	ACCESSION:AX181957
577	83	15.1	250	1	BD077323	ACCESSION:BD077323
578	83	15.1	250	1	BD077324	ACCESSION:BD077324
579	83	15.1	250	1	BD077325	ACCESSION:BD077325
580	83	15.1	256	1	AF228538	ACCESSION:AF228538
581	80	14.6	250	1	AX181958	ACCESSION:AX181958
582	80	14.6	250	1	BD077326	ACCESSION:BD077326
583	78	14.2	249	1	AF407560	ACCESSION:AF407560
584	78	14.2	249	1	AF407567	ACCESSION:AF407567
585	78	14.2	249	1	AF505860	ACCESSION:AF505860
586	76	13.8	244	1	AF407562	ACCESSION:AF407562
587	76	13.8	246	1	AF407561	ACCESSION:AF407561
588	76	13.8	247	1	AF407564	ACCESSION:AF407564
589	76	13.8	247	1	AF407569	ACCESSION:AF407569
590	76	13.8	249	1	AF505861	ACCESSION:AF505861
591	76	13.8	250	1	AF407570	ACCESSION:AF407570
592	75	13.7	247	1	AF407563	ACCESSION:AF407563
593	74	13.5	239	1	AF407568	ACCESSION:AF407568
594	70	12.8	227	1	AY753554	ACCESSION:AY753554
595	69	12.6	249	1	AF407566	ACCESSION:AF407566
596	69	12.6	251	1	AF407565	ACCESSION:AF407565
597	68	12.4	212	1	AF347692	ACCESSION:AF347692
598	68	12.4	217	1	AF505859	ACCESSION:AF505859
599	66	12.0	250	1	AX181959	ACCESSION:AX181959
600	66	12.0	250	1	BD077327	ACCESSION:BD077327
601	64	11.7	197	1	AX181929	ACCESSION:AX181929
602	64	11.7	197	1	AX181933	ACCESSION:AX181933
603	64	11.7	197	1	AX181963	ACCESSION:AX181963
604	64	11.7	197	1	AX181971	ACCESSION:AX181971
605	64	11.7	197	1	BD077306	ACCESSION:BD077306
606	64	11.7	197	1	BD077308	ACCESSION:BD077308
607	63	11.5	197	1	AX181869	ACCESSION:AX181869
608	63	11.5	197	1	AX181899	ACCESSION:AX181899
609	63	11.5	197	1	BD077269	ACCESSION:BD077269
610	63	11.5	197	1	BD077288	ACCESSION:BD077288
611	61	11.1	189	1	AY626041	ACCESSION:AY626041
612	61	11.1	189	1	AY626042	ACCESSION:AY626042
c 613	65.5	11.9	1643	1	E03815	ACCESSION:E03815
c 614	59	10.7	1647	1	AR170406	ACCESSION:AR170406
c 615	59	10.7	1647	1	E17105	ACCESSION:E17105
c 616	59	10.7	1658	1	AR278918	ACCESSION:AR278918
c 617	59	10.7	1666	1	AB082545	ACCESSION:AB082545
c 618	59	10.7	1686	1	AR278920	ACCESSION:AR278920
c 619	60	10.9	2173	1	AF065061	ACCESSION:AF065061
c 620	59	10.7	1983	1	I73139	ACCESSION:I73139
c 621	59	10.7	1983	1	E17107	ACCESSION:E17107
c 622	59	10.7	1983	1	AF124407	ACCESSION:AF124407
c 623	59	10.7	1984	1	AR278906	ACCESSION:AR278906
c 624	59	10.7	2049	1	AR002160	ACCESSION:AR002160
c 625	59	10.7	2049	1	AR170404	ACCESSION:AR170404
c 626	59	10.7	2049	1	AR232465	ACCESSION:AR232465
c 627	59	10.7	2094	1	AR002158	ACCESSION:AR002158
c 628	59	10.7	2094	1	AR232463	ACCESSION:AR232463
c 629	57	10.4	1649	1	HPEPPG	ACCESSION:D90274
c 630	58	10.6	2082	1	HEU22532	ACCESSION:U22532
c 631	58	10.6	2104	1	AF051351	ACCESSION:AF051351
c 632	58	10.6	2106	1	AF051352	ACCESSION:AF051352
c 633	56	10.2	1644	1	AR170407	ACCESSION:AR170407
c 634	56	10.2	1946	1	HEVBCN6	ACCESSION:AF058684
c 635	56	10.2	1980	1	I73140	ACCESSION:I73140
c 636	52	9.5	1402	1	AF151963	ACCESSION:AF151963
c 637	51	9.3	1497	1	AF151962	ACCESSION:AF151962
c 638	50	9.1	1311	1	AR002166	ACCESSION:AR002166
c 639	50	9.1	1311	1	AR232471	ACCESSION:AR232471
c 640	49	8.9	1308	1	AR002167	ACCESSION:AR002167
c 641	49	8.9	1308	1	AR232472	ACCESSION:AR232472
c 642	48	8.7	1309	1	AF141652	ACCESSION:AF141652
c 643	43	7.8	1117	1	HEU40044	ACCESSION:U40044
c 644	42	7.7	984	1	AR002164	ACCESSION:AR002164
c 645	42	7.7	984	1	AR170408	ACCESSION:AR170408
c 646	42	7.7	984	1	I73145	ACCESSION:I73145
c 647	42	7.7	984	1	AR232469	ACCESSION:AR232469
c 648	42	7.7	1020	1	AX181847	ACCESSION:AX181847
c 649	42	7.7	1020	1	BD077247	ACCESSION:BD077247
c 650	41	7.5	981	1	AR002165	ACCESSION:AR002165
c 651	41	7.5	981	1	AR232470	ACCESSION:AR232470
c 652	41	7.5	984	1	AR170409	ACCESSION:AR170409
c 653	41	7.5	984	1	I73146	ACCESSION:I73146
c 654	40	7.3	1026	1	AX181910	ACCESSION:AX181910
c 655	40	7.3	1026	1	AX181913	ACCESSION:AX181913
c 656	40	7.3	1026	1	BD077295	ACCESSION:BD077295
c 657	40	7.3	1026	1	BD077298	ACCESSION:BD077298
658	37	6.7	849	1	HEU40045	ACCESSION:U40045
c 659	37	6.7	899	1	AX181742	ACCESSION:AX181742
c 660	37	6.7	899	1	BD077145	ACCESSION:BD077145
c 661	36	6.6	860	1	AF516178	ACCESSION:AF516178
c 662	36	6.6	960	1	AX181806	ACCESSION:AX181806
c 663	36	6.6	960	1	BD077209	ACCESSION:BD077209
c 664	35	6.4	803	1	AR278919	ACCESSION:AR278919
c 665	35	6.4	860	1	AF516179	ACCESSION:AF516179
c 666	35	6.4	860	1	AF527942	ACCESSION:AF527942
c 667	34	6.2	890	1	AX181903	ACCESSION:AX181903
c 668	34	6.2	890	1	BD077292	ACCESSION:BD077292
c 669	33	6.0	745	1	HPEBCAP	ACCESSION:D10333
c 670	32	5.8	680	1	AF020603	ACCESSION:AF020603
c 671	32	5.8	680	1	AF020606	ACCESSION:AF020606
c 672	32	5.8	680	1	AF020607	ACCESSION:AF020607
c 673	32	5.8	680	1	AF020608	ACCESSION:AF020608
c 674	32	5.8	680	1	AF020605	ACCESSION:AF020605
c 675	33	6.0	901	1	AX181871	ACCESSION:AX181871
c 676	33	6.0	901	1	BD077271	ACCESSION:BD077271
c 677	33	6.0	919	1	AX181904	ACCESSION:AX181904
c 678	33	6.0	919	1	BD077293	ACCESSION:BD077293
c 679	32	5.8	775	1	HPECCAP	ACCESSION:D10332
c 680	31	5.6	680	1	AF020604	ACCESSION:AF020604
c 681	29	5.3	617	1	AF170450	ACCESSION:AF170450
c 682	29	5.3	720	1	AY714267	ACCESSION:AY714267

c 683	29	5.3	720	1	AY714269	ACCESSION:AY714269
c 684	29	5.3	720	1	AY714270	ACCESSION:AY714270
c 685	29	5.3	720	1	AY714272	ACCESSION:AY714272
c 686	29	5.3	720	1	AY714268	ACCESSION:AY714268
c 687	29	5.3	720	1	AY714271	ACCESSION:AY714271
c 688	27	4.9	506	1	HEU62654	ACCESSION:U62654
c 689	28	5.1	720	1	AY641398	ACCESSION:AY641398
c 690	27	4.9	678	1	AX181828	ACCESSION:AX181828
c 691	27	4.9	678	1	BD077228	ACCESSION:BD077228
c 692	23	4.2	409	1	AY568362	ACCESSION:AY568362
c 693	23	4.2	438	1	AY160125	ACCESSION:AY160125
c 694	23	4.2	448	1	AF020495	ACCESSION:AF020495
c 695	23	4.2	448	1	AF020497	ACCESSION:AF020497
c 696	23	4.2	448	1	AF020496	ACCESSION:AF020496
c 697	23	4.2	473	1	AF503511	ACCESSION:AF503511
c 698	22	4.0	412	1	AB079763	ACCESSION:AB079763
c 699	22	4.0	412	1	AB094216	ACCESSION:AB094216
c 700	22	4.0	412	1	AB154829	ACCESSION:AB154829
c 701	22	4.0	412	1	AB094226	ACCESSION:AB094226
c 702	22	4.0	412	1	AB094227	ACCESSION:AB094227
c 703	22	4.0	412	1	AB094228	ACCESSION:AB094228
c 704	22	4.0	412	1	AB094229	ACCESSION:AB094229
c 705	22	4.0	412	1	AB094230	ACCESSION:AB094230
c 706	22	4.0	412	1	AB094231	ACCESSION:AB094231
c 707	22	4.0	412	1	AB094232	ACCESSION:AB094232
c 708	22	4.0	412	1	AB094233	ACCESSION:AB094233
c 709	22	4.0	412	1	AB094234	ACCESSION:AB094234
c 710	22	4.0	412	1	AB094235	ACCESSION:AB094235
c 711	22	4.0	412	1	AB094236	ACCESSION:AB094236
c 712	22	4.0	412	1	AB094237	ACCESSION:AB094237
c 713	22	4.0	412	1	AB094250	ACCESSION:AB094250
c 714	22	4.0	412	1	AB094251	ACCESSION:AB094251
c 715	22	4.0	412	1	AB094252	ACCESSION:AB094252
c 716	22	4.0	412	1	AB094253	ACCESSION:AB094253
c 717	22	4.0	421	1	AB073911	ACCESSION:AB073911
c 718	22	4.0	421	1	AB073909	ACCESSION:AB073909
c 719	22	4.0	421	1	AB073910	ACCESSION:AB073910
c 720	22	4.0	436	1	AB080579	ACCESSION:AB080579
c 721	22	4.0	448	1	AF020492	ACCESSION:AF020492
c 722	22	4.0	448	1	AF020493	ACCESSION:AF020493
c 723	22	4.0	448	1	AF020494	ACCESSION:AF020494
c 724	22	4.0	473	1	AF503512	ACCESSION:AF503512
c 725	22	4.0	476	1	AF332620	ACCESSION:AF332620
c 726	22	4.0	476	1	AF336290	ACCESSION:AF336290
c 727	22	4.0	476	1	AF336292	ACCESSION:AF336292
c 728	22	4.0	476	1	AF336294	ACCESSION:AF336294
c 729	22	4.0	476	1	AF336296	ACCESSION:AF336296
c 730	22	4.0	476	1	AF336299	ACCESSION:AF336299
c 731	21	3.8	405	1	AF396860	ACCESSION:AF396860
c 732	21	3.8	409	1	AY568357	ACCESSION:AY568357
c 733	21	3.8	409	1	AY568358	ACCESSION:AY568358
c 734	21	3.8	409	1	AY568363	ACCESSION:AY568363
c 735	21	3.8	409	1	AY596462	ACCESSION:AY596462
c 736	21	3.8	409	1	AY568360	ACCESSION:AY568360
c 737	21	3.8	412	1	AB116178	ACCESSION:AB116178
c 738	21	3.8	412	1	AB116180	ACCESSION:AB116180
c 739	21	3.8	412	1	AB116183	ACCESSION:AB116183
c 740	21	3.8	412	1	AB116185	ACCESSION:AB116185
c 741	21	3.8	412	1	AB116191	ACCESSION:AB116191
c 742	21	3.8	412	1	AB116192	ACCESSION:AB116192
c 743	21	3.8	412	1	AB082561	ACCESSION:AB082561
c 744	21	3.8	412	1	AB082562	ACCESSION:AB082562
c 745	21	3.8	412	1	AB082564	ACCESSION:AB082564
c 746	21	3.8	412	1	AB082565	ACCESSION:AB082565
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c 858	21	3.8	451	1	AY370686	ACCESSION:AY370686
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c1047	17	3.1	301	1	AF466671	ACCESSION:AF466671
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c1051	17	3.1	304	1	AF093896	ACCESSION:AF093896
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c1065	16	2.9	265	1	AY697427	ACCESSION:AY697427
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c1067	18	3.3	409	1	AY568365	ACCESSION:AY568365
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ALIGNMENTS

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DEFINITION  Sequence 3 from patent US 6291641.
ACCESSION   AR170406
VERSION     AR170406.1  GI:17908365
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1647)
  AUTHORS   Fuerst,T.R., McAtee,C.Patrick., Yarbough,P.O. and Zhang,Y.-F.
  TITLE     Hepatitis E virus antigens and uses therefor
  JOURNAL   Patent: US 6291641-A 3 18-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .1647
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:                0.606          Length:          1647
Score:                    549.00         Matches:         549
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-15 (1-549) x AR170406 (1-1647)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
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Db          1 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 60

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
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Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr  80
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Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db        241 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 300

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        301 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 360

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Db        361 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 420

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
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Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
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Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
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Qy        541 MetLysValGlyLysThrArgGluLeu 549
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RESULT 2
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LOCUS       I73139                  1983 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 1 from patent US 5686239.
ACCESSION   I73139
VERSION     I73139.1  GI:3009278
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1983)
  AUTHORS   Reyes,G.R., Tam,A.W. and Yarbough,P.O.
  TITLE     Hepatitis E virus peptides and methods
  JOURNAL   Patent: US 5686239-A 1 11-NOV-1997;
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:                0.614          Length:          1983
Score:                    549.00         Matches:         549
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-15 (1-549) x I73139 (1-1983)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
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Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
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Db        394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
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Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
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Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db        754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180

Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        874 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

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Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260

Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db       1114 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320

Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

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Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

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Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520

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Qy        541 MetLysValGlyLysThrArgGluLeu 549

Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTG 1980
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RESULT 3
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LOCUS	E17105	1647 bp	DNA	linear	PAT 28-JUL-1999

DEFINITION DNA encoding HEV hollow particle.
ACCESSION E17105
VERSION E17105.1 GI:5711788
KEYWORDS JP 1998234383-A/1.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 1647)
AUTHORS Takeda,N., Ri,T. and Miyamura,T.
TITLE HEPATITIS E VIRUS HOLLOW PARTICLE, GENE ENCODING THE SAME AND PREPARATION OF RECOMBINATION VECTOR CONTAINING THE GENE AND UTILIZATION OF THE RECOMBINATION VECTOR
JOURNAL Patent: JP 1998234383-A 1 08-SEP-1998;
DENKA SEIKEN CO LTD, KOKURITSU KANSENSHIYOU KENKYUSHO
COMMENT OS Hepatitis E virus
PN JP 1998234383-A/1
PD 08-SEP-1998
PF 28-FEB-1997 JP 1997062445
PI TAKEDA NAOKAZU, RI TENSEI, MIYAMURA TATSUO
PC C12N15/09,C07K14/08,C12N5/10,C12P21/02;
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
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FT source 1. .1647
FT /organism='Hepatitis E virus' FT mat_peptide
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source 1. .1647
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Alignment Scores:

Pred. No.:	0.615	Length:	1647
Score:	548.00	Matches:	548
Percent Similarity:	99.82%	Conservative:	0
Best Local Similarity:	99.82%	Mismatches:	1
Query Match:	99.82%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x E17105 (1-1647)

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Db         61 TTGCGCCGGCAGTATAATCTATCAACATCTCCCCTCACCTCTTCCGTGGCCACCGGCACT 120

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60

Db        121 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAAT 180

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

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Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

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Db        481 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAACACA 540

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        541 CCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 600

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

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Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320

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Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

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Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1261 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1320

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Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500

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Db       1501 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1560

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

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Qy        541 MetLysValGlyLysThrArgGluLeu 549

Db       1621 ATGAAGGTGGGTAAAACTCGGGAGTTA 1647
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RESULT 4
AR002160

LOCUS	AR002160	2049 bp	DNA	linear	PAT 04-DEC-1998
DEFINITION	Sequence 3 from patent US 5741490.				
ACCESSION	AR002160				
VERSION	AR002160.1 GI:3963714				
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
	Unclassified.				
REFERENCE	1 (bases 1 to 2049)				
AUTHORS	Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W., Krawczynski,K.Z. and Yarbough,P.D.				
TITLE	Hepatitis E virus vaccine and method				
JOURNAL	Patent: US 5741490-A 3 21-APR-1998;				
FEATURES	Location/Qualifiers				
source	1. .2049				
	/organism="unknown"				
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Alignment Scores:

Pred. No.:	0.615	Length:	2049
Score:	549.00	Matches:	549
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AR002160 (1-2049)

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Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
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Db        394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60

Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db        754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180

Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        874 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

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Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260

Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

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Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320

Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

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Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

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Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

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Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480

Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500

Db       1774 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

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Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTG 1980
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RESULT 5
AR170404

LOCUS	AR170404	2049 bp DNA linear	PAT 17-DEC-2001
DEFINITION	Sequence 1 from patent US 6291641.		
ACCESSION	AR170404		
VERSION	AR170404.1 GI:17908363		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
	Unclassified.		
REFERENCE	1 (bases 1 to 2049)		
AUTHORS	Fuerst,T.R., McAtee,C.Patrick., Yarbough,P.O. and Zhang,Y.-F.		
TITLE	Hepatitis E virus antigens and uses therefor		
JOURNAL	Patent: US 6291641-A 1 18-SEP-2001;		

FEATURES Location/Qualifiers
source 1. .2049
/organism="unknown"
/mol_type="unassigned DNA"

Alignment Scores:

Pred. No.:	0.615	Length:	2049
Score:	549.00	Matches:	549
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AR170404 (1-2049)

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Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40

Db        394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
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Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

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Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        874 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db        934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db        994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1053

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260

Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db       1114 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320

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Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420

Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460

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Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480

Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500

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Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

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Qy        541 MetLysValGlyLysThrArgGluLeu 549

Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTG 1980
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RESULT 6
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LOCUS AR232465 2049 bp mRNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6455492.
ACCESSION AR232465
VERSION AR232465.1 GI:27274534
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2049)
AUTHORS Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W., Krawczynski,K.Z. and Yarbough,P.O.
TITLE Hepatitis E virus vaccine and method
JOURNAL Patent: US 6455492-A 3 24-SEP-2002;
FEATURES Location/Qualifiers
source 1. .2049
/organism="unknown"
/mol_type="mRNA"

Alignment Scores:

Pred. No.:	0.615	Length:	2049
Score:	549.00	Matches:	549
Percent Similarity:	100.00%	Conservative:	0
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Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AR232465 (1-2049)

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Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr  40

Db        394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn  60

Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr  80
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Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Db        754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
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Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Db        874 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Db        934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Db        994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1053

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db       1114 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
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Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653
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Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
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Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
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Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
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Db       1774 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
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Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
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Db       1894 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 MetLysValGlyLysThrArgGluLeu 549
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Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTG 1980

RESULT 7
AR002158
LOCUS       AR002158                2094 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 1 from patent US 5741490.
ACCESSION   AR002158
VERSION     AR002158.1  GI:3963712
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2094)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.D.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 5741490-A 1 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .2094
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Alignment Scores:
Pred. No.:                0.616          Length:          2094
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Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-15 (1-549) x AR002158 (1-2094)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
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Db        379 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 438

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 498

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Db        499 AACCTGGTTCTTTATGCCGCCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 558

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 618

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        619 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 678

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Db        679 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 738

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

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Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

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Db        859 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 918

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        919 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 978

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

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Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db       1039 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1098

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260

Db       1099 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1158

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

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Db       1219 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1278

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Db       1279 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1338

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Db       1339 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1398

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Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1459 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1518

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1519 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1578

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420

Db       1579 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1638

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1639 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1698

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460

Db       1699 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1758

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480

Db       1759 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1818

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500

Db       1819 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1878

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1879 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1938

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1939 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1998

Qy        541 MetLysValGlyLysThrArgGluLeu 549

Db       1999 ATGAAGGTGGGTAAAACTCGGGAGTTG 2025
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RESULT 8
AR232463
LOCUS AR232463 2094 bp mRNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6455492.
ACCESSION AR232463
VERSION AR232463.1 GI:27274532
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2094)
AUTHORS Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W., Krawczynski,K.Z. and Yarbough,P.O.
TITLE Hepatitis E virus vaccine and method
JOURNAL Patent: US 6455492-A 1 24-SEP-2002;
FEATURES Location/Qualifiers
source 1. .2094
/organism="unknown"
/mol_type="mRNA"

Alignment Scores:

Pred. No.:	0.616	Length:	2094
Score:	549.00	Matches:	549
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AR232463 (1-2094)

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Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40

Db        439 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 498

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60

Db        499 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 558

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

Db        559 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 618

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        619 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 678

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        679 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 738

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db        739 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 798

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db        799 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 858

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180

Db        859 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 918

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        919 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 978

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db        979 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 1038

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db       1039 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1098

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260

Db       1099 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1158

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db       1159 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1218

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db       1219 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1278

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320

Db       1279 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1338

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db       1339 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1398

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1399 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1458

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1459 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1518

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1519 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1578

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420

Db       1579 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1638

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1639 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1698

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460

Db       1699 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1758

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480

Db       1759 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1818

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500

Db       1819 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1878

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1879 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1938

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

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Qy        541 MetLysValGlyLysThrArgGluLeu 549

Db       1999 ATGAAGGTGGGTAAAACTCGGGAGTTG 2025
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RESULT 9
E17107

LOCUS	E17107 1983 bp DNA linear PAT 28-JUL-1999
DEFINITION	Hepatitis E virus ORF2.
ACCESSION	E17107
VERSION	E17107.1 GI:5711790
KEYWORDS	JP 1998234383-A/3.
SOURCE	unidentified
ORGANISM	unidentified unclassified.
REFERENCE	1 (bases 1 to 1983)
AUTHORS	Takeda,N., Ri,T. and Miyamura,T.
TITLE	HEPATITIS E VIRUS HOLLOW PARTICLE, GENE ENCODING THE SAME AND PREPARATION OF RECOMBINATION VECTOR CONTAINING THE GENE AND UTILIZATION OF THE RECOMBINATION VECTOR
JOURNAL	Patent: JP 1998234383-A 3 08-SEP-1998; DENKA SEIKEN CO LTD, KOKURITSU KANSENSHIYOU KENKYUSHO
COMMENT	OS Hepatitis E virus PN JP 1998234383-A/3 PD 08-SEP-1998 PF 28-FEB-1997 JP 1997062445 PI TAKEDA NAOKAZU, RI TENSEI, MIYAMURA TATSUO PC C12N15/09,C07K14/08,C12N5/10,C12P21/02; CC strandedness: Double; CC topology: Linear;

FH Key Location/Qualifiers
FH
FT source 1. .1983
FT /organism='Hepatitis E virus' FT CDS
1. .1983
FT /product='structural protein'.

FEATURES Location/Qualifiers
source 1. .1983
/organism="unidentified"
/mol_type="genomic DNA"
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Alignment Scores:

Pred. No.:	0.623	Length:	1983
Score:	548.00	Matches:	548
Percent Similarity:	99.82%	Conservative:	0
Best Local Similarity:	99.82%	Mismatches:	1
Query Match:	99.82%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x E17107 (1-1983)

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Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20

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Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40

Db        394 TTGCGCCGGCAGTATAATCTATCAACATCTCCCCTCACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
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Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
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Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Db        754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
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Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAACACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Db        934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Db        994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAG 1053

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
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Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db       1114 CTGTTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCGGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
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Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
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Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
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Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
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Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
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Db       1774 CCCGTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
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Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
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Db       1894 CCTCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 MetLysValGlyLysThrArgGluLeu 549
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RESULT 10
AR278920
LOCUS       AR278920               1686 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 19 from patent US 6514690.
ACCESSION   AR278920
VERSION     AR278920.1  GI:29713554
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1686)
  AUTHORS   Li,F., Hui,Z., Anderson,D.A., Logarnini,S.A. and Torresi,J.
  TITLE     Immunoreactive antigens of Hepatitis E Virus
  JOURNAL   Patent: US 6514690-A 19 04-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .1686
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Alignment Scores:
Pred. No.:                0.625          Length:          1686
Score:                    547.00         Matches:         547
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Best Local Similarity:    99.64%         Mismatches:      2
Query Match:              99.64%         Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-15 (1-549) x AR278920 (1-1686)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
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Db         38 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 97

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
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Db         98 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 157

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
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Db        158 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 217

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
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Db        218 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 277
Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
Db        338 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 397
Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
Db        398 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 457
Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
Db        458 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 517
Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
Db        518 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 577
Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
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Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
Db        818 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 877
Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
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Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
Db       1058 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1117
Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
Db       1118 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1177
Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
Db       1178 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1237
Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
Db       1238 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1297
Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
Db       1298 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1357

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
Db       1358 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1417
Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
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Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
Db       1478 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCCGCGCTAGCATTGCTTGAG 1537
Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
Db       1538 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1597
Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
Db       1598 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1657
Qy        541 MetLysValGlyLysThrArgGluLeu 549
Db       1658 ATGAAGGTGGGTAAAACTCGGGAGTTA 1684
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RESULT 11
AF124407

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LOCUS       AF124407               1983 bp    RNA     linear   VRL 24-JUL-1999
DEFINITION  Hepatitis E virus isolate AKL-90 ORF-2 gene, complete cds.
ACCESSION   AF124407
VERSION     AF124407.1  GI:5579229
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 1983)
  AUTHORS   Arankalle,V.A., Paranjape,S., Emerson,S.U., Purcell,R.H. and
            Walimbe,A.M.
  TITLE     Phylogenetic analysis of hepatitis E virus isolates from India
            (1976-1993)
  JOURNAL   J. Gen. Virol. 80 (Pt 7), 1691-1700 (1999)
  MEDLINE   99350000
   PUBMED   10423137
REFERENCE   2  (bases 1 to 1983)
  AUTHORS   Arankalle,V.A., Paranjape,S., Emerson,S.U., Purcell,R.H. and
            Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JAN-1999) Hepatitis, National Institute of Virology,
            20-A Dr. Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:                0.632          Length:         1983
Score:                    547.00         Matches:        547
Percent Similarity:       99.64%         Conservative:   0
Best Local Similarity:    99.64%         Mismatches:     2
Query Match:              99.64%         Indels:         0
DB:                       1              Gaps:           0

US-09-769-066-15 (1-549) x AF124407 (1-1983)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
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Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCGGTGCCTGATGTCGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
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Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGCCCGCTTTTACCCCTTCAGGACGGCACCAAC 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
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Db        514 ACTCATATAATGGCCACGGAAGCTTCTAATTATGCCCAATACCGAGTTGCCCGTGCCACG 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db        574 ATCCGTTACCGCCCGCTGGTCCCCAACGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

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Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Db        754 CACTATCGTAACCAGGGTTGGCGCTCTGTCGAGACCTCCGGGGTGGCCGAGGAGGAGGCC 813

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Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Db        874 CCTTACACCGGTGCCCTTGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Db        934 ACCCCCGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

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Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
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Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGACCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Db       1414 TGGCTCTCCCTCACCGCTGCCGAGTATGACCAGTCCACCTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTCAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
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Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
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Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTACAACACCACTGCTAGCGACCAATTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
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Db       1714 GAGAATGCCGCCGGGCACCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

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Db       1774 CCCGTCTCTATTTCTGCGGTTGCAGTCTTCGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
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Db       1834 GATACCTTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

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Qy        541 MetLysValGlyLysThrArgGluLeu 549
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RESULT 12
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LOCUS       AR278906                1984 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 1 from patent US 6514690.
ACCESSION   AR278906
VERSION     AR278906.1  GI:29713540
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1984)
  AUTHORS   Li,F., Hui,Z., Anderson,D.A., Logarnini,S.A. and Torresi,J.
  TITLE     Immunoreactive antigens of Hepatitis E Virus
  JOURNAL   Patent: US 6514690-A 1 04-FEB-2003;
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:                0.632          Length:         1984
Score:                    547.00         Matches:        547
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Percent Similarity:     99.64%          Conservative:  0
Best Local Similarity:  99.64%          Mismatches:    2
Query Match:            99.64%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-15 (1-549) x AR278906 (1-1984)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
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Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
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Db        514 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db        574 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Db        874 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
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Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Db       1294 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       1474 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
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Db       1534 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Db       1594 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
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Db       1654 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1713

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Db       1714 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
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Db       1774 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCCGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
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Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
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Qy        541 MetLysValGlyLysThrArgGluLeu 549
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RESULT 13
AF065061
LOCUS       AF065061               2173 bp    DNA     linear   VRL 29-JAN-1999
DEFINITION  Hepatitis E virus structural protein 2 precursor, gene, complete
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ACCESSION   AF065061
VERSION     AF065061.1  GI:4204235
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 2173)
  AUTHORS   Meng,J., Cong,M., Dai,X., Pillot,J., Purdy,M.A., Fields,H.A. and
            Khudyakov,Y.E.
  TITLE     Primary structure of open reading frame 2 and 3 of the hepatitis E
            virus isolated from Morocco
  JOURNAL   J. Med. Virol. 57 (2), 126-133 (1999)
  MEDLINE   99107414
   PUBMED   9892396
REFERENCE   2  (bases 1 to 2173)
  AUTHORS   Meng,J., Cong,M., Dai,X., Pillot,J., Purdy,M., Fields,H.A. and
            Khudyakov,Y.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-MAY-1998) Hepatitis Branch, CDC, 1600 Clifton Rd.,
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FEATURES             Location/Qualifiers
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Alignment Scores:
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Query Match:              99.64%         Indels:          0
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US-09-769-066-15 (1-549) x AF065061 (1-2173)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
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Db        467 GCGGTTGCTCCGGCCCATGATACCCCGCCTGTGCCCGATGTTGATTCTCGCGGCGCTATC 526

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
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Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
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Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Db        887 CATTATCGCAACCAGGGTTGGCGCTCTGTTGAAACCTCCGGGGTGGCGGAGGAGGAGGCC 946

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
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Db       1007 CCTTACACTGGTGCCCTCGGGTTGTTGGATTTTGCTCTCGAGCTTGAGTTCCGCAACCTC 1066

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Db       1067 ACCCCTGGTAACACCAATACACGGGTTTCCCGCTACTCTAGCACCGCCCGCCACCGTCTT 1126

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Db       1127 CGCCGTGGCGCAGACGGGACTGCCGAGCTCACCACCACGGCTGCGACTCGCTTTATGAAG 1186

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
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Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db       1247 CTGTTTAATCTTGCTGACACCCTGCTTGGCGGCCTACCGACAGAATTGATTTCGTCGGCT 1306

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Db       1307 GGTGGCCAACTGTTTTACTCTCGCCCGGTCGTCTCAGCCAATGGCGAGCCGACTGTCAAG 1366

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
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Db       1367 CTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCTCACGACATC 1426

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Db       1427 GACCTTGGGGAATCTCGTGTAGTCATCCAGGATTATGACAATCAGCATGAGCAGGACCGT 1486

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Db       1487 CCGACACCTTCCCCAGCCCCGTCTCGCCCTTTTTCTGTTCTCCGGGCCAATGATGTGCTT 1546

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       1607 GTCTATGTCTCCGACTCTGTGACCTTGGTCAATGTTGCGACCGGCGCGCAGGCCGTTGCT 1666

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
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Db       1667 CGGTCGCTTGACTGGACTAAGGTCACACTTGATGGCCGCCCTCTTTCTACTATCCAGCAG 1726

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Db       1727 TATTCGAAGACTTTCTTTGTCCTGCCGCTTCGTGGTAAACTTTCCTTCTGGGAGGCAGGT 1786

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
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Db       1787 ACCACTAAAGCCGGGTACCCTTACAATTATAATACTACTGCTAGTGACCAACTGCTCGTT 1846

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
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Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
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Db       1907 CCTGTCTCCATTTCTGCGGTGGCTGTCCTGGCCCCCCACTCTGCGTTAGCACTGCTTGAG 1966

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
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Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
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Db       2027 CCCCTCGGCCTCCAGGGCTGCGCCTTTCAGTCCACTGTCGCTGAGCTCCAGCGGCTTAAG 2086

Qy        541 MetLysValGlyLysThrArgGluLeu 549
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Db       2087 ATGAAGGTGGGTAAAACTCGGGAGTTA 2113

RESULT 14
AF051351
LOCUS       AF051351                2104 bp    RNA     linear   VRL 08-AUG-2001
DEFINITION  Hepatitis E virus strain 93-Egypt RNA-polymerase gene, partial cds;
            and ORF-3 and structural protein genes, complete cds.
ACCESSION   AF051351
VERSION     AF051351.1  GI:3603261
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 2104)
  AUTHORS   Tsarev,S.A., Binn,L.N., Gomatos,P.J., Arthur,R.R., Monier,M.K., van
            Cuyck-Gandre,H., Longer,C.F. and Innis,B.L.
  TITLE     Phylogenetic analysis of hepatitis E virus isolates from Egypt
  JOURNAL   J. Med. Virol. 57 (1), 68-74 (1999)
  MEDLINE   99105430
   PUBMED   9890424
REFERENCE   2  (bases 1 to 2104)
  AUTHORS   Tsarev,S.A., Binn,L.N., Gomatos,P.J., Arthur,R.R., Monier,M.K., van
            Cuyck-Gandre,H., Longer,C.F. and Innis,B.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-FEB-1998) Department of Virus Diseases, Walter Reed
            Army Institute of Research, Washington, DC 20307
FEATURES             Location/Qualifiers.
     source          1. .2104
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
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                     /country="Egypt:Cairo"
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                     SPLLPLQDGTNTHIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTT
                     PTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLV
                     MLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRG
                     ADGTAELTTTAATRFMKDLYFSSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAG
                     GQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQD
                     RPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQ
                     AVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTSS
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Alignment Scores:
Pred. No.:                0.663          Length:          2104
Score:                    544.00         Matches:         544
Percent Similarity:       99.09%         Conservative:    0
Best Local Similarity:    99.09%         Mismatches:      5
Query Match:              99.09%         Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-15 (1-549) x AF051351 (1-2104)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
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Db        455 GCGGTCGCTCCGGCCCATGACACCCCGCCGGTGCCTGATGTTGACTCTCGCGGCGCCATC 514

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 TTGCGCCGACAGTATAATCTTTCAACATCCCCCCTCACTTCCTCCGTGGCCACTGGCACC 574

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
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Db        575 AATTTGGTTCTTTACGCCGCCCCCCTCAGCCCGCTCTTACCCCTTCAGGACGGCACCAAT 634

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 ACCCATATTATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGTTCGTGCCACA 694

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db        695 ATCCGTTACCGTCCGCTAGTCCCTAATGCTGTTGGTGGCTATGCAATTTCCATCTCGTTC 754

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        755 TGGCCACAGACTACCACCACCCCGACGTCCGTCGACATGAATTCCATAACTTCGACGGAT 814

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Db        815 GTTCGTATCCTTGTCCAGCCCGGTATAGCCTCCGAGCTTGTGATCCCAAGTGAGCGCCTG 874

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        875 CACTACCGCAACCAGGGCTGGCGTTCCGTTGAGACCTCTGGGGTGGCAGAGGAGGAGGCC 934

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
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Db        935 ACTTCTGGCCTTGTTATGCTCTGTATACATGGCTCACCTGTCAATTCTTACACTAATACA 994

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Db        995 CCCTATACCGGTGCCCTTGGCTTGCTGGATTTCGCTCTTGAGCTTGAGTTCCGCAACCTC 1054

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Db       1115 CGCCGCGGCGCAGACGGAACCGCTGAGCTTACCACTACGGCTGCAACCCGCTTCATGAAG 1174

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
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Db       1175 GACCTCTATTTTTCTAGTACTAATGGTGTCGGCGAGATTGGCCGCGGGATTGCCCTTACC 1234

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Db       1295 GGTGGCCAATTGTTCTATTCTCGTCCAGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1354

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
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Db       1355 CTATACACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCTATCCCGCATGACATC 1414

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Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1475 CCGACACCTTCCCCAGCCCCGTCGCGCCCTTTCTCTGTTCTTCGGGCTAACGATGTGCTC 1534

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1535 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACCTATGGCTCTTCGACTGGCCCA 1594

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1595 GTCTATGTTTCTGACTCCGTGACCTTGGTCAATGTTGCGACCGGCGCGCAGGCCGTTGCT 1654

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420

Db       1655 CGGTCGCTCGACTGGACTAAGGTCACGCTCGATGGTCGCCCTCTTTCTACCATTCAGCAG 1714

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1715 TATTCGAAGACTTTCTTCGTCCTGCCCCTCCGTGGCAAGCTCTCCTTCTGGGAGGCAGGT 1774

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460

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Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480

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Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500

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Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520

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Qy        541 MetLysValGlyLysThrArgGluLeu 549

Db       2075 ATGAAGGTGGGTAAAACTCGGGAGTTA 2101

RESULT 15
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LOCUS       AF051352               2106 bp    RNA     linear   VRL 08-AUG-2001
DEFINITION  Hepatitis E virus strain 94-Egypt RNA-polymerase gene, partial cds;
            and ORF-3 and structural protein genes, complete cds.
ACCESSION   AF051352
VERSION     AF051352.1  GI:3603265
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 2106)
  AUTHORS   Tsarev,S.A., Binn,L.N., Gomatos,P.J., Arthur,R.R., Monier,M.K., van
            Cuyck-Gandre,H., Longer,C.F. and Innis,B.L.
  TITLE     Phylogenetic analysis of hepatitis E virus isolates from Egypt
  JOURNAL   J. Med. Virol. 57 (1), 68-74 (1999)
  MEDLINE   99105430
   PUBMED   9890424
REFERENCE   2  (bases 1 to 2106)
  AUTHORS   Tsarev,S.A., Binn,L.N., Gomatos,P.J., Arthur,R.R., Monier,M.K., van
            Cuyck-Gandre,H., Longer,C.F. and Innis,B.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-FEB-1998) Department of Virus Diseases, Walter Reed
            Army Institute of Research, Washington, DC 20307
FEATURES             Location/Qualifiers
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                     /strain="94-Egypt"
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Alignment Scores:
Pred. No.:                0.663          Length:          2106
Score:                    544.00         Matches:         544
Percent Similarity:       99.09%         Conservative:    0
Best Local Similarity:    99.09%         Mismatches:      5
Query Match:              99.09%         Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-15 (1-549) x AF051352 (1-2106)

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Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40

Db        517 TTGCGCCGACAGTATAATCTTTCAACATCCCCCCTCACTTCTTCCGTGGCCACTGGCACC 576

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60

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Qy       121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Qy       181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
Db       997 CCTTATACCGGTGCCCTTGGGCTGCTGGACTTTGCCCTCGAGCTTGAGTTCCGCAACCTC 1056

Qy       201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
Db       1057 ACCCCCGGCAATACCAACACGCGGGTCTCCCGTTACTCTAGCACTGCGCGCCACCGTCTT 1116

Qy       221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
Db       1117 CGCCGCGGCGCGGACGGAACTGCTGAGCTCACTACCACGGCCGCAACCCGCTTCATGAAG 1176

Qy       241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
Db       1177 GACCTTTATTTTTCTAGTACTAATGGTGTCGGCGAGATCGGCCGCGGGATTGCCCTTACC 1236

Qy       261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
Db       1237 CTGTTTAACCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAACTGATTTCGTCGGCC 1296

Qy       281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
Db       1297 GGTGGCCAACTGTTCTATTCTCGTCCAGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1356

Qy       301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
Db       1357 CTATATACATCTGTAGAGAATGCTCAGCAGGACAAGGGTATTGCTATCCCGCATGACATC 1416

Qy       321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
Db       1417 GACCTCGGGGAATCCCGAGTAGTTATCCAGGACTATGACAACCAACATGAGCAAGATCGG 1476

Qy       341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
Db       1477 CCGACACCTTCCCCAGCCCCGTCGCGCCCTTTCTCTGTCCTTCGGGCCAACGATGTGCTT 1536

Qy       361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
Db       1537 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACCTATGGCTCCTCGACTGGCCCA 1596

Qy       381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
Db       1597 GTCTATGTTTCTGACTCCGTGACCTTGGTCAACGTTGCGACCGGCGCGCAGGCCGTTGCT 1656

Qy       401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
Db       1657 CGGTCGCTCGATTGGACTAAGGTCACGCTCGATGGTCGCCCCCTTTCTACCATTCAGCAG 1716

Qy       421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
Db       1717 TACTCGAAGACTTTCTTTGTCCTGCCCCTCCGTGGCAAGCTCTCCTTTTGGGAGGCAGGT 1776

Qy       441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
Db       1777 ACTACTAAAGCCGGGTACCCTTATAATTACAATACCACTGCTAGCGACCAATTGCTTATC 1836

Qy       461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
Db       1837 GAGAACGCCACCGGGCATCGGGTGGCTATTTCTACTTACACTACTAGCTTAGGTGCTGGC 1896

Qy       481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
Db       1897 CCTGTTTCCATTTCTGCGGTTGCTGTTCTGGCCCCCCACTCTGCTTTAGCACTGCTTGAG 1956

Qy       501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
Db       1957 GATACCCTGGACTACCCTGCCCGCGCCCACACTTTTGATGATTTCTGCCCGGAGTGCCGT 2016

Qy       521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
Db       2017 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCCACTGTCGCTGAGCTCCAGCGGCTTAAG 2076

Qy       541 MetLysValGlyLysThrArgGluLeu 549
Db       2077 ATGAAGGTGGGTAAAACTCGGGAGTTA 2103
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RESULT 16
HEU22532

LOCUS	HEU22532 2082 bp RNA linear VRL 17-APR-1996
DEFINITION	Hepatitis E virus ORF-3 structural protein and ORF-2 structural protein genes, complete cds.
ACCESSION	U22532
VERSION	U22532.1 GI:726509
KEYWORDS	.
SOURCE	Hepatitis E virus
ORGANISM	Hepatitis E virus Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE	1 (bases 1 to 2082)
AUTHORS	Panda,S.K., Nanda,S.K., Zafrullah,M., Ansari,I.H., Ozdener,M.H. and Jameel,S.
TITLE	An Indian strain of hepatitis E virus (HEV): cloning, sequence, and expression of structural region and antibody responses in sera from individuals from an area of high-level HEV endemicity
JOURNAL	J. Clin. Microbiol. 33 (10), 2653-2659 (1995)
MEDLINE	96087204
PUBMED	8567900
REFERENCE	2 (bases 1 to 2082)
AUTHORS	Panda,S.K.
TITLE	Direct Submission
JOURNAL	Submitted (14-MAR-1995) Subrat K. Panda, Department of Pathology, All India Institute of Medical Sciences, New Delhi, 110029, India

FEATURES	Location/Qualifiers
source	1. .2082 /organism="Hepatitis E virus" /mol_type="genomic RNA" /isolate="Hyderabad (India)" /db_xref="taxon:12461"
CDS	1. .372 /note="ORF-3; structural protein; Method: conceptual translation supplied by author." /codon_start=1 /protein_id="AAA97365.1" /db_xref="GI:726510" /translation="MDNMSFAAPMGSRPWALGLFCCCSSCFCLCCSRHRPVSRLAAVV GGAAAVPAVVSGVTGLILSPSQSPIFIQPTPSPRMSPLRPGLDLVFANPSDHSAPLGA TRPSAPPLPHVVDLPQLGPRR"
CDS	42. .2024 /note="ORF-2; structural protein; Method: conceptual translation supplied by author." /codon_start=1 /protein_id="AAA97366.1" /db_xref="GI:726511" /translation="MGPRPILLLFLMFLPMLLAPPPGQPSGRRRGRRSGGSGGGFWGD RVDSQPFAIPYIHPTNPFAPNVTAAAGAGPRVRQPVRPLGSAWRDQAQRPAAASRRRP TTAGAAPLTAVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPL SPLLPLQDGTNTHIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTPT PTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLV MLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRG

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                RPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQ
                AVARSLDWTKVTLDGRPLSTIQQYSKIFFVLPLRGKLSFWEAGTTRPGYPYNYNTTAS
                DQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLGPHSALALLEDTLDYPARAHTFD
                DFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTREL"

Alignment Scores:
Pred. No.:              0.682           Length:         2082
Score:                  542.00          Matches:        542
Percent Similarity:     98.72%          Conservative:   0
Best Local Similarity:  98.72%          Mismatches:     7
Query Match:            98.72%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x HEU22532 (1-2082)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
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Db        375 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 434

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
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Db        435 TTGCGCCGGCAGTACAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGTACT 494

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
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Db        495 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGTACCAAT 554

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        555 ACTCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACG 614

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db        615 ATCCGTTACCGCCCGCTGGTCCCCAACGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 674

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        675 TGGCCACAGACTACCCCCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 734

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Db        735 GTTCGCATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGCGAGCGCCTA 794

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Db        795 CACTATCGTAACCAAGGTTGGCGCTCTGTCGAGACCTCCGGGGTGGCCGAGGAGGAGGCC 854

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
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Db        855 ACCTCCGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAATACA 914

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Db        915 CCCTATACCGGTGCCCTTGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 974

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Db        975 ACCCCCGGTAATACTAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 1034

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
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Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
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Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Db       1395 CCGACGCCTTCTCCAGCCCCGTCGCGCCCTTTCTCTGTTCTTCGAGCTAATGATGTGCTT 1454

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Db       1455 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACCTATGGCTCTTCGACTGGCCCA 1514

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       1515 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCCACCGGCGCGCAGGCCGTTGCC 1574

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
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Db       1575 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCTCTCTCCACCATCCAGCAG 1634

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Db       1635 TATTCGAAGATCTTCTTTGTCCTGCCGCTCCGCGGGAAGCTCTCTTTCTGGGAGGCAGGC 1694

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
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Db       1695 ACAACTAGGCCCGGGTACCCTTATAATTACAACACCACTGCAAGCGACCAACTGCTTGTC 1754

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
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Db       1755 GAGAATGCCGCCGGGCACCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGC 1814

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
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Db       1815 CCCGTCTCTATTTCTGCGGTTGCCGTCTTAGGCCCCCACTCTGCGCTAGCATTGCTTGAG 1874

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
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Db       1875 GATACTTTGGATTACCCTGCCCGCGCCCATACTTTTGATGACTTCTGCCCAGAGTGCCGC 1934

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
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Db       1935 CCCCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTCCAGCGCCTTAAG 1994

Qy        541 MetLysValGlyLysThrArgGluLeu 549
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Db       1995 ATGAAGGTGGGTAAAACTCGGGAGTTA 2021
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RESULT 17
AR278918
LOCUS       AR278918                1658 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 15 from patent US 6514690.
ACCESSION   AR278918
VERSION     AR278918.1  GI:29713552
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1658)
  AUTHORS   Li,F., Hui,Z., Anderson,D.A., Logarnini,S.A. and Torresi,J.
  TITLE     Immunoreactive antigens of Hepatitis E Virus
  JOURNAL   Patent: US 6514690-A 15 04-FEB-2003;
FEATURES             Location/Qualifiers
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Alignment Scores:

Pred. No.:	0.711	Length:	1658
Score:	538.00	Matches:	538
Percent Similarity:	99.63%	Conservative:	0
Best Local Similarity:	99.63%	Mismatches:	2
Query Match:	98.00%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AR278918 (1-1658)

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Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
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Db         38 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 97

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
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Db         98 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 157

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
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Db        158 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 217

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
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Db        218 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 277

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db        278 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 337

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        338 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 397

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Db        398 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 457

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Db        458 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 517

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
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Db        518 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 577

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Db        638 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 697

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Db        698 CGTCGCGGTGCAGATGGGACTGCCGAGCTTACCACCACGGCTGCTACCCGCTTCATGAAG 757

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Db        758 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 817

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        818 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 877

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Db        878 GGTGGCCAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 937

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
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Db        938 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 997

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Db        998 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1057

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Db       1058 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1117

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Db       1118 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1177

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       1178 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1237

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
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Db       1238 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1297

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Db       1298 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1357

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
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Db       1358 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1417

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
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Db       1418 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1477

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
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Db       1538 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1597

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
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Db       1598 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1657
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RESULT 18
HPEPPG

LOCUS	HPEPPG 1649 bp RNA linear VRL 24-JAN-2003
DEFINITION	Hepatitis E virus gene for polyprotein, partial cds.
ACCESSION	D90274
VERSION	D90274.1 GI:221702
KEYWORDS	.
SOURCE	Hepatitis E virus
ORGANISM	Hepatitis E virus Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE	1
AUTHORS	Uchida,T., Suzuki,K., Hayashi,N., Iida,F., Hara,T., Oo,S.S., Wang,C., Shikata,T., Ichikawa,M., Rikihisa,T., Mizuno,K. and Win,K.M.
TITLE	Hepatitis E virus: cDNA cloning and expression
JOURNAL	Microbiol. Immunol. 36 (1), 67-79 (1992)
MEDLINE	92261377
PUBMED	1584074
REFERENCE	2 (bases 1 to 1649)
AUTHORS	Uchida,T.
TITLE	Direct Submission
JOURNAL	Submitted (25-DEC-1990) Toshikazu Uchida, Nihon University School of Medicine, 1st Department of Pathology; 30-1 Oyaguchi-Kamimachi, Itabashi-ku, Tokyo 173, Japan (Tel:81-3-3972-8111, Fax:81-3-3972-8830)

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US-09-769-066-15 (1-549) x HPEPPG (1-1649)

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Qy        162 SerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrPro 181
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LOCUS       AB082545               1666 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, complete cds,
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ACCESSION   AB082545
VERSION     AB082545.1  GI:22759586
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            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 1666)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
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VERSION     AR170407.1  GI:17908366
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SOURCE      Unknown.
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            Unclassified.
REFERENCE   1  (bases 1 to 1644)
  AUTHORS   Fuerst,T.R., McAtee,C.Patrick., Yarbough,P.O. and Zhang,Y.-F.
  TITLE     Hepatitis E virus antigens and uses therefor
  JOURNAL   Patent: US 6291641-A 4 18-SEP-2001;
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US-09-769-066-15 (1-549) x AR170407 (1-1644)

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Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
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Db        301 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 360

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
Db        361 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 420

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
Db        421 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 480

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
Db        481 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 540

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
Db        541 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 600

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
Db        601 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCAC---TCC 657

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
Db        658 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 717

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
Db        718 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 777

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
Db        778 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 837

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
Db        838 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 897

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
Db        898 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 957

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
Db        958 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1017

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
Db       1018 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1077

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
Db       1078 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1137

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
Db       1138 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1197

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
Db       1198 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1257

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
Db       1258 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1317

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
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Db       1318 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1377

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480

Db       1378 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1437

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500

Db       1438 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1497

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1498 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1557

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1558 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1617

Qy        541 MetLysValGlyLysThrArgGluLeu 549

Db       1618 GTTAAGGTGGGTAAAACTCGGGAGTTG 1644

RESULT 21
I73140
LOCUS       I73140                  1980 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 2 from patent US 5686239.
ACCESSION   I73140
VERSION     I73140.1  GI:3009279
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1980)
  AUTHORS   Reyes,G.R., Tam,A.W. and Yarbough,P.O.
  TITLE     Hepatitis E virus peptides and methods
  JOURNAL   Patent: US 5686239-A 2 11-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .1980
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:              1.14          Length:          1980
Score:                  506.50        Matches:         517
Percent Similarity:     94.17%        Conservative:    0
Best Local Similarity:  94.17%        Mismatches:      31
Query Match:            92.26%        Indels:          1
DB:                     1             Gaps:            1

US-09-769-066-15 (1-549) x I73140 (1-1980)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20

Db        334 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40

Db        394 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60

Db        454 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

Db        514 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        574 ATCCGTTACCGGCCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        634 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db        694 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db        754 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180

Db        814 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        874 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 933

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db        934 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCAC---TCC 990

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db        991 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1050

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260

Db       1051 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1110

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db       1111 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1170

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db       1171 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1230

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320

Db       1231 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1290

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db       1291 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1350

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1351 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1410

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1411 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1470

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1471 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1530

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420

Db       1531 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1590

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1591 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1650

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460

Db       1651 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1710

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
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Db       1711 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1770

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
              ||||||   |||||||||   ||||||||||||||   ||||||||||||||||||||||
Db       1771 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1830

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||   |||||||||   ||||||||||||||||||||||||||||||||||||||
Db       1831 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1890

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1891 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1950

Qy        541 MetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||
Db       1951 GTTAAGGTGGGTAAAACTCGGGAGTTG 1977
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RESULT 22
HEVBCN6
LOCUS       HEVBCN6                 1946 bp    RNA     linear   VRL 17-NOV-1998
DEFINITION  Hepatitis E virus nonstructural polyprotein and structural protein
            genes, partial cds; and unknown gene.
ACCESSION   AF058684
VERSION     AF058684.1  GI:3882959
KEYWORDS    .
SEGMENT     6 of 7
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 1946)
  AUTHORS   Pina,S., Jofre,J., Emerson,S.U., Purcell,R.H. and Girones,R.
  TITLE     Characterization of a strain of infectious hepatitis E virus
            isolated from sewage in an area where hepatitis E is not endemic
  JOURNAL   Appl. Environ. Microbiol. 64 (11), 4485-4488 (1998)
  MEDLINE   99013657
   PUBMED   9797311
REFERENCE   2  (bases 1 to 1946)
  AUTHORS   Pina,S., Jofre,J., Shapiro,M., Emerson,S.U., Purcell,R.H. and
            Girones,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-APR-1998) Department of Microbiology, School of
            Biology, University of Barcelona, Diagonal Avenue 645, Barcelona
            08028, Spain
FEATURES             Location/Qualifiers
     source          1. .1946
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                     /mol_type="genomic RNA"
                     /strain="BCN"
                     /db_xref="taxon:12461"
                     /country="Spain:Barcelona"
     CDS             <1. .95
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                     /product="nonstructural polyprotein"
                     /protein_id="AAC77805.1"
                     /db_xref="GI:3882967"
                     /translation="LQAVADGKAHFTESVKPVLDLTNSILCRVE"
     misc_feature    <1. .92
                     /note="Region: putative RNA-directed RNA polymerase"
     CDS             92. .463
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                     /product="unknown"
                     /protein_id="AAC77807.1"
                     /db_xref="GI:3882969"
                     /translation="MNNMSFAAPMGSRPCALGLFCCCSSCFCLCCPRHRPVSRLAAVV
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                     /db_xref="GI:3882970"
                     /translation="MRPRPILLLFLMFLPMLPAPPPGQSSGRRRGRRSGGSGGGFWGD
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                     TTTGAAPLTAVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPL
                     SPLLPLQDGTNTHIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTT
                     PTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQGRRSVETSGVAQEEATSGLV
                     MLCIHGSPVNSYSNTPYTGALGLLDFALELELRNLTPGNTNTRVSRYSSTARHRLRRG
                     ADGTAELTTTAATRFMKDLYFTSNNGVGEIGRGIALTLFNLADTLLGGLPTELISSAG
                     GQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQD
                     RPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQ
                     AVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTAS
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     misc_feature    133. .>1946
                     /note="Region: putative capsid protein"
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Alignment Scores:
Pred. No.:                1.5          Length:          1946
Score:                    487.00       Matches:         487
Percent Similarity:       98.78%       Conservative:    0
Best Local Similarity:    98.78%       Mismatches:      6
Query Match:              88.71%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-15 (1-549) x HEVBCN6 (1-1946)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 525

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 TTGCGCCGGCAGTACAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 585

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 AACCTGGTTCTTTATGCCGCCCCTCTCAGTCCGCTTTTACCCCTCCAGGACGGTACCAAT 645

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 ACTCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACG 705

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 ATCCGTTACCGCCCGTTGGTTCCCAACGCTGTCGGCGGTTACGCCATTTCCATCTCATTC 765

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 825

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 GTTCGTATTCTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGCGAGCGCCTA 885

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||  ||||||||||||||||||||||||||||   |||||||||
Db        886 CACTACCGTAACCAAGGTAGGCGCTCCGTCGAGACCTCCGGGGTGGCTCAGGAGGAGGCC 945

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||   ||||||||||||   ||||||
Db        946 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATAGTAATACA 1005

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db       1006 CCATACACCGGCGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGCTTCGCAACCTT 1065

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Db       1066 ACCCCCGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 1125

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Db       1126 CGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1185

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260

Db       1186 GACCTCTATTTCACTAGTAATAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1245

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db       1246 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1305

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db       1306 GGTGGCCAGCTGTTCTACTCCCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1365

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320

Db       1366 CTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATCGCAATCCCGCATGATATT 1425

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db       1426 GACCTCGGAGAGTCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGACCGG 1485

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1486 CCGACGCCTTCTCCAGCCCCCTCGCGCCCTTTCTCTGTTCTTCGAGCTAATGATGTGCTT 1545

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1546 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACCTATGGCTCTTCGACTGGCCCA 1605

Qy        381 ValTyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1606 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1665

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420

Db       1666 CGGTCGCTCGACTGGACCAAGGTCACACTTGACGGTCGCCCTCTCTCCACCATCCAGCAG 1725

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1726 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGCAAGCTCTCTTTCTGGGAGGCGGGC 1785

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460

Db       1786 ACAACTAAGGCCGGGTACCCTTATAATTACAACACCACTGCTAGCGACCAACTGCTTGTC 1845

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480

Db       1846 GAGAATGCCGCCGGGCACCGGGTTGCCATCTCCACTTACACCACTAGCCTGGGTGCTGGC 1905

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHis 493

Db       1906 CCCGTCTCCATTTCTGCGGTTGCCGTCTTAGCCCCCCAC 1944

RESULT 23
E03815
LOCUS       E03815                  1643 bp    RNA     linear   PAT 29-SEP-1997
DEFINITION  cDNA encoding a part of type non-A non-B hepatitis virus genome.
ACCESSION   E03815
VERSION     E03815.1  GI:2172029
KEYWORDS    JP 1992200388-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1643)
  AUTHORS   Uchida,T., Shikata,T., Ichikawa,M., Araki,M., Rikihisa,T. and
            Mizuno,K.
  TITLE     EPIDEMIC NON-A NON-B HEPATITIS VIRUS ANTIGEN PEPTIDE AND NUCLEIC
            ACID FRAGMENT CODING THE SAME
  JOURNAL   Patent: JP 1992200388-A 1 21-JUL-1992;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Type non-A non-B hepatitis virus
            PN   JP 1992200388-A/1
            PD   21-JUL-1992
            PF   29-NOV-1990 JP 1990334835
            PI   UCHIDA TOSHIKAZU, SHIKATA TOSHIO, ICHIKAWA MUNETAKA, PI
            ARAKI MASAYASU,
            PI   RIKIHISA TETSUJI, MIZUNO KYOSUKE
            PC   C12N15/51,C07K13/00,C12P21/02,C12Q1/68,C12Q1/70,G01N33/569, PC
              G01N33/576//
            PC   A61K39/29,(C12P21/02,C12R1:19);
            CC   strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            CC   *source: clone=HT-4;
            FH   Key             Location/Qualifiers
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            FT                   /note='a part of type non-A non-B hepatitis
            FT                   virus genome'.
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:                1.59          Length:          1643
Score:                    482.50        Matches:         506
Percent Similarity:       95.83%        Conservative:    0
Best Local Similarity:    95.83%        Mismatches:      21
Query Match:              87.89%        Indels:          2
DB:                       1             Gaps:            1

US-09-769-066-15 (1-549) x E03815 (1-1643)

Qy         22 ArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThrAsn 41

Db          3 CGCCGGCAGTATAATCTATCAACATCTCCCCTCACTTCTTCCGTGGCCACCGGCACTAAC 62

Qy         42 LeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsnThr 61

Db         63 CTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAATACC 122

Qy         62 HisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIle 81

Db        123 CATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGTCCGTGCCACAATC 182

Qy         82 ArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrp 101

Db        183 CGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTCTGG 242

Qy        102 ProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAspVal 121

Db        243 CCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGATGTT 302

Qy        122 ArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeuHis 141

Db        303 CGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACAC 362

Qy        142 TyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaThr 161

Db        363 TATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCTACC 422

Qy        162 SerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrPro 181

Db        423 TCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAACACACCC 482

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201

Db        483 TATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTTACC 542

Qy        202 ProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221

Db        543 CCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGT 602
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Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 CGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAGGAC 662

Qy        242 LeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeu 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        663 CTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTG 722

Qy        262 PheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGly 281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 TTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGT 782

Qy        282 GlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeu 301
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        783 GGCCAGCTGTTCTACTCCCGTCCCGTCGTCTCGGCCCATGGCGAGCCGACTGTTAAGTTG 842

Qy        302 TyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAsp 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 TATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGAC 902

Qy        322 LeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgPro 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGGCCG 962

Qy        342 ThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrp 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 ACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGG 1022

Qy        362 LeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProVal 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1023 CTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTT 1082

Qy        382 TyrValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArg 401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1083 TATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGG 1142

Qy        402 SerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyr 421
              ||||||||||||||||||||||||||||||||||||   |||
Db       1143 TCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCC---TCTCCACCATCCAGCAGT 1199

Qy        422 SerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThr 441
                                  ||||||||||||||||||||||||||||||||||
Db       1200 ACCCGAAGACCTTCTTTGTCCTGCGCTCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACA 1259

Qy        442 ThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGlu 461
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1260 ACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAG 1319

Qy        462 AsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyPro 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1320 AATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCC 1379

Qy        482 ValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAsp 501
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Db       1380 GTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGAT 1439

Qy        502 ThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgPro 521
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db       1440 ACCTTGGACTACCCTGCCTGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCT 1499

Qy        522 LeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMet 541
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1500 CTTGGCCTCCA-GGGTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGANN 1558

Qy        542 LysValGlyLysThrArgGluLeu 549
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Db       1559 NAGGTGGGTAAAACTCGGGAGTTA 1582

RESULT 24
AF151962
LOCUS       AF151962               1497 bp    RNA     linear   VRL 30-JUN-1999
DEFINITION  Hepatitis E virus strain Ch-T11 ORF2 gene, partial cds.
ACCESSION   AF151962
VERSION     AF151962.1  GI:5281444
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 1497)
  AUTHORS   Yang,J., Zhang,H., Wang,Y. and Li,H.
  TITLE     Identification of a Novel Hepatitis E virus Responsible for
            Sporadic Acute Hepatitis in China
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1497)
  AUTHORS   Yang,J., Zhang,H., Wang,Y. and Li,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-MAY-1999) Department of Hepatitis, National Institute
            for the Control of Pharmaceutical and Biological Products, 2 Tian
            Tan Xi Li, Beijing, Hebei 100050, P. R. China
FEATURES             Location/Qualifiers
     source          1. .1497
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="Ch-T11"
                     /db_xref="taxon:12461"
                     /country="China"
     CDS             <1. .1463
                     /codon_start=3
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                     /protein_id="AAD41518.1"
                     /db_xref="GI:5281445"
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                     MLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRG
                     ADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPTELISSAG
                     GQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQD
                     RPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQTTYGSSTNPMYVSDTVTFVNVATGAQ
                     GVSRSLDWSKVTLDGRPLTTIQQYSKTFYVLPLRGKLSFWEAGTTKAGYPYNYNTTAS
                     DQILIENAAGHRVCISTYTTNLGSGPVSISAVGVLAPHSALAALEDTVDYHARAHTFD
                     DFCPECRALGLQGCAFQSTVAELQRLKMKVGKTREY"
     3'UTR           1464. .>1497

Alignment Scores:
Pred. No.:              2.25          Length:          1497
Score:                  458.00        Matches:         458
Percent Similarity:     94.43%        Conservative:    0
Best Local Similarity:  94.43%        Mismatches:      27
Query Match:            83.42%        Indels:          0
DB:                     1             Gaps:            0

US-09-769-066-15 (1-549) x AF151962 (1-1497)

Qy         64 MetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyr 83
              ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db          3 ATGGCTACTGAAGCCTCAAATTATGCCCAATACCGTGTTGTCCGTGCCACCATCCGGTAT 62

Qy         84 ArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGln 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGCCCTCTGGTGCCGAATGCTGTGGGTGGGTATGCTATTTCTATTTCTTTTTGGCCCCAA 122

Qy        104 ThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAspValArgIle 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACGACGACCACCCCGACGTCTGTGGACATGAATTCCATCACGTCCACCGATGTCCGTATT 182

Qy        124 LeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeuHisTyrArg 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 TTAGTTCAACCCGGCATAGCCTCCGAGCTGGTGATTCCCAGTGAGCGCCTGCATTACCGC 242

Qy        144 AsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaThrSerGly 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AACCAGGGCTGGCGCTCGGTTGAGACCTCCGGTGTCGCCGAGGAGGAGGCTACCTCCGGT 302

Qy        164 LeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThr 183
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
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Db        303 CTTGTTATGCTTTGTATCCATGGGTCACCTGTGAATTCTTATACTAATACACCTTATACT 362

Qy        184 GlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGly 203

Db        363 GGCGCCCTTGGCTTGCTTGATTTTGCGCTTGAGCTTGAGTTCCGCAATTTGACACCCGGT 422

Qy        204 AsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGly 223

Db        423 AATACAAACACGCGTGTTTCTCGTTATTCGAGTAGCGCACGTCACAAATTGCGCCGAGGG 482

Qy        224 AlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyr 243

Db        483 GCCGATGGTACTGCTGAGTTAACTACTACTGCTGCTACACGGTTTATGAAGGATCTCCAT 542

Qy        244 PheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsn 263

Db        543 TTTACAGGGACTAACGGAGTTGGTGAGGTTGGCCGTGGTATAGCGCTTACCCTGTTTAAT 602

Qy        264 LeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGln 283

Db        603 CTTGCTGACACACTTCTCGGCGGGCTCCCGACAGAATTGATTTCGTCGGCTGGTGGTCAG 662

Qy        284 LeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThr 303

Db        663 TTGTTTTATTCCCGCCCCGTCGTCTCGGCCAATGGCGAGCCGACAGTGAAACTTTACACC 722

Qy        304 SerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeuGly 323

Db        723 TCAGTCGAGAATGCTCAGCAGGATAAAGGGATTGCTATTCCACATGACATTGATCTTGGT 782

Qy        324 GluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrPro 343

Db        783 GAGTCCCGAGTTGTTATCCAAGATTATGATAATCAACATGAGCAAGACCGCCCTACTCCT 842

Qy        344 SerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSer 363

Db        843 TCCCCCGCCCCTTCTCGTCCCTTTTCTGTGCTCCGTGCTAATGATGTACTTTGGCTCTCT 902

Qy        364 LeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrVal 383

Db        903 CTTACAGCTGCTGAGTATGACCAGACTACCTATGGTTCCTCTACTAATCCTATGTATGTC 962

Qy        384 SerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeu 403

Db        963 TCTGATACTGTGACGTTTGTCAATGTGGCTACCGGTGCCCAGGGGGTTTCGCGCTCTTTG 1022

Qy        404 AspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLys 423

Db       1023 GACTGGTCTAAGGTCACCCTTGACGGGCGCCCACTTACTACTATCCAGCAATACTCTAAG 1082

Qy        424 ThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLys 443

Db       1083 ACTTTCTATGTTTTGCCCCTTCGTGGTAAGCTTTCTTTCTGGGAGGCTGGCACCACTAAG 1142

Qy        444 AlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAla 463

Db       1143 GCCGGTTACCCTTATAATTACAACACTACTGCTAGTGATCAGATTCTGATTGAGAATGCA 1202

Qy        464 AlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProValSer 483

Db       1203 GCCGGACACCGTGTCTGCATCTCTACTTACACTACTAATCTGGGCTCTGGACCCGTCTCT 1262

Qy        484 IleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThrLeu 503

Db       1263 ATCTCGGCCGTCGGTGTCCTCGCACCTCATTCTGCATTAGCCGCTTTAGAGGACACTGTC 1322

Qy        504 AspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeuGly 523

Db       1323 GATTATCATGCTCGCGCTCACACCTTTGATGACTTCTGCCCTGAGTGCCGTGCACTCGGC 1382

Qy        524 LeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLysVal 543

Db       1383 CTTCAGGGTTGTGCTTTCCAGTCAACTGTTGCTGAGCTGCAGCGTCTCAAAATGAAGGTG 1442

Qy        544 GlyLysThrArgGlu 548

Db       1443 GGTAAAACTCGGGAG 1457

RESULT 25
AF151963
LOCUS       AF151963               1402 bp    RNA     linear   VRL 30-JUN-1999
DEFINITION  Hepatitis E virus strain Ch-T21 ORF2 gene, partial cds.
ACCESSION   AF151963
VERSION     AF151963.1  GI:5281446
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 1402)
  AUTHORS   Yang,J., Zhang,H., Wang,Y. and Li,H.
  TITLE     Identification of a Novel Hepatitis E virus Responsible for
            Sporadic Acute Hepatitis in China
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1402)
  AUTHORS   Yang,J., Zhang,H., Wang,Y. and Li,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-MAY-1999) Department of Hepatitis, National Institute
            for the Control of Pharmaceutical and Biological Products, 2 Tian
            Tan Xi Li, Beijing, Hebei 100050, P. R. China
FEATURES             Location/Qualifiers
     source          1. .1402
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="Ch-T21"
                     /db_xref="taxon:12461"
                     /country="China"
     CDS             <1. .>1402
                     /codon_start=3
                     /product="ORF2"
                     /protein_id="AAD41519.1"
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                     /translation="YRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQ
                     PGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTPYTG
                     ALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGADGTAELTTTAATRFMKDL
                     HFTGTNGVGEVGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK
                     LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRAND
                     VLWLSLTAAEYDQTTYGSSTNPMYVSDTVTFVNVATGAQGVSRSLDWSKVTLDGRPLT
                     TIQQYSKTFYVLPLRGKLSFWETGTTKAGYPYNYNTTASDQILIENAAGHRVCISTYT
                     TNLGSGPVSISAVGVLAPHSALAALEDTVDYPARAHTFDDFCPECRALGLQGCAFQST
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Alignment Scores:
Pred. No.:              2.9             Length:         1402
Score:                  440.00          Matches:        440
Percent Similarity:     94.42%          Conservative:   0
Best Local Similarity:  94.42%          Mismatches:     26
Query Match:            80.15%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF151963 (1-1402)

Qy         83 TyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpPro 102

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Qy        103 GlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAspValArg 122

Db         63 CAAACAACTACCACCCCGACGTCCGTGGATATGAACTCCATCACTTCCACTGATGTCCGT 122

Qy        123 IleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeuHisTyr 142

Db        123 ATTCTTGTCCAACCCGGTATAGCCTCCGAGTTGGTGATCCCCAGTGAGCGCTTGCATTAT 182

Qy        143 ArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaThrSer 162
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Db        183 CGCAATCAGGGCTGGCGCTCAGTTGAGACCTCTGGCGTTGCTGAGGAGGAGGCTACTTCC 242

Qy        163 GlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyr 182

Db        243 GGTCTTGTTATGCTTTGTATACATGGGTCACCTGTGAACTCCTACACTAATACACCTTAT 302

Qy        183 ThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrPro 202

Db        303 ACTGGTGCTCTCGGCCTGCTCGATTTTGCACTTGAGCTTGAGTTTCGTAATCTGACACCT 362

Qy        203 GlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArg 222

Db        363 GGCAATACAAACACGCGCGTCTCTCGTTATTCGAGCAGTGCGCGCCATAAACTGCGCCGA 422

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242

Db        423 GGGGCCGACGGCACTGCTGAGCTAACTACTACTGCTGCTACACGGTTTATGAAGGATCTT 482

Qy        243 TyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPhe 262

Db        483 CATTTTACAGGGACTAATGGCGTTGGTGAGGTTGGCCGTGGGATAGCGCTTACCTTGTTT 542

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282

Db        543 AACCTTGCTGACACACTTCTCGGCGGGCTCCCGACAGAATTGATTTCGTCGGCTGGTGGT 602

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302

Db        603 CAGTTGTTTTATTCCCGCCCCGTCGTCTCGGCCAATGGCGAGCCGACAGTGAAACTTTAC 662

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322

Db        663 ACCTCAGTCGAGAATGCTCAGCAGGATAAAGGGATTGCTATTCCACATGACATTGATCTT 722

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342

Db        723 GGTGAGTCCCGAGTTGTTATCCAAGATTATGATAATCAACATGAGCAAGACCGCCCTACT 782

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362

Db        783 CCTTCCCCCGCCCCTTCTCGTCCCTTTTCTGTGCTCCGTGCTAATGATGTACTTTGGCTC 842

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382

Db        843 TCTCTTACAGCTGCTGAGTATGACCAGACTACCTATGGTTCCTCTACTAATCCTATGTAT 902

Qy        383 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402

Db        903 GTCTCTGATACTGTGACGTTTGTCAATGTGGCTACCGGTGCCCAGGGGGTTTCGCGCTCT 962

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422

Db        963 TTGGACTGGTCTAAGGTCACCCTTGACGGGCGCCCACTTACTACTATCCAGCAATACTCT 1022

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442

Db       1023 AAGACTTTCTATGTTTTGCCCCTTCGTGGTAAGCTTTCTTTCTGGGAGACTGGCACCACT 1082

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462

Db       1083 AAGGCCGGTTACCCTTATAATTACAACACTACTGCTAGTGATCAGATTCTGATTGAGAAT 1142

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482

Db       1143 GCAGCCGGACACCGTGTCTGCATCTCTACTTACACTACTAATCTGGGCTCTGGACCCGTC 1202

Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThr 502

Db       1203 TCTATCTCGGCCGTCGGTGTCCTCGCACCTCATTCTGCATTAGCCGCTTTAGAGGACACT 1262

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522

Db       1263 GTCGATTATCCTGCTCGCGCTCACACCTTTGATGACTTCTGCCCTGAGTGCCGTGCACTC 1322

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLys 542

Db       1323 GGCCTTCAGGGCTGTGCTTTCCAGTCAACTGTTGCTGAGCTGCAGCGTCTCAAAATGAAG 1382

Qy        543 ValGlyLysThrArgGlu 548

Db       1383 GTGGGTAAAACTCGGGAG 1400

RESULT 26
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LOCUS       AR002166               1311 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 9 from patent US 5741490.
ACCESSION   AR002166
VERSION     AR002166.1  GI:3963720
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1311)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.D.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 5741490-A 9 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .1311
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:                3.06          Length:          1311
Score:                    436.00        Matches:         436
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              79.42%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x AR002166 (1-1311)

Qy        114 AsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGluLeu 133

Db          1 AATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTT 60

Qy        134 ValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThrSer 153

Db         61 GTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCT 120

Qy        154 GlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeu 173

Db        121 GGGGTGGCTGAGGAGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTC 180

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193

Db        181 GTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTT 240

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213

Db        241 GAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCC 300

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233

Db        301 AGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACG 360

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253

Db        361 GCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 420

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273

Db        421 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCG 480

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
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Db        481 ACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCC 540

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313

Db        541 AATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGT 600

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333

Db        601 ATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGAT 660

Qy        334 AsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgProPheSerVal 353

Db        661 AACCAACATGAACAAGATCGGCCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTC 720

Qy        354 LeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThr 373

Db        721 CTTCGAGCTAATGATGTGCTTTGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACT 780

Qy        374 TyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeuValAsnValAla 393

Db        781 TATGGCTCTTCGACTGGCCCAGTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCG 840

Qy        394 ThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArg 413

Db        841 ACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGC 900

Qy        414 ProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLys 433

Db        901 CCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAG 960

Qy        434 LeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThr 453

Db        961 CTCTCTTTCTGGGAGGCAGGCACAACTAAAGCCGGGTACCCTTATAATTATAACACCACT 1020

Qy        454 AlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyr 473

Db       1021 GCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTAC 1080

Qy        474 ThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAlaProHis 493

Db       1081 ACCACTAGCCTGGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCAC 1140

Qy        494 SerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAsp 513

Db       1141 TCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGAT 1200

Qy        514 AspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrVal 533

Db       1201 GATTTCTGCCCAGAGTGCCGCCCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTC 1260

Qy        534 AlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArgGluLeu 549

Db       1261 GCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTG 1308
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RESULT 27
AR232471
LOCUS       AR232471                1311 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 9 from patent US 6455492.
ACCESSION   AR232471
VERSION     AR232471.1  GI:27274540
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1311)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.O.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 6455492-A 9 24-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .1311
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Alignment Scores:
Pred. No.:                3.06          Length:          1311
Score:                    436.00        Matches:         436
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              79.42%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x AR232471 (1-1311)

Qy        114 AsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGluLeu 133

Db          1 AATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTT 60

Qy        134 ValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThrSer 153

Db         61 GTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCT 120

Qy        154 GlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeu 173

Db        121 GGGGTGGCTGAGGAGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTC 180

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193

Db        181 GTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTT 240

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213

Db        241 GAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCC 300

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233

Db        301 AGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACG 360

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253

Db        361 GCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 420

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273

Db        421 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCG 480

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293

Db        481 ACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCC 540

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313

Db        541 AATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGT 600

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333

Db        601 ATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGAT 660

Qy        334 AsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgProPheSerVal 353

Db        661 AACCAACATGAACAAGATCGGCCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTC 720

Qy        354 LeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThr 373

Db        721 CTTCGAGCTAATGATGTGCTTTGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACT 780

Qy        374 TyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeuValAsnValAla 393

Db        781 TATGGCTCTTCGACTGGCCCAGTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCG 840

Qy        394 ThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArg 413

Db        841 ACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGC 900

Qy        414 ProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLys 433
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Db        901 CCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAG 960

Qy        434 LeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThr 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTCTCTTTCTGGGAGGCAGGCACAACTAAAGCCGGGTACCCTTATAATTATAACACCACT 1020

Qy        454 AlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyr 473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTAC 1080

Qy        474 ThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAlaProHis 493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ACCACTAGCCTGGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCAC 1140

Qy        494 SerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAsp 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGAT 1200

Qy        514 AspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrVal 533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GATTTCTGCCCAGAGTGCCGCCCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTC 1260

Qy        534 AlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArgGluLeu 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTG 1308

RESULT 28
AF141652
LOCUS       AF141652               1309 bp    RNA     linear   VRL 01-JUN-1999
DEFINITION  Hepatitis E virus structural protein gene, partial cds.
ACCESSION   AF141652
VERSION     AF141652.1  GI:4929147
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 1309)
  AUTHORS   Jiang,L., Yang,G. and Shen,X.L.
  TITLE     Cloning and sequence analysis of the 1.3Kb cDNA fragment from open
            reading frame 2 (ORF2) of hepatitis E virus (HEV)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1309)
  AUTHORS   Jiang,L., Yang,G. and Shen,X.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-APR-1999) Fourth Lab, Lanzhou Institute of Biological
            Products, Yanchang Road, Lanzhou, Gansu 730046, P.R.China
FEATURES             Location/Qualifiers
     source          1. .1309
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="China"
                     /db_xref="taxon:12461"
                     /note="isolated from patient serum"
     CDS             <1. .>1309
                     /function="viral particle assembly"
                     /note="ORF2; capsid protein homolog"
                     /codon_start=2
                     /product="structural protein"
                     /protein_id="AAD33878.1"
                     /db_xref="GI:4929148"
                     /translation="NSINSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAE
                     EEATSGLVMLCIHGSPVNSYTNTPYTGALGLSDFALELEFRNLTPGNTNTRVSRYSST
                     ARHRLRRGTDGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP
                     TELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDVGESRVVIQD
                     YDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTL
                     VNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAWYP
                     YNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLEDTMDY
                     PARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTREL"

Alignment Scores:
Pred. No.:          3.39          Length:       1309
Score:              429.00        Matches:      429
Percent Similarity:     98.39%          Conservative:  0
Best Local Similarity:  98.39%          Mismatches:    7
Query Match:            78.14%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-15 (1-549) x AF141652 (1-1309)

Qy        114 AsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGluLeu 133
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 AATTCAATAAACTCGACGGATGTCCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTT 61

Qy        134 ValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThrSer 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 GTTATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCC 121

Qy        154 GlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeu 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GGGGTGGCGGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCT 181

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db        182 GTAAATTCTTATACTAACACACCTTATACCGGTGCCCTTGGGCTGTCGGACTTTGCCCTC 241

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GAACTTGAGTTCCGCAACCTCACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCC 301

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        302 AGCACTGCCCGTCACCGCCTTCGTCGCGGTACAGATGGGACTGCCGAGCTCACCACCACG 361

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 GCTGCTACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 421

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GGCCGCGGGATAGCGCTTACCCTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCG 481

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 ACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCTCGCCCCGTCGTCTCAGCC 541

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
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Db        542 AATGGCGAGCCGACTGTTAAGCTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGT 601

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        602 ATTGCAATCCCGCATGACATCGACGTCGGGGAATCTCGAGTTGTTATTCAGGATTATGAC 661

Qy        334 AsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgProPheSerVal 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 AACCAACATGAGCAGGACCGACCGACACCTTCCCCAGCCCCATCGCGTCCTTTTTCTGTC 721

Qy        354 LeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThr 373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 CTCCGAGCTAATGATGTGCTGTGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACT 781

Qy        374 TyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeuValAsnValAla 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 TACGGCTCTTCGACCGGCCCAGTCTATGTCTCCGACTCTGTGACCTTGGTTAATGTTGCG 841

Qy        394 ThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArg 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 ACCGGCGCGCAGGCCGTTGCCCGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGC 901

Qy        414 ProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLys 433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 CCCCTTTCCACCATCCAGCAGTATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAG 961

Qy        434 LeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThr 453
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
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Db        962 CTCTCCTTTTGGGAGGCAGGTACTACTAAAGCCTGGTACCCTTATAATTATAATACCACT 1021

Qy        454 AlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyr 473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 GCTAGTGACCAACTGCTCGTTGAGAATGCCGCCGGGCATCGGGTTGCTATTTCCACTTAT 1081

Qy        474 ThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAlaProHis 493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 ACCACTAGCCTGGGTGCTGGCCCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCAC 1141

Qy        494 SerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAsp 513
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db       1142 TCTGCGCTAGCATTGCTTGAGGATACCATGGACTACCCTGCCCGCGCCCATACTTTCGAT 1201

Qy        514 AspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrVal 533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 GACTTCTGCCCGGAGTGCCGCCCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTC 1261

Qy        534 AlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 GCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTA 1309

RESULT 29
AR002167
LOCUS       AR002167                1308 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 10 from patent US 5741490.
ACCESSION   AR002167
VERSION     AR002167.1  GI:3963721
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1308)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.D.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 5741490-A 10 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .1308
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                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:                5.35          Length:          1308
Score:                    397.50        Matches:         408
Percent Similarity:       93.58%        Conservative:    0
Best Local Similarity:    93.58%        Mismatches:      27
Query Match:              72.40%        Indels:          1
DB:                       1             Gaps:            1

US-09-769-066-15 (1-549) x AR002167 (1-1308)

Qy        114 AsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGluLeu 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATTCCATTACTTCCACTGATGTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTG 60

Qy        134 ValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThrSer 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTCATCCCAAGCGAGCGCCTTCACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCT 120

Qy        154 GlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeu 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTGTTGCTGAGGAGGAAGCCACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCA 180

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTTAACTCCTATACCAATACCCCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTA 240

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        241 GAGCTTGAGTTTCGCAATCTCACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCC 300

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGCACTGCTCGTCAC---TCCGCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACT 357

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||
Db        358 GCAGCCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTC 417

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        418 GGCCGCGGGATAGCTCTAACATTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCG 477

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 ACAGAATTAATTTCGTCGGCTGGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCC 537

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AATGGCGAGCCAACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGT 597

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        598 GTTGCTATCCCCCACGATATCGATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGAC 657

Qy        334 AsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgProPheSerVal 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 AACCAGCATGAGCAGGATCGGCCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTT 717

Qy        354 LeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThr 373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 CTCCGAGCAAATGATGTACTTTGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACT 777

Qy        374 TyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeuValAsnValAla 393
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        778 TACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCG 837

Qy        394 ThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArg 413
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        838 ACTGGCGCGCAGGCCGTAGCCCGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGG 897

Qy        414 ProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLys 433
              ||||||  |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 CCCCTCCCGACTGTTGAGCAATATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAG 957

Qy        434 LeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThr 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 CTCTCCTTTTGGGAGGCCGGCACAACAAAAGCAGGTTATCCTTATAATTATAATACTACT 1017

Qy        454 AlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyr 473
              ||||||||||||  |||  ||||||||||||||||||||||||||||||||||||||||||||
Db       1018 GCTAGTGACCAGATTCTGATTGAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTAT 1077

Qy        474 ThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAlaProHis 493
              ||||||  ||||||||||||||||||  |||||||||  ||||||||||||||||||||||
Db       1078 ACCACCAGGCTTGGGGCCGGTCCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGC 1137

Qy        494 SerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAsp 513
              ||||||||||||||||||||||||||  |||||||||  ||||||||||||||||||||||
Db       1138 TCCGCCCTGGCTCTGCTGGAGGATACTTTTGATTATCCGGGGCGGGCGCACACATTTGAT 1197

Qy        514 AspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrVal 533
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db       1198 GACTTCTGCCCTGAATGCCGCGCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTC 1257

Qy        534 AlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArgGluLeu 549
              ||||||||||||||||||||||  ||||||||||||||||||||||||
Db       1258 GCTGAGCTCCAGCGCCTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTG 1305

RESULT 30
AR232472
LOCUS       AR232472                1308 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 10 from patent US 6455492.
ACCESSION   AR232472
VERSION     AR232472.1  GI:27274541
```

```
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1308)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.O.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 6455492-A 10 24-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .1308
                     /organism="unknown"
                     /mol_type="mRNA"

Alignment Scores:
Pred. No.:                5.35          Length:          1308
Score:                    397.50        Matches:         408
Percent Similarity:       93.58%        Conservative:    0
Best Local Similarity:    93.58%        Mismatches:      27
Query Match:              72.40%        Indels:          1
DB:                       1             Gaps:            1

US-09-769-066-15 (1-549) x AR232472 (1-1308)

Qy        114 AsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGluLeu 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATTCCATTACTTCCACTGATGTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTG 60

Qy        134 ValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThrSer 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTCATCCCAAGCGAGCGCCTTCACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCT 120

Qy        154 GlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeu 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTGTTGCTGAGGAGGAAGCCACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCA 180

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTTAACTCCTATACCAATACCCCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTA 240

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||      ||||||||||||||||||||||||||||||||||||||
Db        241 GAGCTTGAGTTTCGCAATCTCACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCC 300

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||      ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGCACTGCTCGTCAC---TCCGCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACT 357

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 GCAGCCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTC 417

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
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Db        418 GGCCGCGGGATAGCTCTAACATTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCG 477

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 ACAGAATTAATTTCGTCGGCTGGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCC 537

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AATGGCGAGCCAACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGT 597

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
              ||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||
Db        598 GTTGCTATCCCCCACGATATCGATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGAC 657

Qy        334 AsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgProPheServal 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 AACCAGCATGAGCAGGATCGGCCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTT 717

Qy        354 LeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThr 373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 CTCCGAGCAAATGATGTACTTTGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACT 777

Qy        374 TyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeuValAsnValAla 393
              ||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        778 TACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCG 837

Qy        394 ThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArg 413
              ||||||||||||||||||||||||||||||||||||    ||||||||||||||||||||
Db        838 ACTGGCGCGCAGGCCGTAGCCCGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGG 897

Qy        414 ProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLys 433
              ||||||   |||      ||||||||||||||||||||||||||||||||||||||||||||
Db        898 CCCCTCCCGACTGTTGAGCAATATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAG 957

Qy        434 LeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThr 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 CTCTCCTTTTGGGAGGCCGGCACAACAAAAGCAGGTTATCCTTATAATTATAATACTACT 1017

Qy        454 AlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyr 473
              ||||||||||||   |||   ||||||||||||||||||||||||||||||||||||||||||||
Db       1018 GCTAGTGACCAGATTCTGATTGAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTAT 1077

Qy        474 ThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAlaProHis 493
              ||||||   ||||||||||||||||||   |||||||||   |||||||||||||||
Db       1078 ACCACCAGGCTTGGGGCCGGTCCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGC 1137

Qy        494 SerAlaLeuAlaLeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAsp 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 TCCGCCCTGGCTCTGCTGGAGGATACTTTTGATTATCCGGGGCGGGCGCACACATTTGAT 1197

Qy        514 AspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrVal 533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1198 GACTTCTGCCCTGAATGCCGCGCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTC 1257

Qy        534 AlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArgGluLeu 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1258 GCTGAGCTCCAGCGCCTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTG 1305

RESULT 31
HEU40044
LOCUS       HEU40044                1117 bp    DNA     linear   VRL 26-JAN-1999
DEFINITION  Hepatitis E virus structural protein 2 (orf2) mRNA, partial cds.
ACCESSION   U40044
VERSION     U40044.1  GI:4096791
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 1117)
  AUTHORS   Van Cuyck-Gandre,H., Clements,N.J., Zhang,H.Y., Caudill,J.C.,
            Cohen,S.G., Coursaget,P., Buisson,Y., Warren,R.L. and Longer,C.F.
  TITLE     Partial Sequence of HEV Isolates from North Africa and Pakistan:
            Comparison with Known HEV Sequences
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1117)
  AUTHORS   Van Cuyck-Gandre,H., Clements,N.J., Zhang,H.Y., Caudill,J.C.,
            Cohen,S.G., Coursaget,P., Buisson,Y., Warren,R.L. and Longer,C.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-NOV-1995) Helene Van Cuyck-Gandre, Virus Disease,
            Walter Reed Army Institute of Research, BLD 40, Washington, DC
            20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .1117
                     /organism="Hepatitis E virus"
                     /mol_type="genomic DNA"
                     /strain="2B Abbottabad, Pakistan"
                     /db_xref="taxon:12461"
     CDS             <1. .1035
                     /note="orf2; capsid protein"
                     /codon_start=1
                     /product="structural protein 2"
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                  /db_xref="GI:4096792"
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                  AAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSK
                  TFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGP
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                  KMKVGKTREL"

Alignment Scores:
Pred. No.:                11.5          Length:          1117
Score:                    344.00        Matches:         344
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              62.66%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x HEU40044 (1-1117)

Qy        206 AsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAsp 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATACGCGGGTCTCGCGTTACTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGAC 60

Qy        226 GlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThr 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGGACTGCCGAGCTCACCACCACGGCTGCTACCCGTTTTATGAAGGACCTCTATTTCACT 120

Qy        246 SerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAla 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGTACCAATGGTGTCGGTGAGATCGGCCGCGGGATAGCTCTCACCCTGTTCAACCTTGCT 180

Qy        266 AspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPhe 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACACTCTGCTTGGTGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTC 240

Qy        286 TyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerVal 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAGCTGTATACATCTGTA 300

Qy        306 GluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSer 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGGGAATCT 360

Qy        326 ArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerPro 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGTGGTTATTCAGGACTATGATAACCAACATGAACAGGACCGGCCGACGCCTTCGCCA 420

Qy        346 AlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThr 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCTCCATCGCGCCCTTTTTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTCTCTCTCACC 480

Qy        366 AlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAsp 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGCCGAGTATGACCAATCCACTTATGGCTCTTCGACTGGCCCAGTTTATGTCTCTGAC 540

Qy        386 SerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrp 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCTGTGACCTTGGTTAATGTCGCGACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGG 600

Qy        406 ThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhe 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACCAAGGTCACACTTGACGGCCGCCCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTC 660

Qy        426 PheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGly 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACAACTAAAGCCGGG 720

Qy        446 TyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGly 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TACCCTTATAATTATAATACCACTGCTAGCGACCAACTGCTCGTCGAGAATGCCGCCGGG 780

Qy        466 HisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSer 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CACCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGACCCGTTTCCATTTCT 840

Qy        486 AlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyr 505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGATTAC 900

Qy        506 ProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeuGlyLeuGln 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCCTTGGCCTCCAG 960

Qy        526 GlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLysValGlyLys 545
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGCTGTGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGTCTTAAGATGAAGGTGGGTAAA 1020

Qy        546 ThrArgGluLeu 549
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Db       1021 ACTCGGGAGTTA 1032

RESULT 32
AR002164
LOCUS       AR002164                984 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 7 from patent US 5741490.
ACCESSION   AR002164
VERSION     AR002164.1  GI:3963718
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.D.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 5741490-A 7 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:                14.5          Length:          984
Score:                    327.00        Matches:         327
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              59.56%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x AR002164 (1-984)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTC 60

Qy        243 TyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPhe 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTC 120

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGC 180

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTAT 240

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTC 300

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGGCCGACG 360
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Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTC 420

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
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Db        421 TCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTTAT 480

Qy        383 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCG 540

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAGTACTCG 600

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACAACT 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482
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Db        721 GCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTC 780

Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThr 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACC 840

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCCTT 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549
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Db        961 GTGGGTAAAACTCGGGAGTTG 981
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RESULT 33
AR170408
LOCUS AR170408 984 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 5 from patent US 6291641.
ACCESSION AR170408
VERSION AR170408.1 GI:17908367
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 984)
AUTHORS Fuerst,T.R., McAtee,C.Patrick., Yarbough,P.O. and Zhang,Y.-F.
TITLE Hepatitis E virus antigens and uses therefor
JOURNAL Patent: US 6291641-A 5 18-SEP-2001;
FEATURES Location/Qualifiers
source 1. .984
/organism="unknown"
/mol_type="unassigned DNA"

Alignment Scores:

Pred. No.:	14.5	Length:	984
Score:	327.00	Matches:	327
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	59.56%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AR170408 (1-984)

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Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
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Db          1 GGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTC 60

Qy        243 TyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPhe 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTC 120

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
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Db        121 AACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGC 180

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
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Db        181 CAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTAT 240

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322
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Db        241 ACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTC 300

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
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Db        301 GGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGGCCGACG 360

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTC 420

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTTAT 480

Qy        383 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
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Db        481 GTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCG 540

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422
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Db        541 CTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAGTACTCG 600

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACAACT 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTC 780

Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThr 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACC 840

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCCTT 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549
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Db        961 GTGGGTAAAACTCGGGAGTTG 981
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RESULT 34
I73145
LOCUS I73145 984 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 7 from patent US 5686239.
ACCESSION I73145

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VERSION     I73145.1  GI:3009284
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Reyes,G.R., Tam,A.W. and Yarbough,P.O.
  TITLE     Hepatitis E virus peptides and methods
  JOURNAL   Patent: US 5686239-A 7 11-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:                14.5          Length:          984
Score:                    327.00        Matches:         327
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              59.56%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x I73145 (1-984)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
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Db          1 GGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTC 60

Qy        243 TyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPhe 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTC 120

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGC 180

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTAT 240

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTC 300

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGGCCGACG 360

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTC 420

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTTAT 480

Qy        383 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCG 540

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAGTACTCG 600

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACAACT 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTC 780

Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThr 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACC 840

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCCTT 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||
Db        961 GTGGGTAAAACTCGGGAGTTG 981

RESULT 35
AR232469
LOCUS       AR232469                984 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 7 from patent US 6455492.
ACCESSION   AR232469
VERSION     AR232469.1  GI:27274538
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.O.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 6455492-A 7 24-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .984
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Alignment Scores:
Pred. No.:                14.5          Length:          984
Score:                    327.00        Matches:         327
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              59.56%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x AR232469 (1-984)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
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Db          1 GGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTC 60

Qy        243 TyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPhe 262
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Db         61 TATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTC 120

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGC 180

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTAT 240

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTC 300

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGGCCGACG 360
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Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
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Db        361 CCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTC 420

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTTAT 480

Qy        383 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCG 540

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAGTACTCG 600

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACAACT 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTC 780

Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThr 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACC 840

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCCTT 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549
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Db        961 GTGGGTAAAACTCGGGAGTTG 981
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RESULT 36
AX181847
LOCUS       AX181847                1020 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 129 from Patent WO0146696.
ACCESSION   AX181847
VERSION     AX181847.1  GI:15133167
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 129 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .1020
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="us2-1019"

Alignment Scores:
Pred. No.:              15.6          Length:         1020
Score:                  322.00        Matches:        322
Percent Similarity:     95.55%        Conservative:   0
Best Local Similarity:  95.55%        Mismatches:     15
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Query Match:            58.65%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AX181847 (1-1020)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
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Db          9 GCCGTGTCACCGGCTCCTGACACAGCCCCTGTACCTGATGTTGACTCACGTGGTGCTATT 68

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 CTGCGCCGGCAGTACAATTTGTCCACGTCCCCGCTCACGTCATCTGTCGCTTCGGGTACT 128

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        129 AATTTGGTCCTCTATGCTGCCCCGCTGAATCCCCTCTTGCCTCTCCAGGATGGTACCAAC 188

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 ACTCATATTATGGCTACTGAGGCATCCAATTATGCCCAGTATCGGGTTGTTCGAGCTACA 248

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 ATCCGTTATCGCCCGCTGGTGCCGAATGCCGTTGGTGGCTATGCCATTTCCATTTCTTTC 308

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TGGCCCCAAACTACAACTACCCCTACTTCTGTCGATATGAATTCTATTACTTCCACYGAT 368

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GTTAGGATTTTGGTTCAGCCCGGTATTGCCTCCGAGCTAGTCATCCCCAGTGAGCGCCTT 428

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 CATTACCGTAATCAAGGCTGGCGCTCTGTTGAGACCACGGGTGTGGCTGAGGAGGAGGCT 488

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 ACTTCCGGTCTGGTAATGCTTTGCATTCATGGCTCTCCTGTTAATTCCTACACTAATACA 548

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCACTAGAGCTTGAATTTAGGAATTTG 608

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 ACACCCGGGAACACCAACACCCGTGTTTCCCGGTATACCAGCACAGCCCGCCACCGGCTG 668

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CGCCGTGGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCCACACGTTTCATGAAG 728

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              |||||| |||      ||||||||||||||||||  ||||||||||||||||||||
Db        729 GACCTGCACTTCGCTGGCACGAATGGCGTTGGTGAGGTGGGTCGTGGTATCGCCCTGACA 788

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 CTGTTCAATCTCGCTGATACGCTTCTCGGCGGTTTACCGACAGAATTGATTTCGTCGGCT 848

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 GGGGGCCAACTGTTTTACTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAG 908

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              |||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        909 TTATATACATCTGTTGAGAATGCGCAGCAAGACAAGGGCATCACCATTCCACATGATATA 968

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              |||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        969 GACCTGGGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCAYGAA 1019
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RESULT 37
BD077247
LOCUS       BD077247               1020 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077247
VERSION     BD077247.1  GI:22622850
KEYWORDS    JP 2001520384-A/126.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1020)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 126 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/126
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   us2-1019
            FH   Key             Location/Qualifiers
            FT   source          1. .1020
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                        virus)'.
FEATURES             Location/Qualifiers
     source          1. .1020
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              15.6          Length:         1020
Score:                  322.00        Matches:        322
Percent Similarity:     95.55%        Conservative:   0
Best Local Similarity:  95.55%        Mismatches:     15
Query Match:            58.65%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x BD077247 (1-1020)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              ||||||   ||||||   ||||||   ||||||||||||||||||||||||||||||||
Db          9 GCCGTGTCACCGGCTCCTGACACAGCCCCTGTACCTGATGTTGACTCACGTGGTGCTATT 68

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 CTGCGCCGGCAGTACAATTTGTCCACGTCCCCGCTCACGTCATCTGTCGCTTCGGGTACT 128

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        129 AATTTGGTCCTCTATGCTGCCCCGCTGAATCCCCTCTTGCCTCTCCAGGATGGTACCAAC 188

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||
Db        189 ACTCATATTATGGCTACTGAGGCATCCAATTATGCCCAGTATCGGGTTGTTCGAGCTACA 248

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 ATCCGTTATCGCCCGCTGGTGCCGAATGCCGTTGGTGGCTATGCCATTTCCATTTCTTTC 308

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TGGCCCCAAACTACAACTACCCCTACTTCTGTCGATATGAATTCTATTACTTCCACYGAT 368

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GTTAGGATTTTGGTTCAGCCCGGTATTGCCTCCGAGCTAGTCATCCCCAGTGAGCGCCTT 428

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 CATTACCGTAATCAAGGCTGGCGCTCTGTTGAGACCACGGGTGTGGCTGAGGAGGAGGCT 488

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        489 ACTTCCGGTCTGGTAATGCTTTGCATTCATGGCTCTCCTGTTAATTCCTACACTAATACA 548

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCACTAGAGCTTGAATTTAGGAATTTG 608

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        609 ACACCCGGGAACACCAACACCCGTGTTTCCCGGTATACCAGCACAGCCCGCCACCGGCTG 668

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CGCCGTGGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCCACACGTTTCATGAAG 728

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||   |||      ||||||||||||||||||   ||||||||||||||||||||
Db        729 GACCTGCACTTCGCTGGCACGAATGGCGTTGGTGAGGTGGGTCGTGGTATCGCCCTGACA 788

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 CTGTTCAATCTCGCTGATACGCTTCTCGGCGGTTTACCGACAGAATTGATTTCGTCGGCT 848

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 GGGGGCCAACTGTTTTACTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAG 908

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        909 TTATATACATCTGTTGAGAATGCGCAGCAAGACAAGGGCATCACCATTCCACATGATATA 968

Qy        321 AspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 GACCTGGGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCAYGAA 1019

RESULT 38
AR170409
LOCUS       AR170409               984 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 6 from patent US 6291641.
ACCESSION   AR170409
VERSION     AR170409.1  GI:17908368
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Fuerst,T.R., McAtee,C.Patrick., Yarbough,P.O. and Zhang,Y.-F.
  TITLE     Hepatitis E virus antigens and uses therefor
  JOURNAL   Patent: US 6291641-A 6 18-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:              19.8          Length:         984
Score:                  305.00        Matches:        305
Percent Similarity:     93.27%        Conservative:   0
Best Local Similarity:  93.27%        Mismatches:     22
Query Match:            55.56%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AR170409 (1-984)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
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Db          1 GGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAAGATCTC 60

Qy        243 TyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPhe 262

Db         61 CACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACATTACTT 120

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282

Db        121 AACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCTGGCGGG 180

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302

Db        181 CAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTAT 240

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322

Db        241 ACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATCGATCTT 300

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342

Db        301 GGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGGCCCACC 360

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362

Db        361 CCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTTTGGCTG 420

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382

Db        421 TCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTAT 480

Qy        383 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402

Db        481 ATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCCCGATCG 540

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422

Db        541 CTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAATATTCC 600

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442

Db        601 AAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGCACAACA 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462

Db        661 AAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATTGAAAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482

Db        721 GCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGTCCGGTC 780

Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuGluAspThr 502

Db        781 GCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAGGATACT 840

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522

Db        841 TTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGCGCTTTA 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLys 542

Db        901 GGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549

Db        961 GTGGGTAAAACTCGGGAGTTG 981

RESULT 39
I73146
LOCUS       I73146                  984 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 8 from patent US 5686239.
ACCESSION   I73146
VERSION     I73146.1  GI:3009285
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Reyes,G.R., Tam,A.W. and Yarbough,P.O.
  TITLE     Hepatitis E virus peptides and methods
  JOURNAL   Patent: US 5686239-A 8 11-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:                19.8          Length:          984
Score:                    305.00        Matches:         305
Percent Similarity:       93.27%        Conservative:    0
Best Local Similarity:    93.27%        Mismatches:      22
Query Match:              55.56%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x I73146 (1-984)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242

Db          1 GGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAAGATCTC 60

Qy        243 TyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPhe 262

Db         61 CACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACATTACTT 120

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282

Db        121 AACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCTGGCGGG 180

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302

Db        181 CAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTAT 240

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322

Db        241 ACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATCGATCTT 300

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342

Db        301 GGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGGCCCACC 360

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362

Db        361 CCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTTTGGCTG 420

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382

Db        421 TCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTAT 480

Qy        383 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402

Db        481 ATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCCCGATCG 540

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422

Db        541 CTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAATATTCC 600

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442

Db        601 AAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGCACAACA 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462

Db        661 AAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATTGAAAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482
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Db        721 GCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGTCCGGTC 780

Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThr 502
              |||||||||   ||||||||||||||   ||||||||||||||||||||||||||||||
Db        781 GCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAGGATACT 840

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522
              |||||||||   ||||||||||||||||||||||||||||||||||||||||    |||
Db        841 TTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGCGCTTTA 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db        901 GGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||
Db        961 GTGGGTAAAACTCGGGAGTTG 981

RESULT 40
AX181910
LOCUS       AX181910                1026 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 192 from Patent WO0146696.
ACCESSION   AX181910
VERSION     AX181910.1  GI:15133216
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 192 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .1026
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="cksorf2m-2.seq"

Alignment Scores:
Pred. No.:              19.9          Length:         1026
Score:                  305.00        Matches:        305
Percent Similarity:     93.56%        Conservative:   0
Best Local Similarity:  93.56%        Mismatches:     21
Query Match:            55.56%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AX181910 (1-1026)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCCACACGTTTCATGAAGGACCTG 69

Qy        243 TyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPhe 262
              |||     ||||||||||||||||||   ||||||||||||||||||||||||||||||
Db         70 CACTTCGCTGGCACGAATGGCGTTGGTGAGGTGGGTCGTGGTATCGCCCTGACACTGTTC 129

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 AATCTCGCTGATACGCTTCTCGGCGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGC 189

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CAACTGTTTTACTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATAT 249

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        250 ACATCTGTTGAGAATGCGCAGCAAGACAAGGGCATCACCATTCCACATGATATAGACCTG 309

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCATGAGCAAGACCGACCTACT 369

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CCGTCACCTGCCCCCTCTCGCCCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTT 429

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||   ||||||||||||||||||   |||   |||
Db        430 TCCCTCACTGCCGCTGAGTATGACCAGACTACGTATGGGTCGTCCACCAACCCTATGTAT 489

Qy        383 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GTCTCTGACACAGTTACGCTTGTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCC 549

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422
              |||||||||   ||||||||||||||||||||||||||   ||||||||||||||||||||
Db        550 CTTGATTGGTCTAAAGTTACTCTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCT 609

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 AAGACATTTTATGTTCTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACT 669

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||   |||   ||||||
Db        670 AAGGCCGGCTACCCTTACAATTATAATACTACCGCTAGTGACCAAATTTTGATTGAGAAT 729

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 GCGGCCGGCCACCGTGTCGCTATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACC 789

Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThr 502
              |||||||||||||   ||||||||||||||||||||||||||   ||||||||||||
Db        790 TCGATCTCTGCGGTCGGCGTACTGGCTCCACACTCTGCCCTTGCCGTTCTTGAGGATACT 849

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db        850 ATTGATTACCCCGCCCGTGCCCATACTTTTGATGATTTTTGCCCGGAGTGCCGTACCCTA 909

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLys 542
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        910 GGTTTGCAGGGTTGTGCATTCCAGTCTACTATTGCTGAGCTCCAGCGTTTAAAAATGAAG 969

Qy        543 ValGlyLysThrArgGlu 548
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Db        970 GTAGGTAAAACCCGGGAG 987

RESULT 41
AX181913
LOCUS       AX181913                1026 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 195 from Patent WO0146696.
ACCESSION   AX181913
VERSION     AX181913.1  GI:15133219
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 195 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .1026
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="plorf2.2-6.seq"

Alignment Scores:
Pred. No.:              19.9          Length:         1026
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Score:                  305.00          Matches:        305
Percent Similarity:     93.56%          Conservative:   0
Best Local Similarity:  93.56%          Mismatches:     21
Query Match:            55.56%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AX181913 (1-1026)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCCACACGTTTCATGAAGGACCTG 69

Qy        243 TyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPhe 262
              |||      ||||||||||||||||||   ||||||||||||||||||||||||||||
Db         70 CACTTCGCTGGCACGAATGGCGTTGGTGAGGTGGGTCGTGGTATCGCCCTGACACTGTTC 129

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 AATCTCGCTGATACGCTTCTCGGCGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGC 189

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CAACTGTTTTACTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATAT 249

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        250 ACATCTGTTGAGAATGCGCAGCAAGACAAGGGCATCACCATTCCACATGATATAGACCTG 309

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCATGAGCAAGACCGACCTACT 369

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CCGTCACCTGCCCCCTCTCGCCCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTT 429

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||   ||||||||||||||||||   |||   |||
Db        430 TCCCTCACTGCCGCTGAGTATGACCAGACTACGTATGGGTCGTCCACCAACCCTATGTAT 489

Qy        383 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GTCTCTGACACAGTTACGCTTGTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCC 549

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422
              |||||||||   ||||||||||||||||||||||||||||||   ||||||||||||||||
Db        550 CTTGATTGGTCTAAAGTTACTCTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCT 609

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 AAGACATTTTATGTTCTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACT 669

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||   |||   ||||||
Db        670 AAGGCCGGCTACCCTTACAATTATAATACTACCGCTAGTGACCAAATTTTGATTGAGAAT 729

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 GCGGCCGGCCACCGTGTCGCTATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACC 789

Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThr 502
              ||||||||||||||   ||||||||||||||||||||||||||   ||||||||||||
Db        790 TCGATCTCTGCGGTCGGCGTACTGGCTCCACACTCTGCCCTTGCCGTTCTTGAGGATACT 849

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        850 ATTGATTACCCCGCCCGTGCCCATACTTTTGATGATTTTTGCCCGGAGTGCCGTACCCTA 909

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLys 542
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        910 GGTTTGCAGGGTTGTGCATTCCAGTCTACTATTGCTGAGCTCCAGCGTTTAAAAATGAAG 969

Qy        543 ValGlyLysThrArgGlu 548
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              ||||||||||||||||||
Db        970 GTAGGTAAAACCCGGGAG 987

RESULT 42
BD077295
LOCUS       BD077295                1026 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077295
VERSION     BD077295.1  GI:22622898
KEYWORDS    JP 2001520384-A/174.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 174 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/174
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   cksorf2m-2.seq
            FH   Key             Location/Qualifiers
            FT   source          1. .1026
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                                 virus)'.
FEATURES             Location/Qualifiers
     source          1. .1026
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              19.9            Length:         1026
Score:                  305.00          Matches:        305
Percent Similarity:     93.56%          Conservative:   0
Best Local Similarity:  93.56%          Mismatches:     21
Query Match:            55.56%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x BD077295 (1-1026)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCCACACGTTTCATGAAGGACCTG 69

Qy        243 TyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPhe 262
              |||      ||||||||||||||||||   ||||||||||||||||||||||||||||
Db         70 CACTTCGCTGGCACGAATGGCGTTGGTGAGGTGGGTCGTGGTATCGCCCTGACACTGTTC 129

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 AATCTCGCTGATACGCTTCTCGGCGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGC 189

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CAACTGTTTTACTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATAT 249

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        250 ACATCTGTTGAGAATGCGCAGCAAGACAAGGGCATCACCATTCCACATGATATAGACCTG 309

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        310 GGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCATGAGCAAGACCGACCTACT 369

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CCGTCACCTGCCCCCTCTCGCCCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTT 429

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              |||||||||||||||||||||||||||   ||||||||||||||||||   |||   |||
Db        430 TCCCTCACTGCCGCTGAGTATGACCAGACTACGTATGGGTCGTCCACCAACCCTATGTAT 489

Qy        383 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GTCTCTGACACAGTTACGCTTGTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCC 549

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422
              |||||||||   ||||||||||||||||||||||||||||   ||||||||||||||||||
Db        550 CTTGATTGGTCTAAAGTTACTCTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCT 609

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 AAGACATTTTATGTTCTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACT 669

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||   |||   ||||||
Db        670 AAGGCCGGCTACCCTTACAATTATAATACTACCGCTAGTGACCAAATTTTGATTGAGAAT 729

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 GCGGCCGGCCACCGTGTCGCTATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACC 789

Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThr 502
              |||||||||||||||   ||||||||||||||||||||||||||   ||||||||||||
Db        790 TCGATCTCTGCGGTCGGCGTACTGGCTCCACACTCTGCCCTTGCCGTTCTTGAGGATACT 849

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        850 ATTGATTACCCCGCCCGTGCCCATACTTTTGATGATTTTTGCCCGGAGTGCCGTACCCTA 909

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLys 542
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        910 GGTTTGCAGGGTTGTGCATTCCAGTCTACTATTGCTGAGCTCCAGCGTTTAAAAATGAAG 969

Qy        543 ValGlyLysThrArgGlu 548
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Db        970 GTAGGTAAAACCCGGGAG 987
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RESULT 43
BD077298
LOCUS       BD077298               1026 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077298
VERSION     BD077298.1  GI:22622901
KEYWORDS    JP 2001520384-A/177.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 177 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/177
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   plorf2.2-6.seq
            FH   Key             Location/Qualifiers
            FT   source          1. .1026
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                                 virus)'.
FEATURES             Location/Qualifiers
     source          1. .1026
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
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Alignment Scores:
Pred. No.:                19.9          Length:          1026
Score:                    305.00        Matches:         305
Percent Similarity:       93.56%        Conservative:    0
Best Local Similarity:    93.56%        Mismatches:      21
Query Match:              55.56%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x BD077298 (1-1026)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCCACACGTTTCATGAAGGACCTG 69

Qy        243 TyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPhe 262
              |||   ||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db         70 CACTTCGCTGGCACGAATGGCGTTGGTGAGGTGGGTCGTGGTATCGCCCTGACACTGTTC 129

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 AATCTCGCTGATACGCTTCTCGGCGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGC 189

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CAACTGTTTTACTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATAT 249

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        250 ACATCTGTTGAGAATGCGCAGCAAGACAAGGGCATCACCATTCCACATGATATAGACCTG 309

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCATGAGCAAGACCGACCTACT 369

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CCGTCACCTGCCCCCTCTCGCCCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTT 429

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              |||||||||||||||||||||||||||   ||||||||||||||||||   |||   |||
Db        430 TCCCTCACTGCCGCTGAGTATGACCAGACTACGTATGGGTCGTCCACCAACCCTATGTAT 489

Qy        383 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GTCTCTGACACAGTTACGCTTGTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCC 549

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422
              |||||||||   ||||||||||||||||||||||||||||   ||||||||||||||||||
Db        550 CTTGATTGGTCTAAAGTTACTCTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCT 609

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 AAGACATTTTATGTTCTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACT 669

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||   |||   ||||||
Db        670 AAGGCCGGCTACCCTTACAATTATAATACTACCGCTAGTGACCAAATTTTGATTGAGAAT 729

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 GCGGCCGGCCACCGTGTCGCTATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACC 789
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Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThr 502
              ||||||||||||||||   ||||||||||||||||||||||||||   ||||||||||||
Db        790 TCGATCTCTGCGGTCGGCGTACTGGCTCCACACTCTGCCCTTGCCGTTCTTGAGGATACT 849

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        850 ATTGATTACCCCGCCCGTGCCCATACTTTTGATGATTTTTGCCCGGAGTGCCGTACCCTA 909

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLys 542
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        910 GGTTTGCAGGGTTGTGCATTCCAGTCTACTATTGCTGAGCTCCAGCGTTTAAAAATGAAG 969

Qy        543 ValGlyLysThrArgGlu 548
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Db        970 GTAGGTAAAACCCGGGAG 987

RESULT 44
AR002165
LOCUS       AR002165                 981 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 8 from patent US 5741490.
ACCESSION   AR002165
VERSION     AR002165.1  GI:3963719
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 981)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.D.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 5741490-A 8 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .981
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:              20.1          Length:         981
Score:                  304.00        Matches:        304
Percent Similarity:     93.25%        Conservative:   0
Best Local Similarity:  93.25%        Mismatches:     22
Query Match:            55.37%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AR002165 (1-981)

Qy        224 AlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyr 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAAGATCTCCAC 60

Qy        244 PheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsn 263
              ||||||      ||||||||||||||||   ||||||||||||||||||||||||   |||
Db         61 TTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACATTACTTAAC 120

Qy        264 LeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGln 283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCTGGCGGGCAA 180

Qy        284 LeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThr 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTATACA 240

Qy        304 SerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeuGly 323
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        241 TCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATCGATCTTGGT 300

Qy        324 GluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrPro 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGGCCCACCCCG 360

Qy        344 SerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSer 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTTTGGCTGTCC 420

Qy        364 LeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrVal 383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATC 480

Qy        384 SerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeu 403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCCCGATCGCTT 540

Qy        404 AspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLys 423
              ||||||   ||||||||||||||||||||||||||||   |||      ||||||||||||
Db        541 GACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAATATTCCAAG 600

Qy        424 ThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLys 443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGCACAACAAAA 660

Qy        444 AlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAla 463
              ||||||||||||||||||||||||||||||||||||||||   |||   |||||||||
Db        661 GCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATTGAAAATGCT 720

Qy        464 AlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProValSer 483
              ||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        721 GCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGTCCGGTCGCC 780

Qy        484 IleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThrLeu 503
              |||||||||   ||||||||||||||||   ||||||||||||||||||||||||||||
Db        781 ATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAGGATACTTTT 840

Qy        504 AspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeuGly 523
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        841 GATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGCGCTTTAGGC 900

Qy        524 LeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLysVal 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        901 CTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTG 960

Qy        544 GlyLysThrArgGluLeu 549
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Db        961 GGTAAAACTCGGGAGTTG 978

RESULT 45
AR232470
LOCUS       AR232470                 981 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 8 from patent US 6455492.
ACCESSION   AR232470
VERSION     AR232470.1  GI:27274539
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 981)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.O.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 6455492-A 8 24-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .981
                     /organism="unknown"
                     /mol_type="mRNA"

Alignment Scores:
Pred. No.:              20.1          Length:         981
Score:                  304.00        Matches:        304
Percent Similarity:     93.25%        Conservative:   0
Best Local Similarity:  93.25%        Mismatches:     22
Query Match:            55.37%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AR232470 (1-981)

Qy        224 AlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyr 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db          1 GCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAAGATCTCCAC 60

Qy        244 PheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsn 263

Db         61 TTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACATTACTTAAC 120

Qy        264 LeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGln 283

Db        121 CTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCTGGCGGGCAA 180

Qy        284 LeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThr 303

Db        181 CTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTATACA 240

Qy        304 SerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeuGly 323

Db        241 TCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATCGATCTTGGT 300

Qy        324 GluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrPro 343

Db        301 GATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGGCCCACCCCG 360

Qy        344 SerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSer 363

Db        361 TCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTTTGGCTGTCC 420

Qy        364 LeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrVal 383

Db        421 CTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATC 480

Qy        384 SerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeu 403

Db        481 TCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCCCGATCGCTT 540

Qy        404 AspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLys 423

Db        541 GACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAATATTCCAAG 600

Qy        424 ThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLys 443

Db        601 ACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGCACAACAAAA 660

Qy        444 AlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAla 463

Db        661 GCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATTGAAAATGCT 720

Qy        464 AlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProValSer 483

Db        721 GCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGTCCGGTCGCC 780

Qy        484 IleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThrLeu 503

Db        781 ATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAGGATACTTTT 840

Qy        504 AspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeuGly 523

Db        841 GATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGCGCTTTAGGC 900

Qy        524 LeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLysVal 543

Db        901 CTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTG 960

Qy        544 GlyLysThrArgGluLeu 549

Db        961 GGTAAAACTCGGGAGTTG 978

RESULT 46
AX181742
LOCUS       AX181742                899 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 24 from Patent WO0146696.
ACCESSION   AX181742
VERSION     AX181742.1  GI:15133065
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 24 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .899
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="Clone: df-orf2/3"

Alignment Scores:
Pred. No.:                  26.6          Length:          899
Score:                      284.00        Matches:         284
Percent Similarity:         95.62%        Conservative:    0
Best Local Similarity:      95.62%        Mismatches:      13
Query Match:                51.73%        Indels:          0
DB:                         1             Gaps:            0

US-09-769-066-15 (1-549) x AX181742 (1-899)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20

Db          8 GCCATATCACCAGCCCCTGATACAGCTCCTGTACCTGATGTTGACTCACGTGGTGCTATT 67

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40

Db         68 TTGCGCCGGCAGTACAATTTGTCTACGTCCCCGCTTACATCATCTGTTGCTTCTGGTACT 127

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60

Db        128 AATCTGGTTCTCTATGCTGCCCCGCTGAACCCTCTCTTGCCTCTTCAGGATGGCACCAAC 187

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

Db        188 ACTCATATTATGGCTACTGAGGCATCTAATTACGCCCAGTATCGGGTTGTTCGGGCTACG 247

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        248 ATTCGTTATCGCCCGTTGGTGCCAAATGCTGTTGGTGGTTATGCTATCTCTATTTCTTTC 307

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        308 TGGCCTCAAACTACAACTACCCCTACTTCTGTTGACATGAATTCTATCACTTCTACTGAT 367

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db        368 GTCAGGATCTTGGTCCAGCCCGGTATAGCCTCCGAGTTAGTCATCCCTAGTGAACGCCTT 427

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db        428 CACTACCGCAACCAAGGCTGGCGCTCTGTTGAGACCACGGGTGTGGCCGAAGAGGAGGCT 487

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180

Db        488 ACCTCCGGTCTGGTAATGCTTTGTATTCATGGCTCCCCTGTTAACTCCTACACTAATACA 547

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        548 CCTTACACCGGTGCATTGGGGCTTCTTGATTTTGCATTAGAACTTGAATTTAGAAATTTG 607

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db        608 ACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACTAGCACAGCCCGCCACCGGCTG 667

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Db        668 CGCCGCGGTGCTGATGGGACCGCTGAGCTCACCACCACAGCAGCCACACGCTTCATGAAG 727

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||   ||||||   ||||||||||||||||||   ||||||||||||||||||||
Db        728 GATTTGCATTTTACTGGTACGAACGGCGTTGGTGAGGTGGGTCGTGGTATTGCCCTGACT 787

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CTGTTTAATCTTGCTGATACGCTTCTTGGTGGTTTACCGACAGAATTGATTTCGTCGGCT 847

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 GGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCAGCCAATGGCGAGCCA 898

RESULT 47
BD077145
LOCUS       BD077145                899 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077145
VERSION     BD077145.1  GI:22622748
KEYWORDS    JP 2001520384-A/24.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 899)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 24 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/24
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   Clone: df-orf2/3
            FH   Key             Location/Qualifiers
            FT   source          1. .899
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                        virus)'.
FEATURES             Location/Qualifiers
     source          1. .899
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              26.6          Length:         899
Score:                  284.00        Matches:        284
Percent Similarity:     95.62%        Conservative:   0
Best Local Similarity:  95.62%        Mismatches:     13
Query Match:            51.73%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x BD077145 (1-899)

Qy          1 AlaValAlaProAlaHisAspThrProProValProAspValAspSerArgGlyAlaIle 20
              |||      ||||||   ||||||   ||||||||||||||||||||||||||||||||
Db          8 GCCATATCACCAGCCCCTGATACAGCTCCTGTACCTGATGTTGACTCACGTGGTGCTATT 67

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db         68 TTGCGCCGGCAGTACAATTTGTCTACGTCCCCGCTTACATCATCTGTTGCTTCTGGTACT 127

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        128 AATCTGGTTCTCTATGCTGCCCCGCTGAACCCTCTCTTGCCTCTTCAGGATGGCACCAAC 187

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        188 ACTCATATTATGGCTACTGAGGCATCTAATTACGCCCAGTATCGGGTTGTTCGGGCTACG 247

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 ATTCGTTATCGCCCGTTGGTGCCAAATGCTGTTGGTGGTTATGCTATCTCTATTTCTTTC 307

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 TGGCCTCAAACTACAACTACCCCTACTTCTGTTGACATGAATTCTATCACTTCTACTGAT 367

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 GTCAGGATCTTGGTCCAGCCCGGTATAGCCTCCGAGTTAGTCATCCCTAGTGAACGCCTT 427

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        428 CACTACCGCAACCAAGGCTGGCGCTCTGTTGAGACCACGGGTGTGGCCGAAGAGGAGGCT 487

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        488 ACCTCCGGTCTGGTAATGCTTTGTATTCATGGCTCCCCTGTTAACTCCTACACTAATACA 547

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 CCTTACACCGGTGCATTGGGGCTTCTTGATTTTGCATTAGAACTTGAATTTAGAAATTTG 607

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        608 ACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACTAGCACAGCCCGCCACCGGCTG 667

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CGCCGCGGTGCTGATGGGACCGCTGAGCTCACCACCACAGCAGCCACACGCTTCATGAAG 727

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||   ||||||   ||||||||||||||||||   ||||||||||||||||||||
Db        728 GATTTGCATTTTACTGGTACGAACGGCGTTGGTGAGGTGGGTCGTGGTATTGCCCTGACT 787

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CTGTTTAATCTTGCTGATACGCTTCTTGGTGGTTTACCGACAGAATTGATTTCGTCGGCT 847

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 GGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCAGCCAATGGCGAGCCA 898

RESULT 48
HEU40045/c
LOCUS       HEU40045                849 bp    DNA     linear   VRL 26-JAN-1999
DEFINITION  Hepatitis E virus structural protein 2 (orf2) mRNA, partial cds.
ACCESSION   U40045
VERSION     U40045.1  GI:4096793
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 849)
  AUTHORS   Van Cuyck-Gandre,H., Clements,N.J., Zhang,H.Y., Caudill,J.C.,
            Cohen,S.G., Coursaget,P., Buisson,Y., Warren,R.L. and Longer,C.F.
  TITLE     Partial Sequence of HEV Isolates from North Africa and Pakistan:
            Comparison with Known HEV Sequences
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 849)
  AUTHORS   Van Cuyck-Gandre,H., Clements,N.J., Zhang,H.Y., Caudill,J.C.,
            Cohen,S.G., Coursaget,P., Buisson,Y., Warren,R.L. and Longer,C.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-NOV-1995) Helene Van Cuyck-Gandre, Virus Disease,
            Walter Reed Army Institute of Research, BLD 40, Washington, DC
            20307-5100, USA
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FEATURES             Location/Qualifiers
     source          1. .849
                     /organism="Hepatitis E virus"
                     /mol_type="genomic DNA"
                     /strain="2B NIH Abbottabad, Pakistan"
                     /db_xref="taxon:12461"
                     /note="HEV mRNA from patient feces"
     CDS             complement(<1. .>849)
                     /note="orf2; capsid protein"
                     /codon_start=1
                     /product="structural protein 2"
                     /protein_id="AAD09446.1"
                     /db_xref="GI:4096794"
                     /translation="GLYNGSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMAT
                     EASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRIL
                     VQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTPY
                     TGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK
                     DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPT
                     VKLYRSV"

Alignment Scores:
Pred. No.:                28.9          Length:          849
Score:                    278.00        Matches:         278
Percent Similarity:       98.93%        Conservative:    0
Best Local Similarity:    98.93%        Mismatches:      3
Query Match:              50.64%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x HEU40045 (1-849)

Qy          25 TyrAsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThrAsnLeuValLeu 44
               ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         843 TATAACGGATCCACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACCAACCTGGTTCTT 784

Qy          45 TyrAlaAlaProLeuSerProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMet 64
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         783 TATGCTGCTCCCCTTAGCCCACTTCTACCCCTTCAGGACGGCACTAATACTCATATAATG 724

Qy          65 AlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArg 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         723 GCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACAATCCGTTACCGC 664

Qy          85 ProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThr 104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         663 CCGCTTGTTCCCAACGCTGTCGGCGGTTACGCCATTTCCATCTCATTTTGGCCACAGACC 604

Qy         105 ThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAspValArgIleLeu 124
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         603 ACCACCACCCCGACGTCCGTTGATATGAATTCAATAACTTCGACGGATGTTCGTATTTTA 544

Qy         125 ValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeuHisTyrArgAsn 144
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         543 GTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACACTATCGTAAC 484

Qy         145 GlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeu 164
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         483 CAAGGTTGGCGCTCCGTCGAGACCTCCGGGGTGGCTGAGGAGGAGGCTACCTCTGGTCTT 424

Qy         165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
               ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db         423 GTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTACACTAATACACCTTATACCGGT 364

Qy         185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         363 GCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAATTTCGCAACCTCACCCCCGGTAAC 304

Qy         205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         303 ACTAACACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCG 244

Qy         225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         243 GACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGTTTTATGAAGGACCTCTATTTC 184

Qy         245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         183 ACTAGTACCAATGGTGTCGGTGAGATCGGCCGCGGGATAGCTCTCACCCTGTTCAACCTT 124

Qy         265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeu 284
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         123 GCTGACACTCTGCTTGGTGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTG 64

Qy         285 PheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSer 304
               ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||
Db          63 TTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTATAGATCT 4

Qy         305 Val 305
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Db           3 GTA 1

RESULT 49
AF516179
LOCUS       AF516179                 860 bp    RNA     linear   VRL 07-AUG-2003
DEFINITION  Swine hepatitis E virus isolate KOR2 capsid protein gene, partial
            cds.
ACCESSION   AF516179
VERSION     AF516179.1  GI:21541736
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 860)
  AUTHORS   Choi,I.S., Kwon,H.J., Shin,N.R. and Yoo,H.S.
  TITLE     Identification of Swine Hepatitis E Virus (HEV) and Prevalence of
            Anti-HEV Antibodies in Swine and Human Populations in Korea
  JOURNAL   J. Clin. Microbiol. 41 (8), 3602-3608 (2003)
   PUBMED   12904362
REFERENCE   2  (bases 1 to 860)
  AUTHORS   Choi,I.-S. and Yoo,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAY-2002) Infectious Diseases, College of Veterinary
            Medicine, Seoul National University, 103 Seodun-dong, Suwon
            441-744, Republic of Korea
FEATURES             Location/Qualifiers
     source          1. .860
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="KOR2"
                     /db_xref="taxon:63421"
     CDS             <1. .>860
                     /note="ORF2; structural protein"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM61950.1"
                     /db_xref="GI:21541737"
                     /translation="VPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPLLP
                     LQDGTNTHIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVD
                     MNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETTGVAEEEATSGLVMLCIH
                     GSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTARHRLRRGADGTA
                     ELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPTELISSAGGQLFY
                     SRPVVSANGE"

Alignment Scores:
Pred. No.:                29.4          Length:          860
Score:                    277.00        Matches:         277
Percent Similarity:       96.85%        Conservative:    0
Best Local Similarity:    96.85%        Mismatches:      9
Query Match:              50.46%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x AF516179 (1-860)

Qy          11 ValProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThrSer 30
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 GTACCTGATGTTGACTCACGTGGTGCCATCTTGCGTCGGCAGTACAATTTGTCCACGTCC 61
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Qy         31 ProLeuThrSerSerValAlaThrGlyThrAsnLeuValLeuTyrAlaAlaProLeuSer 50
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db         62 CCGCTCACGTCTTCTGTCGCTTCTGGTACTAATTTAGTTCTCTATGCCGCCCCGCTGAAC 121

Qy         51 ProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSerAsn 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CCTCTCTTGCCCCTTCAGGATGGCACCAATACTCATATCATGGCTACTGAGGCATCCAAT 181

Qy         71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        182 TATGCTCAGTATCGGGTTGTTCGAGCTACGATCCGCTATCGCCCGCTGGTGCCAAATGCT 241

Qy         91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GTTGGTGGTTATGCTATCTCTATTTCTTTCTGGCCTCAAACCACAACTACCCCTACTTCT 301

Qy        111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GTTGACATGAATTCTATTACTTCCACTGATGTTAGGATTTTGGTCCAGCCCGGTATTGCC 361

Qy        131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TCCGAGCTGGTCATCCCTAGCGAGCGTCTTCATTATCGTAATCAAGGCTGGCGCTCTGTT 421

Qy        151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GAGACCACGGGTGTGGCCGAGGAGGAGGCCACTTCCGGTCTAGTAATGCTTTGCATCCAT 481

Qy        171 GlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 GGCTCCCCTGTTAATTCTTACACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGAT 541

Qy        191 PheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSer 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 TTTGCATTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCC 601

Qy        211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 CGGTACACCAGCACAGCCCGCCACCGGCTGCGTCGCGGTGCAGATGGGACCGCTGAGCTT 661

Qy        231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyVal 250
              ||||||||||||||||||||||||||||||  ||||||  ||||||||||||
Db        662 ACTACCACAGCAGCCACACGTTTTATGAAAGATTTGCATTTTACTGGCACGAATGGCGTT 721

Qy        251 GlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGly 270
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GGTGAGGTGGGTCGTGGTATTGCCCTGACACTGTTTAATCTTGCTGATACGCTTCTCGGT 781

Qy        271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProVal 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAGTTGTTCTACTCCCGCCCTGTT 841

Qy        291 ValSerAlaAsnGlyGlu 296
              |||||||||||||||||
Db        842 GTCTCGGCCAATGGCGAG 859

RESULT 50
AF516178
LOCUS       AF516178                860 bp    RNA     linear   VRL 07-AUG-2003
DEFINITION  Swine hepatitis E virus isolate KOR1 capsid protein gene, partial
            cds.
ACCESSION   AF516178
VERSION     AF516178.1  GI:21541734
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 860)
  AUTHORS   Choi,I.S., Kwon,H.J., Shin,N.R. and Yoo,H.S.
  TITLE     Identification of Swine Hepatitis E Virus (HEV) and Prevalence of
            Anti-HEV Antibodies in Swine and Human Populations in Korea
  JOURNAL   J. Clin. Microbiol. 41 (8), 3602-3608 (2003)
   PUBMED   12904362
REFERENCE   2  (bases 1 to 860)
  AUTHORS   Choi,I.-S. and Yoo,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAY-2002) Infectious Diseases, College of Veterinary
            Medicine, Seoul National University, 103 Seodun-dong, Suwon
            441-744, Republic of Korea
FEATURES             Location/Qualifiers
     source          1. .860
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="KOR1"
                     /db_xref="taxon:63421"
     CDS             <1. .>860
                     /note="ORF2; structural protein"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM61949.1"
                     /db_xref="GI:21541735"
                     /translation="VPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLP
                     LQDGTNTHIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVD
                     MNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETTGVAEEEATSGLVMLCIH
                     GSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTARHRLRRGADGTA
                     ELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPTELISSAGGQLFY
                     SRPVVSANGE"

Alignment Scores:
Pred. No.:              29.8          Length:         860
Score:                  276.00        Matches:        276
Percent Similarity:     96.50%        Conservative:   0
Best Local Similarity:  96.50%        Mismatches:     10
Query Match:            50.27%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF516178 (1-860)

Qy         11 ValProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThrSer 30
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GTACCTGATGTTGACTCACGTGGTGCCATCTTGCGTCGGCAGTACAATTTGTCCACGTCC 61

Qy         31 ProLeuThrSerSerValAlaThrGlyThrAsnLeuValLeuTyrAlaAlaProLeuSer 50
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db         62 CCGCTCACGTCTTCTGTCGCTTCTGGTACTAATTTAGTTCTCTATGCCGCCCCGCTGAAC 121

Qy         51 ProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSerAsn 70
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CCTCCCTTGCCCCTTCAGGATGGCACCAATACTCATATCATGGCTACTGAGGCATCCAAT 181

Qy         71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        182 TATGCTCAGTATCGGGTTGTTCGAGCTACGATCCGCTATCGCCCGCTGGTGCCAAATGCT 241

Qy         91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GTTGGTGGTTATGCTATCTCTATTTCTTTCTGGCCTCAAACCACAACTACCCCTACTTCT 301

Qy        111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GTTGACATGAATTCTATTACTTCCACTGATGTTAGGATTTTGGTCCAGCCCGGTATTGCC 361

Qy        131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TCCGAGCTGGTCATCCCTAGCGAGCGTCTTCATTATCGTAATCAAGGCTGGCGCTCTGTT 421

Qy        151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GAGACCACGGGTGTGGCCGAGGAGGAGGCCACTTCCGGTCTAGTAATGCTTTGCATCCAT 481

Qy        171 GlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 GGCTCCCCTGTTAATTCTTACACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGAT 541
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Qy        191 PheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSer 210
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Db        542 TTTGCATTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCC 601

Qy        211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 CGGTACACCAGCACAGCCCGCCACCGGCTGCGTCGCGGTGCAGATGGGACCGCTGAGCTT 661

Qy        231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyVal 250
              |||||||||||||||||||||||||||||||||||  ||||||  ||||||||||||||
Db        662 ACTACCACAGCAGCCACACGTTTTATGAAAGATTTGCATTTTACTGGCACGAATGGCGTT 721

Qy        251 GlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGly 270
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GGTGAGGTGGGTCGTGGTATTGCCCTGACACTGTTCAATCTTGCTGATACGCTTCTCGGT 781

Qy        271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProVal 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAGTTGTTCTACTCCCGCCCTGTT 841

Qy        291 ValSerAlaAsnGlyGlu 296
              |||||||||||||||||
Db        842 GTCTCGGCCAATGGCGAG 859

RESULT 51
AF527942
LOCUS       AF527942                 860 bp    RNA     linear   VRL 07-AUG-2003
DEFINITION  Swine hepatitis E virus isolate KOR3 capsid protein gene, partial
            cds.
ACCESSION   AF527942
VERSION     AF527942.1  GI:22023950
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 860)
  AUTHORS   Choi,I.S., Kwon,H.J., Shin,N.R. and Yoo,H.S.
  TITLE     Identification of Swine Hepatitis E Virus (HEV) and Prevalence of
            Anti-HEV Antibodies in Swine and Human Populations in Korea
  JOURNAL   J. Clin. Microbiol. 41 (8), 3602-3608 (2003)
   PUBMED   12904362
REFERENCE   2  (bases 1 to 860)
  AUTHORS   Choi,I.-S. and Yoo,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUL-2002) Infectious Diseases, College of Veterinary
            Medicine, Seoul National University, 103 Seodun-dong, Suwon
            441-744, Republic of Korea
FEATURES             Location/Qualifiers
     source          1. .860
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="KOR3"
                     /db_xref="taxon:63421"
     CDS             <1. .>860
                     /note="structural protein; ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM89262.1"
                     /db_xref="GI:22023951"
                     /translation="VPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPLLP
                     LQDGTNTHIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVD
                     MNSITSTDVRTLVQPGIASELVIPSERLHYRNQGWRSVETTGVAEEEATSGLVMLCIH
                     GSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTARHRLRRGADGTA
                     ELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPTELISSAGGQLFY
                     SRPVVSANGE"

Alignment Scores:
Pred. No.:              29.8          Length:         860
Score:                  276.00        Matches:        276
Percent Similarity:     96.50%        Conservative:   0
Best Local Similarity:  96.50%        Mismatches:     10
Query Match:            50.27%        Indels:         0

DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF527942 (1-860)

Qy         11 ValProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThrSer 30
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Db          2 GTACCTGATGTTGACTCACGTGGTGCTATCTTGCGCCGGCAATACAATCTTTCCACGTCC 61

Qy         31 ProLeuThrSerSerValAlaThrGlyThrAsnLeuValLeuTyrAlaAlaProLeuSer 50
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db         62 CCGCTTACATCTTCTGTCGCCTCTGGTACTAATTTGGTCCTCTACGCCGCTCCGTTAAAT 121

Qy         51 ProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSerAsn 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CCCCTCCTGCCTCTTCAGGATGGCACCAACACTCATATTATGGCTACTGAAGCATCCAAT 181

Qy         71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        182 TATGCCCAGTATCGGGTTGTTCGAGCTACGATCCGTTACCGCCCGCTAGTGCCAAATGCT 241

Qy         91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GTTGGTGGTTATGCTATTTCTATCTCTTTTTGGCCTCAAACCACAACTACCCCCACCTCT 301

Qy        111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        302 GTTGACATGAATTCTATTACTTCCACTGATGTTAGGACTTTGGTCCAGCCCGGTATTGCC 361

Qy        131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TCCGAGCTAGTCATCCCTAGCGAGCGCCTGCATTACCGTAATCAAGGCTGGCGCTCTGTT 421

Qy        151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GAGACCACGGGTGTCGCTGAGGAGGAGGCTACATCTGGTCTGGTAATGCTTTGCATCCAT 481

Qy        171 GlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 GGCTCTCCTGTTAATTCTTATACTAACACACCTTACACTGGTGCACTGGGGCTTCTTGAT 541

Qy        191 PheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSer 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 TTCGCATTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACCAATACCCGTGTCTCC 601

Qy        211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 CGGTATACCAGCACAGCTCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAACTT 661

Qy        231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyVal 250
              |||||||||||||||||||||||||||||||||||  ||||||  ||||||||||||||
Db        662 ACTACCACAGCAGCCACACGCTTTATGAAAGATCTGCATTTTACTGGCACTAATGGCGTT 721

Qy        251 GlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGly 270
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GGTGAGGTGGGCCGTGGTATTGCTCTGACACTGTTTAATCTCGCTGATACGCTTCTCGGT 781

Qy        271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProVal 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTT 841

Qy        291 ValSerAlaAsnGlyGlu 296
              |||||||||||||||||
Db        842 GTCTCGGCCAATGGCGAG 859

RESULT 52
AR278919
LOCUS       AR278919                 803 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 17 from patent US 6514690.
ACCESSION   AR278919
VERSION     AR278919.1  GI:29713553
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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           Unclassified.
REFERENCE  1  (bases 1 to 803)
  AUTHORS  Li,F., Hui,Z., Anderson,D.A., Logarnini,S.A. and Torresi,J.
  TITLE    Immunoreactive antigens of Hepatitis E Virus
  JOURNAL  Patent: US 6514690-A 17 04-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .803
                     /organism="unknown"
                     /mol_type="genomic DNA"

Alignment Scores:
Pred. No.:              34.2          Length:         803
Score:                  266.00        Matches:        266
Percent Similarity:     99.63%        Conservative:   0
Best Local Similarity:  99.63%        Mismatches:     1
Query Match:            48.45%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AR278919 (1-803)

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAGCTTTAT 60

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATCGACCTC 120

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGACCGACA 180

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTTCCCCAGCCCCATCGCGCCCTTTTCTGTCCTCCGAGCTAATGATGTGCTTTGGCTT 240

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCAGTCTAT 300

Qy        383 ValSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCA 360

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAGTATTCA 420

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGTACTACT 480

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTTGAGAAT 540

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTC 600

Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThr 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCCGCGCTAGCATTGCTTGAGGATACC 660

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGCCCCCTT 720

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAG 780

Qy        543 ValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||
Db        781 GTGGGTAAAACTCGGGAGTTA 801

RESULT 53
AX181806
LOCUS       AX181806                960 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 88 from Patent WO0146696.
ACCESSION   AX181806
VERSION     AX181806.1  GI:15133129
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 88 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .960
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="Clone: HEV 3p RACE"

Alignment Scores:
Pred. No.:              36.6          Length:         960
Score:                  262.00        Matches:        262
Percent Similarity:     93.24%        Conservative:   0
Best Local Similarity:  93.24%        Mismatches:     19
Query Match:            47.72%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AX181806 (1-960)

Qy        268 LeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSer 287
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CTTCTTGGTGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCC 62

Qy        288 ArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsn 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGCCCTGTTGTCTCGGCCAATGGCGAGCCAACAGTAAAGTTATACACATCTGTTGAGAAT 122

Qy        308 AlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSerArgVal 327
              ||||||||||||||||||||  ||||||||||||||||||||||||||  |||||||||
Db        123 GCGCAGCAAGACAAGGGCATCACCATTCCACACGACATAGATTTAGGTGACTCCCGTGTG 182

Qy        328 ValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaPro 347
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GTTATCCAGGATTATGATAACCAGCACGAACAAGATCGACCTACCCCGTCACCTGCCCCC 242

Qy        348 SerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAla 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 TCCCGCCCTTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTCTCTCTCACTGCCGCT 302

Qy        368 GluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerVal 387
              ||||||  |||  ||||||||||||||||||  |||  ||||||||||||  |||
Db        303 GAGTACGRCCAGACCACGTATGGGTCGTCCACCAACCCTATGTATGTCTCTGATACAGTC 362

Qy        388 ThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLys 407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        363 ACGCTTGTTAATGTAGCCACTGGTGCTCAGGCTGTTGCCCGCTCTCTTGACTGGTCTAAA 422

Qy        408 ValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheVal 427
              ||||||||||||||||||||  ||||||||||||||||||||  |||  |||
Db        423 GTTACTCTGGATGGTCGCCCTCTTACTACCATTCAGCAGTATTCTAAGAAATTTTATGTT 482

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 CTCCCGCTTCGSGGGAAGCTGTCCTTTTGGGAGGCTGGTACGACCAAGGCCGGCTACCCG 542
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Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||||||   |||   ||||||||||||||||||||
Db        543 TATAATTATAATACCACTGCTAGTGACCAAATTTTGATTGAGAACGCGGCCGGTCACCGT 602

Qy        468 ValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaVal 487
              ||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||
Db        603 GTCGCCATTTCTACTTATACCACTAGTTTGGGTGCCGGCCCTACCTCGATYTCTGCGGTC 662

Qy        488 AlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAla 507
              ||||||||||||||||||||||||||||   ||||||||||||   ||||||||||||||
Db        663 GGTGTACTAGCTCCACATTCGGCCCTTGCTGTTCTCGAGGATACTGTTGATTATCCTGCT 722

Qy        508 ArgAlaHisThrPheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGlyCys 527
              ||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        723 CGTGCCCATACTTTTGATGATTTCTGCCCGGAGTGTCGCACCCTTGGTCTGCAGGGTTGT 782

Qy        528 AlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArg 547
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        783 GCATTCCAATCTACTATTGCTGAACTTCAGCGTCTTAAAATGAAGGTAGGTAAAACCCGG 842

Qy        548 Glu 548
              |||
Db        843 GAG 845
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RESULT 54
BD077209
LOCUS       BD077209                960 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077209
VERSION     BD077209.1  GI:22622812
KEYWORDS    JP 2001520384-A/88.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 960)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 88 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/88
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   Clone: HEV 3p RACE
            FH   Key             Location/Qualifiers
            FT   source          1. .960
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                        virus)'.
FEATURES             Location/Qualifiers
     source          1. .960
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              36.6          Length:         960
Score:                  262.00        Matches:        262
Percent Similarity:     93.24%        Conservative:   0
Best Local Similarity:  93.24%        Mismatches:     19
Query Match:            47.72%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x BD077209 (1-960)

Qy        268 LeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSer 287
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CTTCTTGGTGGTTTACCGACACGAATTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCC 62

Qy        288 ArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsn 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGCCCTGTTGTCTCGGCCAATGGCGAGCCAACAGTAAAGTTATACACATCTGTTGAGAAT 122

Qy        308 AlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSerArgVal 327
              ||||||||||||||||||   ||||||||||||||||||||||||   |||||||||
Db        123 GCGCAGCAAGACAAGGGCATCACCATTCCACACGACATAGATTTAGGTGACTCCCGTGTG 182

Qy        328 ValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaPro 347
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GTTATCCAGGATTATGATAACCAGCACGAACAAGATCGACCTACCCCGTCACCTGCCCCC 242

Qy        348 SerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAla 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 TCCCGCCCTTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTCTCTCTCACTGCCGCT 302

Qy        368 GluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerVal 387
              ||||||   |||   ||||||||||||||||||   |||   ||||||||||||   |||
Db        303 GAGTACGRCCAGACCACGTATGGGTCGTCCACCAACCCTATGTATGTCTCTGATACAGTC 362

Qy        388 ThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLys 407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        363 ACGCTTGTTAATGTAGCCACTGGTGCTCAGGCTGTTGCCCGCTCTCTTGACTGGTCTAAA 422

Qy        408 ValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheVal 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        423 GTTACTCTGGATGGTCGCCCTCTTACTACCATTCAGCAGTATTCTAAGAAATTTTATGTT 482

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 CTCCCGCTTCGSGGGAAGCTGTCCTTTTGGGAGGCTGGTACGACCAAGGCCGGCTACCCG 542

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||||||   |||   ||||||||||||||||||||
Db        543 TATAATTATAATACCACTGCTAGTGACCAAATTTTGATTGAGAACGCGGCCGGTCACCGT 602

Qy        468 ValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaVal 487
              ||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||
Db        603 GTCGCCATTTCTACTTATACCACTAGTTTGGGTGCCGGCCCTACCTCGATYTCTGCGGTC 662

Qy        488 AlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAla 507
              ||||||||||||||||||||||||||||   ||||||||||||   ||||||||||||||
Db        663 GGTGTACTAGCTCCACATTCGGCCCTTGCTGTTCTCGAGGATACTGTTGATTATCCTGCT 722

Qy        508 ArgAlaHisThrPheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGlyCys 527
              ||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        723 CGTGCCCATACTTTTGATGATTTCTGCCCGGAGTGTCGCACCCTTGGTCTGCAGGGTTGT 782

Qy        528 AlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArg 547
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        783 GCATTCCAATCTACTATTGCTGAACTTCAGCGTCTTAAAATGAAGGTAGGTAAAACCCGG 842

Qy        548 Glu 548
              |||
Db        843 GAG 845
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RESULT 55
HPECCAP
LOCUS       HPECCAP                 775 bp    RNA     linear   VRL 02-FEB-1999
DEFINITION  Hepatitis E virus RNA, capsid region.
ACCESSION   D10332
VERSION     D10332.1  GI:221700
KEYWORDS    structural protein.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (sites)
  AUTHORS   Tam,A.W., Smith,M.M., Guerra,M.E., Huang,C.C., Bradley,D.W.,
            Fry,K.E. and Reyes,G.R.
```

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  TITLE     Hepatitis E virus (HEV): molecular cloning and sequencing of the
            full-length viral genome
  JOURNAL   Virology 185 (1), 120-131 (1991)
  MEDLINE   92024067
   PUBMED   1926770
REFERENCE   2  (bases 1 to 775)
  AUTHORS   Aye,T.T., Uchida,T., Ma,X., Iida,F., Shikata,T., Zhuang,H. and
            Win,K.M.
  TITLE     Sequence comparison of the capsid region of hepatitis E viruses
            isolated from Myanmar and China
  JOURNAL   Microbiol. Immunol. 36 (6), 615-621 (1992)
  MEDLINE   92396046
   PUBMED   1387921
REFERENCE   3  (bases 1 to 775)
  AUTHORS   Uchida,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JAN-1992) Toshikazu Uchida, Nihon University School
            of Medicine, 1st Department of Pathology; 30-1 Oyaguchi-Kamimachi,
            Itabashi-ku, Tokyo 173, Japan (Tel:03-3972-8111, Fax:03-3972-8830)
COMMENT     Submitted (23-Jan-1992) to DDBJ by:
            Toshikazu Uchida
            Ist Department of Pathology
            Nihon University School of Medicine
            30-1 Oyaguchi Kamimachi
            Itabashi-ku, Tokyo 173
            Japan
            Phone:  03-3972-8111
            Fax:    03-3972-8830.
FEATURES             Location/Qualifiers
     source          1. .775
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="ChinaEpi-1-3"
                     /db_xref="taxon:12461"
     CDS             <1. .>775
                     /codon_start=2
                     /product="structural protein"
                     /protein_id="BAA01178.1"
                     /db_xref="GI:391712"
                     /translation="VSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDN
                     QHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTAPVYVSDSVTLVNV
                     ATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNY
                     NTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLEDTMDYPAR
                     AHTFDDFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTRK"

Alignment Scores:
Pred. No.:                39.9          Length:         775
Score:                    255.00        Matches:        255
Percent Similarity:       99.22%        Conservative:   0
Best Local Similarity:    99.22%        Mismatches:     2
Query Match:              46.45%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x HPECCAP (1-775)

Qy         291 ValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGln 310
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 GTCTCAGCCAATGGCGAGCCGACTGTTAAGCTTTATACATCTGTAGAGAATGCTCAGCAG 61

Qy         311 AspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGln 330
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 GATAAGGGTATTGCAATCCCGCATGACATCGACCTCGGGGAGTCTCGTGTAGTTATTCAG 121

Qy         331 AspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgPro 350
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         122 GATTATGACAACCAACATGAGCAGGACCGACCGACACCTTCCCCAGCCCCATCGCGCCCT 181

Qy         351 PheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAsp 370
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         182 TTTTCTGTCCTCCGAGCTAATGATGTGCTTTGGCTTTCTCTCACCGCTGCCGAGTATGAC 241

Qy         371 GlnSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeuVal 390
               |||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||

Db         242 CAGTCCACTTACGGCTCTTCGACGGCCCCAGTCTATGTCTCTGACTCTGTGACCTTGGTT 301

Qy         391 AsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeu 410
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         302 AATGTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCACTCGACTGGACCAAGGTCACACTT 361

Qy         411 AspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeu 430
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         362 GATGGTCGCCCCCTTTCCACCATCCAGCAGTATTCAAAGACCTTCTTTGTCCTGCCGCTC 421

Qy         431 ArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyr 450
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         422 CGCGGTAAGCTCTCCTTTTGGGAGGCAGGTACTACTAAAGCCGGGTACCCTTATAATTAT 481

Qy         451 AsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIle 470
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         482 AACACCACTGCTAGTGACCAACTGCTCGTTGAGAATGCCGCTGGGCATCGGGTTGCTATT 541

Qy         471 SerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeu 490
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         542 TCCACTTACACCACTAGCCTGGGTGCTGGCCCCGTCTCTATTTCCGCGGTTGCTGTTTTA 601

Qy         491 AlaProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHis 510
               ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db         602 GCCCCCCACTCCGCGCTAGCATTGCTTGAGGATACCATGGACTACCCTGCCCGCGCCCAT 661

Qy         511 ThrPheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPheGln 530
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         662 ACTTTCGATGACTTCTGCCCGGAGTGCCGCCCCCTTGGCCTCCAGGGCTGTGCTTTTCAG 721

Qy         531 SerThrValAlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArg 547
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         722 TCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGG 772

RESULT 56
AX181904
LOCUS       AX181904                919 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 186 from Patent WO0146696.
ACCESSION   AX181904
VERSION     AX181904.1  GI:15133214
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 186 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .919
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
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                     /note="z12-3p.con"

Alignment Scores:
Pred. No.:                40.4          Length:         919
Score:                    255.00        Matches:        255
Percent Similarity:       92.73%        Conservative:   0
Best Local Similarity:    92.73%        Mismatches:     20
Query Match:              46.45%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x AX181904 (1-919)

Qy         274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 ACAGAATTAATTTCGTCGGCTGGGGGTCAACTGTTCTACTCCCGCCCTGTCGTCTCAGCC 61

Qy         294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
```

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Db        62 AATGGCGAGCCGACTGTCAAGTTATACACATCTGTTGAGAATGCACAGCAGGATAAGGGG 121

Qy       314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
Db       122 ATAGCTATTCCACATGACATAGATTTGGGCGACTCTCGTTTGGTAATCCAGGATTACGAT 181

Qy       334 AsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgProProheSerVal 353
Db       182 AATCAGCACGAGCAGGACCGGCCCACCCCTTCGCCCGCCCCGTCTCGTCCTTTCTCGGTC 241

Qy       354 LeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThr 373
Db       242 CTCCGCGCTAATGATGCTTTGTGGCTTTCTCTTACCGCTGCTGAGTATGACCAGACTACA 301

Qy       374 TyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeuValAsnValAla 393
Db       302 TATGGGTCGTCCACCAACCCGATGTATGTCTCAGACACTGTTACATTTGTCAATGTGGCC 361

Qy       394 ThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArg 413
Db       362 ACAGGGGCTCAGGCTGTCGCCCGTTCTCTTGATTGGTCTAAAGTTACCCTGGACGGCCGC 421

Qy       414 ProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLys 433
Db       422 CCTCTTACTACCATCCAGCAGTACTCTAAGACATTTTATGTTCTCCCACTTCGCGGGAAG 481

Qy       434 LeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThr 453
Db       482 TTATCTTTTTGGGAGGCTGGCACAACTAAAGCCGGTTACCCTTATAATTATAACACAACT 541

Qy       454 AlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyr 473
Db       542 GCTAGTGACCAGATTCTGATTGAAAACGCGGCTGGCCATCGTGTCGCTATATCTACTTAT 601

Qy       474 ThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAlaProHis 493
Db       602 ACTACTAGCCTGGGCGCCGGCCCTGTGTCAGTTTCTGCGGTTGGTGTGTTAGCCCCACAC 661

Qy       494 SerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAsp 513
Db       662 TCGAGCCTTGCTATTCTTGAAGACACTGTTGACTATCCGGCCCGTGCTCACACTTTTGAT 721

Qy       514 AspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrVal 533
Db       722 GACTTCTGTCCGGAATGCCGTGCCCTGGGTCTGCAGGGGTGTGCTTTTCAATCTACTATC 781

Qy       534 AlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArgGlu 548
Db       782 GCTGAGCTCCAGCGTCTTAAAATGAAGGTAGGCAAAACCCGGGAG 826

RESULT 57
BD077293
LOCUS       BD077293                 919 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077293
VERSION     BD077293.1  GI:22622896
KEYWORDS    JP 2001520384-A/172.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 919)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 172 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/172
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   z12-3p.con
            FH   Key             Location/Qualifiers
            FT   source          1. .919
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                           virus)'.
FEATURES             Location/Qualifiers
     source          1. .919
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:                40.4          Length:          919
Score:                    255.00        Matches:         255
Percent Similarity:       92.73%        Conservative:    0
Best Local Similarity:    92.73%        Mismatches:      20
Query Match:              46.45%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x BD077293 (1-919)

Qy       274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
Db         2 ACAGAATTAATTTCGTCGGCTGGGGGTCAACTGTTCTACTCCCGCCCTGTCGTCTCAGCC 61

Qy       294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
Db        62 AATGGCGAGCCGACTGTCAAGTTATACACATCTGTTGAGAATGCACAGCAGGATAAGGGG 121

Qy       314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
Db       122 ATAGCTATTCCACATGACATAGATTTGGGCGACTCTCGTTTGGTAATCCAGGATTACGAT 181

Qy       334 AsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgProProheSerVal 353
Db       182 AATCAGCACGAGCAGGACCGGCCCACCCCTTCGCCCGCCCCGTCTCGTCCTTTCTCGGTC 241

Qy       354 LeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThr 373
Db       242 CTCCGCGCTAATGATGCTTTGTGGCTTTCTCTTACCGCTGCTGAGTATGACCAGACTACA 301

Qy       374 TyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeuValAsnValAla 393
Db       302 TATGGGTCGTCCACCAACCCGATGTATGTCTCAGACACTGTTACATTTGTCAATGTGGCC 361

Qy       394 ThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArg 413
Db       362 ACAGGGGCTCAGGCTGTCGCCCGTTCTCTTGATTGGTCTAAAGTTACCCTGGACGGCCGC 421

Qy       414 ProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLys 433
Db       422 CCTCTTACTACCATCCAGCAGTACTCTAAGACATTTTATGTTCTCCCACTTCGCGGGAAG 481

Qy       434 LeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThr 453
Db       482 TTATCTTTTTGGGAGGCTGGCACAACTAAAGCCGGTTACCCTTATAATTATAACACAACT 541

Qy       454 AlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyr 473
Db       542 GCTAGTGACCAGATTCTGATTGAAAACGCGGCTGGCCATCGTGTCGCTATATCTACTTAT 601

Qy       474 ThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAlaProHis 493
Db       602 ACTACTAGCCTGGGCGCCGGCCCTGTGTCAGTTTCTGCGGTTGGTGTGTTAGCCCCACAC 661

Qy       494 SerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAsp 513
Db       662 TCGAGCCTTGCTATTCTTGAAGACACTGTTGACTATCCGGCCCGTGCTCACACTTTTGAT 721
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Qy        514 AspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrVal 533
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        722 GACTTCTGTCCGGAATGCCGTGCCCTGGGTCTGCAGGGGTGTGCTTTTCAATCTACTATC 781

Qy        534 AlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArgGlu 548
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GCTGAGCTCCAGCGTCTTAAAATGAAGGTAGGCAAAACCCGGGAG 826

RESULT 58
HPEBCAP
LOCUS       HPEBCAP                  745 bp    RNA     linear   VRL 02-FEB-1999
DEFINITION  Hepatitis E virus RNA, capsid region.
ACCESSION   D10333
VERSION     D10333.1  GI:221699
KEYWORDS    structural protein.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (sites)
  AUTHORS   Tam,A.W., Smith,M.M., Guerra,M.E., Huang,C.C., Bradley,D.W.,
            Fry,K.E. and Reyes,G.R.
  TITLE     Hepatitis E virus (HEV): molecular cloning and sequencing of the
            full-length viral genome
  JOURNAL   Virology 185 (1), 120-131 (1991)
  MEDLINE   92024067
   PUBMED   1926770
REFERENCE   2  (bases 1 to 745)
  AUTHORS   Aye,T.T., Uchida,T., Ma,X., Iida,F., Shikata,T., Zhuang,H. and
            Win,K.M.
  TITLE     Sequence comparison of the capsid region of hepatitis E viruses
            isolated from Myanmar and China
  JOURNAL   Microbiol. Immunol. 36 (6), 615-621 (1992)
  MEDLINE   92396046
   PUBMED   1387921
REFERENCE   3  (bases 1 to 745)
  AUTHORS   Uchida,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JAN-1992) Toshikazu Uchida, Nihon University School
            of Medicine, 1st Department of Pathology; 30-1 Oyaguchi-Kamimachi,
            Itabashi-ku, Tokyo 173, Japan (Tel:03-3972-8111, Fax:03-3972-8830)
COMMENT     Submitted (23-Jan-1992) to DDBJ by:
            Toshikazu Uchida
            1st Department of Pathology
            Nihon University School of Medicine
            30-1 Oyaguchi Kamimachi
            Itabashi-ku, Tokyo 173
            Japan
            Phone:  03-3972-8111
            Fax:    03-3972-8830.
FEATURES             Location/Qualifiers
     source          1. .745
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="BurmaEpi-1-3"
                     /db_xref="taxon:12461"
     CDS             <1. .>745
                     /codon_start=1
                     /product="structural protein"
                     /protein_id="BAA01179.1"
                     /db_xref="GI:391711"
                     /translation="EPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQD
                     RPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQ
                     AVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTAS
                     DQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLEDTLDYPACAHTFD
                     DFCPECRPLGLQGCAFQSTVAELQRLKMKV"

Alignment Scores:
Pred. No.:              44.6          Length:        745
Score:                  247.00        Matches:       247
Percent Similarity:     99.60%        Conservative:  0
Best Local Similarity:  99.60%        Mismatches:    1

Query Match:            44.99%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x HPEBCAP (1-745)

Qy        296 GluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAla 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGCCGACTGTTAAGCTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCA 60

Qy        316 IleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGln 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCCCGCATGATATTGACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAA 120

Qy        336 HisGluGlnAspArgProThrProSerProAlaProSerArgProPheSerValLeuArg 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGAACAAGACCGGCCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTTCTTCGA 180

Qy        356 AlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGly 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCTAATGATGTGCTCTGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACCTATGGC 240

Qy        376 SerSerThrGlyProValTyrValSerAspSerValThrLeuValAsnValAlaThrGly 395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTTCGACTGGCCCAGTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGC 300

Qy        396 AlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeu 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTC 360

Qy        416 SerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSer 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCT 420

Qy        436 PheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSer 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCTGGGAGGCAGGCACAACTAAGGCCGGGTACCCTTATAATTACAACACCACTGCTAGC 480

Qy        456 AspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThr 475
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTTGCTATTTCTACTTACACTACT 540

Qy        476 SerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAla 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCCTGGGCGCTGGCCCCGTCTCCATTTCTGCGGTTGCCGTCTTAGCCCCCCACTCTGCG 600

Qy        496 LeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPhe 515
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTAGCATTGCTTGAGGATACTTTGGACTACCCTGCCTGCGCCCATACTTTTGATGATTTC 660

Qy        516 CysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGlu 535
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGCCCAGAGTGCCGCCCCCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAG 720

Qy        536 LeuGlnArgLeuLysMetLysVal 543
              |||||||||||||||||||||||
Db        721 CTTCAGCGCCTTAAGATGAAGGTG 744

RESULT 59
AX181871
LOCUS       AX181871                 901 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 153 from Patent WO0146696.
ACCESSION   AX181871
VERSION     AX181871.1  GI:15133192
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 153 28-JUN-2001;
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           ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .901
                     /organism="Hepatitis E virus"
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                     /note="us2-3p"

Alignment Scores:
Pred. No.:                48.5          Length:          901
Score:                    242.00        Matches:         242
Percent Similarity:       93.44%        Conservative:    0
Best Local Similarity:    93.44%        Mismatches:      17
Query Match:              44.08%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x AX181871 (1-901)

Qy        290 ValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGln 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATATACATCTGTTGAGAATGCGCAG 60

Qy        310 GlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIle 329
              ||||||||||||||||  ||||||||||||||||||||||||  ||||||||||||||||
Db         61 CAAGACAAGGGCATCACCATTCCACATGATATAGACCTGGGTGACTCCCGTGTGGTTATC 120

Qy        330 GlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArg 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGGATTATGATAACCAGCAYGAGCAAGACCGACCTACTCCGTCACCTGCCCCCTCTCGC 180

Qy        350 ProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyr 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTTTCCCTCACTGCCGCTGAGTAT 240

Qy        370 AspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeu 389
              ||||||  ||||||||||||||||||  |||  ||||||||||||  ||||||||||||||
Db        241 GACCAGACTACGTATGGGTCGTCCACCAACCCTATGTATGTCTCTGACACAGTTACGCTT 300

Qy        390 ValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThr 409
              ||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||||||
Db        301 GTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCCCTTGATTGGTCTAAAGTTACT 360

Qy        410 LeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuPro 429
              ||||||||||||||||  ||||||||||||||||||||||||||||  |||||||||||||
Db        361 CTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCTAAGACATTTTATGTTCTCCCG 420

Qy        430 LeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsn 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACTAAGGCCGGCTACCCTTACAAT 480

Qy        450 TyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAla 469
              ||||||||||||||||||||||  |||  ||||||||||||||||||||||||||||||||
Db        481 TATAATACTACCGCTAGTGACCAAATTTTGATTGAGAATGCGGCCGGCCACCGTGTCGCT 540

Qy        470 IleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaVal 489
              ||||||||||||||||||||||||||||||||||  ||||||||||||||  |||||||||
Db        541 ATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACCTCGATCTCTGCGGTCGGCGTA 600

Qy        490 LeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAla 509
              ||||||||||||||||||||||  ||||||||||||  ||||||||||||||||||||||||
Db        601 CTGGCTCCACACTCTGCCCTTGCCGTTCTTGAGGATACTATTGATTACCCCGCCCGTGCC 660

Qy        510 HisThrPheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPhe 529
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        661 CATACTTTTGATGATTTTTGCCCGGAGTGCCGTACCCTAGGTTTGCAGGGTTGTGCATTC 720

Qy        530 GlnSerThrValAlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArgGlu 548
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGTCTACTATTGCTGAGCTCCAGCGTTTAAAAATGAAGGTAGGTAAAACCCGGGAG 777

RESULT 60
BD077271
LOCUS       BD077271                901 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077271
VERSION     BD077271.1  GI:22622874
KEYWORDS    JP 2001520384-A/150.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 901)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 150 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/150
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   us2-3p
            FH   Key             Location/Qualifiers
            FT   source          1. .901
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                                 virus)'.
FEATURES             Location/Qualifiers
     source          1. .901
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:                48.5          Length:          901
Score:                    242.00        Matches:         242
Percent Similarity:       93.44%        Conservative:    0
Best Local Similarity:    93.44%        Mismatches:      17
Query Match:              44.08%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x BD077271 (1-901)

Qy        290 ValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGln 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATATACATCTGTTGAGAATGCGCAG 60

Qy        310 GlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIle 329
              ||||||||||||||||  ||||||||||||||||||||||||  ||||||||||||||||
Db         61 CAAGACAAGGGCATCACCATTCCACATGATATAGACCTGGGTGACTCCCGTGTGGTTATC 120

Qy        330 GlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArg 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGGATTATGATAACCAGCAYGAGCAAGACCGACCTACTCCGTCACCTGCCCCCTCTCGC 180

Qy        350 ProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyr 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTTTCCCTCACTGCCGCTGAGTAT 240

Qy        370 AspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeu 389
              ||||||  ||||||||||||||||||  |||  ||||||||||||  ||||||||||||||
Db        241 GACCAGACTACGTATGGGTCGTCCACCAACCCTATGTATGTCTCTGACACAGTTACGCTT 300

Qy        390 ValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThr 409
              ||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||||||
Db        301 GTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCCCTTGATTGGTCTAAAGTTACT 360

Qy        410 LeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuPro 429
              ||||||||||||||||  ||||||||||||||||||||||||||||  |||||||||||||
Db        361 CTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCTAAGACATTTTATGTTCTCCCG 420
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Qy        430 LeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsn 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACTAAGGCCGGCTACCCTTACAAT 480

Qy        450 TyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAla 469
              |||||||||||||||||||||||||   |||   ||||||||||||||||||||||||||||
Db        481 TATAATACTACCGCTAGTGACCAAATTTTGATTGAGAATGCGGCCGGCCACCGTGTCGCT 540

Qy        470 IleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaVal 489
              |||||||||||||||||||||||||||||||||||   ||||||||||||||||   |||
Db        541 ATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACCTCGATCTCTGCGGTCGGCGTA 600

Qy        490 LeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAla 509
              ||||||||||||||||||||||||   ||||||||||||   ||||||||||||||||||||
Db        601 CTGGCTCCACACTCTGCCCTTGCCGTTCTTGAGGATACTATTGATTACCCCGCCCGTGCC 660

Qy        510 HisThrPheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPhe 529
              |||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        661 CATACTTTTGATGATTTTTGCCCGGAGTGCCGTACCCTAGGTTTGCAGGGTTGTGCATTC 720

Qy        530 GlnSerThrValAlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArgGlu 548
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGTCTACTATTGCTGAGCTCCAGCGTTTAAAAATGAAGGTAGGTAAAACCCGGGAG 777

RESULT 61
AX181903
LOCUS       AX181903                890 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 185 from Patent WO0146696.
ACCESSION   AX181903
VERSION     AX181903.1  GI:15133213
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 185 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .890
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="z12-3p.race"

Alignment Scores:
Pred. No.:              50.6          Length:         890
Score:                  239.00        Matches:        239
Percent Similarity:     92.28%        Conservative:   0
Best Local Similarity:  92.28%        Mismatches:     20
Query Match:            43.53%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AX181903 (1-890)

Qy        290 ValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGln 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCGTCTCGGCCAATGGCGAGCCGACTGTCAAGTTATACACATCTGTTGAGAATGCACAG 60

Qy        310 GlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIle 329
              |||||||||||||||||||||||||||||||||||||||   ||||||   ||||||
Db         61 CAGGATAAGGGGATAGCTATTCCACATGACATAGATTTGGGCGACTCTCGTTTGGTAATC 120

Qy        330 GlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArg 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGGATTACGATAATCAGCACGAGCAGGACCGGCCCACCCCTTCGCCCGCCCCGTCTCGT 180

Qy        350 ProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyr 369
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        181 CCTTTCTCGGTCCTCCGCGCTAATGATGCTTTGTGGCTTTCTCTTACCGCTGCTGAGTAT 240

Qy        370 AspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeu 389
              ||||||   ||||||||||||||||||   |||   ||||||||||||   ||||||
Db        241 GACCAGACTACATATGGGTCGTCCACCAACCCGATGTATGTCTCAGACACTGTTACATTT 300

Qy        390 ValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThr 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        301 GTCAATGTGGCCACAGGGGCTCAGGCTGTCGCCCGTTCTCTTGATTGGTCTAAAGTTACC 360

Qy        410 LeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuPro 429
              ||||||||||||||||||   ||||||||||||||||||||||||||||||   |||||||||
Db        361 CTGGACGGCCGCCCTCTTACTACCATCCAGCAGTACTCTAAGACATTTTATGTTCTCCCA 420

Qy        430 LeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsn 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTTCGCGGGAAGTTATCTTTTTGGGAGGCTGGCACAACTAAAGCCGGTTACCCTTATAAT 480

Qy        450 TyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAla 469
              |||||||||||||||||||||||||   |||   ||||||||||||||||||||||||||||
Db        481 TATAACACAACTGCTAGTGACCAGATTCTGATTGAAAACGCGGCTGGCCATCGTGTCGCT 540

Qy        470 IleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaVal 489
              |||||||||||||||||||||||||||||||||||   ||||||||||||||||   |||
Db        541 ATATCTACTTATACTACTAGCCTGGGCGCCGGCCCTGTGTCAGTTTCTGCGGTTGGTGTG 600

Qy        490 LeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAla 509
              ||||||||||||||||   ||||||   ||||||||||||   ||||||||||||||||||||
Db        601 TTAGCCCCACACTCGAGCCTTGCTATTCTTGAAGACACTGTTGACTATCCGGCCCGTGCT 660

Qy        510 HisThrPheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPhe 529
              |||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        661 CACACTTTTGATGACTTCTGTCCGGAATGCCGTGCCCTGGGTCTGCAGGGGTGTGCTTTT 720

Qy        530 GlnSerThrValAlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArgGlu 548
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAATCTACTATCGCTGAGCTCCAGCGTCTTAAAATGAAGGTAGGCAAAACCCGGGAG 777

RESULT 62
BD077292
LOCUS       BD077292                890 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077292
VERSION     BD077292.1  GI:22622895
KEYWORDS    JP 2001520384-A/171.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 890)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 171 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/171
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   z12-3p.race
            FH   Key             Location/Qualifiers
            FT   source          1. .890
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                        virus)'.
FEATURES             Location/Qualifiers
     source          1. .890
                     /organism="unidentified"
                     /mol_type="genomic DNA"
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/db_xref="taxon:32644"

Alignment Scores:

Pred. No.:	50.6	Length:	890
Score:	239.00	Matches:	239
Percent Similarity:	92.28%	Conservative:	0
Best Local Similarity:	92.28%	Mismatches:	20
Query Match:	43.53%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x BD077292 (1-890)

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Qy        290 ValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGln 309
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Db          1 GTCGTCTCGGCCAATGGCGAGCCGACTGTCAAGTTATACACATCTGTTGAGAATGCACAG 60

Qy        310 GlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIle 329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGATAAGGGGATAGCTATTCCACATGACATAGATTTGGGCGACTCTCGTTTGGTAATC 120

Qy        330 GlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArg 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGGATTACGATAATCAGCACGAGCAGGACCGGCCCACCCCTTCGCCCGCCCCGTCTCGT 180

Qy        350 ProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyr 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTTTCTCGGTCCTCCGCGCTAATGATGCTTTGTGGCTTTCTCTTACCGCTGCTGAGTAT 240

Qy        370 AspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeu 389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACCAGACTACATATGGGTCGTCCACCAACCCGATGTATGTCTCAGACACTGTTACATTT 300

Qy        390 ValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThr 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTCAATGTGGCCACAGGGGCTCAGGCTGTCGCCCGTTCTCTTGATTGGTCTAAAGTTACC 360

Qy        410 LeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuPro 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGGACGGCCGCCCTCTTACTACCATCCAGCAGTACTCTAAGACATTTTATGTTCTCCCA 420

Qy        430 LeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsn 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTTCGCGGGAAGTTATCTTTTTGGGAGGCTGGCACAACTAAAGCCGGTTACCCTTATAAT 480

Qy        450 TyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAla 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TATAACACAACTGCTAGTGACCAGATTCTGATTGAAAACGCGGCTGGCCATCGTGTCGCT 540

Qy        470 IleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaVal 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATATCTACTTATACTACTAGCCTGGGCGCCGGCCCTGTGTCAGTTTCTGCGGTTGGTGTG 600

Qy        490 LeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAla 509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTAGCCCCACACTCGAGCCTTGCTATTCTTGAAGACACTGTTGACTATCCGGCCCGTGCT 660

Qy        510 HisThrPheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPhe 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACACTTTGATGACTTCTGTCCGGAATGCCGTGCCCTGGGTCTGCAGGGGTGTGCTTTT 720

Qy        530 GlnSerThrValAlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArgGlu 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAATCTACTATCGCTGAGCTCCAGCGTCTTAAAATGAAGGTAGGCAAAACCCGGGAG 777
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RESULT 63
AY714267
LOCUS AY714267 720 bp RNA linear VRL 15-SEP-2004
DEFINITION Hepatitis E virus isolate hKOR-JMA capsid protein gene, partial cds.
ACCESSION AY714267
VERSION AY714267.1 GI:51980112
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 720)
AUTHORS Ahn,J.M. and Yoo,H.S.
TITLE Identification of human Hepatitis E virus (HEV) and prevalence of anti-HEV antibodies in human populations in Korea
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 720)
AUTHORS Ahn,J.M. and Yoo,H.S.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-2004) Infectious Diseases, College of Veterinary Medicine and School of Agricultural Biotechnology, Seoul National University, Shinlim-Dong, San56-1, Seoul, Kwanak-Gu 151-742, South Korea

FEATURES Location/Qualifiers
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/db_xref="taxon:12461"
/country="South Korea"
CDS <1. .>720
/note="ORF2; structural protein"
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/protein_id="AAU20758.1"
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SRYTSTARHRLRRGADGTAELTTTAATRFMKDLYFTGTNGVGEVGRGIALTLFNLADT
LLGGLPTELISSAGGQLFYSRP"

Alignment Scores:

Pred. No.:	55	Length:	720
Score:	232.00	Matches:	232
Percent Similarity:	97.07%	Conservative:	0
Best Local Similarity:	97.07%	Mismatches:	7
Query Match:	42.26%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AY714267 (1-720)

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Qy         51 ProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSerAsn 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 CCTCTCTTGCCTCTTCAGGATGGCACCAACACTCATATTATGGCTACTGAAGCATCCAAT 63

Qy         71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 TATGCCCAGTATCGGGTTGTTCGAGCTACGATCCGTTACCGCCCGCTAGTGCCAAATGCT 123

Qy         91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 GTTGGTGGTTATGCTATTTCTATCTCTTTTTGGCCTCAAACCACAACTACCCCCACCTCT 183

Qy        111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GTTGACATGAATTCTATTACTTCCACTGATGTTAGGACTTTGGTCCAGCCCGGTATTGCC 243

Qy        131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 TCCGAGCTAGTCATCCCTAGCGAGCGCCTGCATTACCGTAATCAAGGCTGGCGCTCTGTT 303

Qy        151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAGACCACGGGTGTCGCTGAGGAGGAGGCTACATCTGGTCTGGTAATGCTTTGCATCCAT 363

Qy        171 GlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 GGCTCTCCTGTTAATTCTTATACTAACACACCTTACACTGGTGCACTAGGGCTTCTTGAT 423

Qy        191 PheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSer 210
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Db        424 TTCGCATTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACCAATACCCGTGTCTCC 483

Qy        211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230

Db        484 CGGTATACCAGCACAGCTCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAACTT 543

Qy        231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyVal 250

Db        544 ACTACCACAGCAGCCACACGCTTTATGAAAGATCTGTATTTTACTGGCACTAATGGCGTT 603

Qy        251 GlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGly 270

Db        604 GGTGAGGTGGGCCGTGGTATTGCTCTGACACTGTTTAATCTCGCTGATACGCTTCTCGGT 663

Qy        271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgPro 289

Db        664 GGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCT 720

RESULT 64
AY714269
LOCUS       AY714269                720 bp    RNA     linear   VRL 15-SEP-2004
DEFINITION  Hepatitis E virus isolate hKOR-SGK capsid protein gene, partial
            cds.
ACCESSION   AY714269
VERSION     AY714269.1  GI:51980116
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Identification of human Hepatitis E virus (HEV) and prevalence of
            anti-HEV antibodies in human populations in Korea
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2004) Infectious Diseases, College of Veterinary
            Medicine and School of Agricultural Biotechnology, Seoul National
            University, Shinlim-Dong, San56-1, Seoul, Kwanak-Gu 151-742, South
            Korea
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
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                     /isolate="hKOR-SGK"
                     /db_xref="taxon:12461"
                     /country="South Korea"
     CDS             <1. .>720
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                     /codon_start=1
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                     /protein_id="AAU20760.1"
                     /db_xref="GI:51980117"
                     /translation="NPLLPLQDGTNTHIMATEASNYAQYRVVRATIRYRPLVPNAVGG
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                     LLGGLPTELISSAGGQLFYSRP"

Alignment Scores:
Pred. No.:              55              Length:         720
Score:                  232.00          Matches:        232
Percent Similarity:     97.07%          Conservative:   0
Best Local Similarity:  97.07%          Mismatches:     7
Query Match:            42.26%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AY714269 (1-720)

Qy         51 ProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSerAsn 70

Db          4 CCTCTCTTGCCTCTTCAGGATGGCACCAACACTCATATTATGGCTACTGAAGCATCCAAT 63

Qy         71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90

Db         64 TATGCCCAGTATCGGGTTGTTCGAGCTACGATCCGTTACCGCCCGCTAGTGCCAAATGCT 123

Qy         91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110

Db        124 GTTGGTGGTTATGCTATTTCTATCTCTTTTTGGCCTCAAACCACAACTACCCCCACCTCT 183

Qy        111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130

Db        184 GTTGACATGAATTCTATTACTTCCACTGATGTCAGGACTTTGGTCCAGCCCGGTATTGCC 243

Qy        131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150

Db        244 TCCGAGCTAGTCATCCCTAGCGAGCGCCTGCATTACCGTAATCAAGGCTGGCGCTCTGTT 303

Qy        151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170

Db        304 GAGACCACGGGTGTCGCTGAGGAGGAGGCTACATCTGGTCTGGTAATGCTTTGCATCCAT 363

Qy        171 GlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190

Db        364 GGCTCTCCTGTTAATTCTTATACTAACACACCTTACACTGGTGCACTAGGGCTTCTTGAT 423

Qy        191 PheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSer 210

Db        424 TTCGCATTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACCAATACCCGTGTCTCC 483

Qy        211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230

Db        484 CGGTATACCAGCACAGCTCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAACTT 543

Qy        231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyVal 250

Db        544 ACTACCACAGCAGCCACACGCTTTATGAAAGATCTGTATTTTACTGGCACTAATGGCGTT 603

Qy        251 GlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGly 270

Db        604 GGTGAGGTGGGCCGTGGTATTGCTCTGACACTGTTTAATCTCGCTGATACGCTTCTCGGT 663

Qy        271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgPro 289

Db        664 GGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCT 720

RESULT 65
AY714270
LOCUS       AY714270                720 bp    RNA     linear   VRL 15-SEP-2004
DEFINITION  Hepatitis E virus isolate hKOR-DYL capsid protein gene, partial
            cds.
ACCESSION   AY714270
VERSION     AY714270.1  GI:51980118
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Identification of human Hepatitis E virus (HEV) and prevalence of
            anti-HEV antibodies in human populations in Korea
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2004) Infectious Diseases, College of Veterinary
            Medicine and School of Agricultural Biotechnology, Seoul National
            University, Shinlim-Dong, San56-1, Seoul, Kwanak-Gu 151-742, South
            Korea
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:                55              Length:         720
Score:                    232.00          Matches:        232
Percent Similarity:       97.07%          Conservative:   0
Best Local Similarity:    97.07%          Mismatches:     7
Query Match:              42.26%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AY714270 (1-720)

Qy         51 ProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSerAsn 70
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Qy         71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
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Qy        111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
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Db        484 CGGTATACCAGCACAGCTCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAACTT 543

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Db        664 GGTTTACCGACAGAATTGATTTCGTCAGCTGGGGGTCAACTGTTTTACTCCCGCCCT 720

RESULT 66
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DEFINITION  Hepatitis E virus isolate hKOR-HJY capsid protein gene, partial
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ACCESSION   AY714272
VERSION     AY714272.1  GI:51980122
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Identification of human Hepatitis E virus (HEV) and prevalence of
            anti-HEV antibodies in human populations in Korea
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2004) Infectious Diseases, College of Veterinary
            Medicine and School of Agricultural Biotechnology, Seoul National
            University, Shinlim-Dong, San56-1, Seoul, Kwanak-Gu 151-742, South
            Korea
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Alignment Scores:
Pred. No.:                55              Length:         720
Score:                    232.00          Matches:        232
Percent Similarity:       97.07%          Conservative:   0
Best Local Similarity:    97.07%          Mismatches:     7
Query Match:              42.26%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AY714272 (1-720)

Qy         51 ProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSerAsn 70
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Qy        171 GlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
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Db        664 GGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCT 720

RESULT 67
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LOCUS       AY641398                720 bp    RNA     linear   VRL 03-JUL-2004
DEFINITION  Hepatitis E virus isolate hKOR capsid protein gene, partial cds.
ACCESSION   AY641398
VERSION     AY641398.1  GI:49339406
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Identification of human Hepatitis E virus (HEV) and prevalence of
            anti-HEV antibodies in human populations in Korea
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-MAY-2004) Department of Infectious Diseases, College
            of Veterinary Medicine and School of Agricultural Biotechnology,
            Seoul National University, Shinlim-dong, san56-1, Seoul, Kwanak-Gu
            151-742, South Korea
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Alignment Scores:

Pred. No.:              55.8          Length:         720
Score:                  231.00        Matches:        231
Percent Similarity:     96.65%        Conservative:   0
Best Local Similarity:  96.65%        Mismatches:     8
Query Match:            42.08%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AY641398 (1-720)

Qy         51 ProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSerAsn 70
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Qy         71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
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Db         64 TATGCTCAGTATCGGGTTGTTCGAGCTACGATCCGCTATCGCCCGCTGGTGCCAAATGCT 123

Qy         91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
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Db        124 GTTGGTGGTTATGCTATCTCTATTTCTTTCTGGCCTCAAACCACAACCACCCCTACTTCT 183

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Qy        131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
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Qy        211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
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DEFINITION  Hepatitis E virus isolate hKOR-HSY capsid protein gene, partial
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ACCESSION   AY714268
VERSION     AY714268.1  GI:51980114
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Identification of human Hepatitis E virus (HEV) and prevalence of
            anti-HEV antibodies in human populations in Korea
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  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2004) Infectious Diseases, College of Veterinary
            Medicine and School of Agricultural Biotechnology, Seoul National
            University, Shinlim-Dong, San56-1, Seoul, Kwanak-Gu 151-742, South
            Korea
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                     LLGGLPTELISSAGGQLFYSRP"

Alignment Scores:
Pred. No.:                55.8          Length:          720
Score:                    231.00        Matches:         231
Percent Similarity:       96.65%        Conservative:    0
Best Local Similarity:    96.65%        Mismatches:      8
Query Match:              42.08%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x AY714268 (1-720)

Qy          51 ProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSerAsn 70
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Qy          71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
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Qy         111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
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Db         184 GTTGACATGAATTCTATTACTTCCACTGATGTTAGGACTTTGGTCCAGCCCGGTATTGCC 243

Qy         131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
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Db         244 TCCGAGCTAGTCATCCCTAGCGAGCGCCTGCATTACCGTAATCAAGGCTGGCGCTCTGTT 303

Qy         151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
               ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         304 GAGACCACGGGTGTCGCTGAGGAGGAGGCTACATCTGGTCTGGTAATGCTTTGCATCCAT 363

Qy         171 GlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
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Qy         191 PheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSer 210
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Qy         251 GlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGly 270
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Db         604 GGTGAGGTGGGCCGTGGTATTGCCCTGACACTGTTTAATCTCGCTGATACGCTTCTCGGT 663

Qy         271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgPro 289
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Db         664 GGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCT 720

RESULT 69
AY714271
LOCUS       AY714271                720 bp    RNA     linear   VRL 15-SEP-2004
DEFINITION  Hepatitis E virus isolate hKOR-NAB capsid protein gene, partial
            cds.
ACCESSION   AY714271
VERSION     AY714271.1  GI:51980120
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Identification of human Hepatitis E virus (HEV) and prevalence of
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  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2004) Infectious Diseases, College of Veterinary
            Medicine and School of Agricultural Biotechnology, Seoul National
            University, Shinlim-Dong, San56-1, Seoul, Kwanak-Gu 151-742, South
            Korea
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                     /note="ORF2; structural protein"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAU20762.1"
                     /db_xref="GI:51980121"
                     /translation="NPLLPLQDGTNTHIMATEASNYAQYRVVRATIRYRPLVPNAVGG
                     YAISISFWPQTTTTPTSVDMNSITSTDVRTLVQPGIASELVIPSERLHYRNQGWRSVE
                     TTGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRV
                     SRYTSTARHWLRRGADGTAELTTTAATRFMKDLYFTGTNGVGEVGRGIALTLFNLADT
                     LLGGLPTELISAAGGQLFYSRP"

Alignment Scores:
Pred. No.:                56.6          Length:          720
Score:                    230.00        Matches:         230
Percent Similarity:       96.23%        Conservative:    0
Best Local Similarity:    96.23%        Mismatches:      9
Query Match:              41.89%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x AY714271 (1-720)

Qy          51 ProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSerAsn 70
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           4 CCTCTCTTGCCTCTTCAGGATGGCACCAACACTCATATTATGGCTACTGAAGCATCCAAT 63

Qy          71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
               |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db          64 TATGCCCAGTATCGGGTTGTTCGAGCTACGATCCGTTACCGCCCGCTAGTGCCAAATGCT 123
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Qy          91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         124 GTTGGTGGTTATGCTATTTCTATCTCTTTTTGGCCTCAAACCACAACTACCCCCACCTCT 183

Qy         111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
               |||||||||||||||||||||||||||||||||||    ||||||||||||||||||||
Db         184 GTTGACATGAATTCTATTACTTCCACTGATGTTAGGACTTTGGTCCAGCCCGGTATTGCC 243

Qy         131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         244 TCCGAGCTAGTCATCCCTAGCGAGCGCCTGCATTACCGTAATCAAGGCTGGCGCTCTGTT 303

Qy         151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
               ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         304 GAGACCACGGGTGTCGCTGAGGAGGAGGCTACATCTGGTCTGGTAATGCTTTGCATCCAT 363

Qy         171 GlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
               ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         364 GGCTCTCCTGTTAATTCTTATACTAACACACCTTACACTGGTGCACTAGGGCTTCTTGAT 423

Qy         191 PheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSer 210
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         424 TTCGCATTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACCAATACCCGTGTCTCC 483

Qy         211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
               ||||||   ||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         484 CGGTATACCAGCACAGCTCGCCACTGGCTGCGCCGCGGTGCTGATGGGACCGCTGAACTT 543

Qy         231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyVal 250
               ||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||
Db         544 ACTACCACAGCAGCCACACGCTTTATGAAAGATCTGTATTTTACTGGCACTAATGGCGTT 603

Qy         251 GlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGly 270
               ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         604 GGTGAGGTGGGCCGTGGTATTGCTCTGACACTGTTTAATCTCGCTGATACGCTTCTCGGT 663

Qy         271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgPro 289
               ||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db         664 GGTTTACCGACAGAATTGATTTCGGCGGCTGGGGGTCAACTGTTTTACTCCCGCCCT 720

RESULT 70
AF020603
LOCUS       AF020603                680 bp    RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus TK104/91/Nepal capsid protein gene, partial cds.
ACCESSION   AF020603
VERSION     AF020603.1  GI:2731803
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 680)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 680)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th & Dahlia St, Washington, DC 20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .680
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TK104/91/Nepal"
                     /db_xref="taxon:12461"
     CDS             <1. .>680
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAB93554.1"
                     /db_xref="GI:2731804"
                     /translation="YAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMN
                     SITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGS
                     PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAEL
                     TTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSR
                     PVVSANGEP"

Alignment Scores:
Pred. No.:              60.5          Length:         680
Score:                  225.00        Matches:        225
Percent Similarity:     99.56%        Conservative:   0
Best Local Similarity:  99.56%        Mismatches:     1
Query Match:            40.98%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF020603 (1-680)

Qy          71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
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Db           1 TATGCCCAGTACCGGGTTGCCCGTGCCACGATCCGTTACCGCCCGTTGGTTCCCAACGCT 60

Qy          91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GTCGGCGGTTACGCCATCTCCATCTCATTCTGGCCACAGACCACCACCACCCCGACGTCC 120

Qy         111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GTTGATATGAATTCAATAACCTCGACGGATGTTCGTATCTTAGTCCAGCCCGGCATAGCC 180

Qy         131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TCTGAGCTTGTGATCCCAAGCGAGCGCCTACACTACCGTAACCAAGGTTGGCGCTCCGTC 240

Qy         151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GAGACCTCCGGGGTGGCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACAT 300

Qy         171 GlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
               ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 GGCTCACCCGTAAATTCCTATACTAATACACCTTATACCGGTGCCCTCGGGCTGCTGGAC 360

Qy         191 PheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSer 210
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TTTGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCC 420

Qy         211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 CGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTC 480

Qy         231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyVal 250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 ACCACCACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTT 540

Qy         251 GlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGly 270
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGC 600

Qy         271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProVal 290
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTT 660

Qy         291 ValSerAlaAsnGlyGlu 296
               ||||||||||||||||
Db         661 GTCTCAGCCAATGGCGAG 678

RESULT 71
AF020606
LOCUS       AF020606                680 bp    RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus TK4/95/Nepal capsid protein gene, partial cds.
ACCESSION   AF020606
VERSION     AF020606.1  GI:2731809
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KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 680)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 680)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th & Dahlia St, Washington, DC 20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .680
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TK4/95/Nepal"
                     /db_xref="taxon:12461"
     CDS             <1. .>680
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAB93557.1"
                     /db_xref="GI:2731810"
                     /translation="YAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMN
                     SITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGS
                     PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAEL
                     TTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSR
                     PVVSANGEP"

Alignment Scores:
Pred. No.:                60.5          Length:          680
Score:                    225.00        Matches:         225
Percent Similarity:       99.56%        Conservative:    0
Best Local Similarity:    99.56%        Mismatches:      1
Query Match:              40.98%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x AF020606 (1-680)

Qy         71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TATGCCCAGTACCGGGTTGCCCGTGCCACGATCCGTTACCGCCCGTTGGTTCCCAACGCT 60

Qy         91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTCGGCGGTTACGCCATCTCCATCTCATTCTGGCCACAGACCACCACCACCCCGACGTCC 120

Qy        111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTTGATATGAATTCAATAACCTCGACGGATGTTCGTATTCTAGTCCAGCCCGGCATAGCC 180

Qy        131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCTGAGCTTGTGATCCCAAGCGAGCGCCTACACTACCGTAACCAAGGTTGGCGCTCCGTC 240

Qy        151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGACCTCCGGGGTGGCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACAT 300

Qy        171 GlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCTCACCCGTAAATTCCTATACTAATACACCTTATACCGGTGCCCTCGGGCTGCTGGAC 360

Qy        191 PheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSer 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCC 420

Qy        211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTC 480

Qy        231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyVal 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCACCACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTT 540

Qy        251 GlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGly 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGC 600

Qy        271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProVal 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTT 660

Qy        291 ValSerAlaAsnGlyGlu 296
              ||||||||||||||||||
Db        661 GTCTCAGCCAATGGCGAG 678

RESULT 72
AF020607
LOCUS       AF020607                 680 bp    RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus Nep4/94/Nepal capsid protein gene, partial cds.
ACCESSION   AF020607
VERSION     AF020607.1  GI:2731811
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 680)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 680)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th & Dahlia St, Washington, DC 20307-5100, USA
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="Nep4/94/Nepal"
                     /db_xref="taxon:12461"
     CDS             <1. .>680
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                     /codon_start=1
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                     /protein_id="AAB93558.1"
                     /db_xref="GI:2731812"
                     /translation="YAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMN
                     SITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGS
                     PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAEL
                     TTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSR
                     PVVSANGEP"

Alignment Scores:
Pred. No.:                60.5          Length:          680
Score:                    225.00        Matches:         225
Percent Similarity:       99.56%        Conservative:    0
Best Local Similarity:    99.56%        Mismatches:      1
Query Match:              40.98%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x AF020607 (1-680)
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Qy          71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
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Db           1 TATGCCCAGTACCGGGTTGCCCGTGCCACGATCCGTTACCGCCCGTTGGTTCCCAACGCT 60

Qy          91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GTCGGCGGTTACGCCATTTCCATATCATTCTGGCCACAGACCACCACCACCCCGACGTCC 120

Qy         111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GTTGATATGAATTCAATAACCTCGACGGATGTTCGTATTCTAGTCCAGCCCGGCATAGCC 180

Qy         131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TCTGAGCTTGTGATCCCAAGCGAGCGCCTACACTACCGTAACCAAGGTTGGCGCTCCGTC 240

Qy         151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GAGACCTCCGGGGTGGCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACAT 300

Qy         171 GlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
               ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 GGCTCACCCGTAAATTCCTATACTAATACACCTTATACCGGTGCCCTCGGGCTGCTGGAC 360

Qy         191 PheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSer 210
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TTTGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCC 420

Qy         211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 CGTTACTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTC 480

Qy         231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyVal 250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 ACCACCACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTT 540

Qy         251 GlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGly 270
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGC 600

Qy         271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProVal 290
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTT 660

Qy         291 ValSerAlaAsnGlyGlu 296
               |||||||||||||||||
Db         661 GTCTCAGCCAATGGCGAG 678
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RESULT 73
AF020608
LOCUS       AF020608                680 bp    RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus TK78/87/Nepal capsid protein gene, partial cds.
ACCESSION   AF020608
VERSION     AF020608.1  GI:2731813
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 680)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 680)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th & Dahlia St, Washington, DC 20307-5100, USA
FEATURES             Location/Qualifiers
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                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAB93559.1"
                     /db_xref="GI:2731814"
                     /translation="YAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMN
                     SITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGS
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                     TTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSR
                     PVVSANGEP"
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Alignment Scores:
Pred. No.:              60.5          Length:         680
Score:                  225.00        Matches:        225
Percent Similarity:     99.56%        Conservative:   0
Best Local Similarity:  99.56%        Mismatches:     1
Query Match:            40.98%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF020608 (1-680)

Qy          71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 TATGCCCAGTACCGGGTTGCCCGTGCCACAATCCGTTACCGCCCGCTGGTCCCAAACGCT 60

Qy          91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
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Db          61 GTCGGCGGTTACGCCATCTCCATCTCATTCTGGCCACAGACCACCACCACCCCGACGTCC 120

Qy         111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GTTGATATGAATTCAATAACCTCGACGGATGTTCGTATCTTAGTCCAGCCTGGCATAGCC 180

Qy         131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
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Db         181 TCTGAGCTTGTGATCCCAAGCGAGCGCCTACACTATCGTAACCAGGGTTGGCGCTCCGTC 240

Qy         151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GAGACCTCCGGGGTGGCTGAGGAGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATACAT 300

Qy         171 GlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
               ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 GGCTCACCCGTAAATTCCTATACTAATACACCCTACACCGGTGCCCTCGGGCTGCTGGAC 360

Qy         191 PheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSer 210
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TTTGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCC 420

Qy         211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 CGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTC 480

Qy         231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyVal 250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 ACCACCACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTC 540

Qy         251 GlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGly 270
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGC 600

Qy         271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProVal 290
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTT 660

Qy         291 ValSerAlaAsnGlyGlu 296
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Db        661 GTCTCAGCCAATGGCGAG 678

RESULT 74
AF020604
LOCUS       AF020604                680 bp    RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus TK15/92/Nepal capsid protein gene, partial cds.
ACCESSION   AF020604
VERSION     AF020604.1  GI:2731805
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 680)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 680)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th & Dahlia St, Washington, DC 20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .680
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TK15/92/Nepal"
                     /db_xref="taxon:12461"
     CDS             <1. .>680
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAB93555.1"
                     /db_xref="GI:2731806"
                     /translation="YAQYRVARAAIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMN
                     SITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGS
                     PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAEL
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                     PVVSANGEP"

Alignment Scores:
Pred. No.:              61.4          Length:        680
Score:                  224.00        Matches:       224
Percent Similarity:     99.12%        Conservative:  0
Best Local Similarity:  99.12%        Mismatches:    2
Query Match:            40.80%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AF020604 (1-680)

Qy          71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
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Db           1 TATGCCCAGTACCGGGTTGCCCGTGCCGCGATCCGTTACCGCCCGTTGGTTCCCAACGCT 60

Qy          91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GTCGGCGGTTACGCCATCTCCATCTCATTCTGGCCACAGACCACCACCACCCCGACGTCC 120

Qy         111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GTTGATATGAATTCAATAACCTCGACGGATGTTCGTATTCTAGTCCAGCCCGGCATAGCC 180

Qy         131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TCTGAGCTTGTGATCCCAAGCGAGCGCCTACACTACCGTAACCAAGGTTGGCGCTCCGTC 240

Qy         151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GAGACCTCCGGGGTGGCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACAT 300

Qy         171 GlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
               ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 GGCTCACCCGTAAATTCCTATACTAATACACCTTATACCGGTGCCCTCGGGCTGCTGGAC 360

Qy         191 PheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSer 210
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TTTGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCC 420

Qy         211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 CGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTC 480

Qy         231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyVal 250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 ACCACCACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTT 540

Qy         251 GlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGly 270
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGC 600

Qy         271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProVal 290
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTT 660

Qy         291 ValSerAlaAsnGlyGlu 296
               |||||||||||||||||
Db         661 GTCTCAGCCAATGGCGAG 678

RESULT 75
AF020605
LOCUS       AF020605                680 bp    RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus TK5/95/Nepal capsid protein gene, partial cds.
ACCESSION   AF020605
VERSION     AF020605.1  GI:2731807
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 680)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 680)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th & Dahlia St, Washington, DC 20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .680
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TK5/95/Nepal"
                     /db_xref="taxon:12461"
     CDS             <1. .>680
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAB93556.1"
                     /db_xref="GI:2731808"
                     /translation="YAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMN
                     SITSMDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGS
                     PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAEL
                     TTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSR
                     PVVSANGEP"

Alignment Scores:
Pred. No.:              61.4          Length:        680
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Score:                  224.00          Matches:        224
Percent Similarity:     99.12%          Conservative:   0
Best Local Similarity:  99.12%          Mismatches:     2
Query Match:            40.80%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF020605 (1-680)

Qy         71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
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Db          1 TATGCCCAGTACCGGGTTGCCCGTGCCACGATCCGTTACCGCCCGTTGGTTCCCAACGCT 60

Qy         91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTCGGCGGTTACGCCATCTCCATCTCATTCTGGCCACAGACCACCACCACCCCGACGTCC 120

Qy        111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
              |||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db        121 GTTGATATGAATTCAATAACCTCGATGGATGTTCGTATTCTAGTCCAGCCCGGCATAGCC 180

Qy        131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCTGAGCTTGTGATCCCAAGCGAGCGCCTACACTACCGTAACCAAGGTTGGCGCTCCGTC 240

Qy        151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGACCTCCGGGGTGGCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACAT 300

Qy        171 GlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
              ||||||    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCTCACCCGTAAATTCCTATACTAATACACCTTATACCGGTGCCCTCGGGCTGCTGGAC 360

Qy        191 PheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSer 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCC 420

Qy        211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTC 480

Qy        231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyVal 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCACCACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTT 540

Qy        251 GlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGly 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGC 600

Qy        271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProVal 290
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Db        601 GGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTT 660

Qy        291 ValSerAlaAsnGlyGlu 296
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Db        661 GTCTCAGCCAATGGCGAG 678

RESULT 76
AX181828
LOCUS       AX181828                678 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 110 from Patent WO0146696.
ACCESSION   AX181828
VERSION     AX181828.1  GI:15133148
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 110 28-JUN-2001;
            ABBOTT LABORATORIES (US)

FEATURES             Location/Qualifiers
     source          1. .678
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
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                     /note="us2-667"

Alignment Scores:
Pred. No.:              72.6            Length:         678
Score:                  212.00          Matches:        212
Percent Similarity:     94.22%          Conservative:   0
Best Local Similarity:  94.22%          Mismatches:     13
Query Match:            38.62%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AX181828 (1-678)

Qy        268 LeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSer 287
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CTTCTTGGTGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGCCAACTGTTTTACTCC 62

Qy        288 ArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsn 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATATACATCTGTTGAGAAT 122

Qy        308 AlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSerArgVal 327
              ||||||||||||||||||    ||||||||||||||||||||||    |||||||||
Db        123 GCGCAGCAAGACAAGGGCATCACCATTCCACATGATATAGACCTGGGTGACTCCCGTGTG 182

Qy        328 ValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaPro 347
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GTTATCCAGGATTATGATAACCAGCAYGAGCAAGACCGACCTACTCCGTCACCTGCCCCC 242

Qy        348 SerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAla 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 TCTCGCCCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTTTCCCTCACTGCCGCT 302

Qy        368 GluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerVal 387
              ||||||||||||    ||||||||||||||||||    |||    ||||||||||||    |||
Db        303 GAGTATGACCAGACTACGTATGGGTCGTCCACCAACCCTATGTATGTCTCTGACACAGTT 362

Qy        388 ThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLys 407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db        363 ACGCTTGTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCCCTTGATTGGTCTAAA 422

Qy        408 ValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheVal 427
              ||||||||||||||||||||||    ||||||||||||||||||||||||||||    |||
Db        423 GTTACTCTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCTAAGACATTTTATGTT 482

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 CTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACTAAGGCCGGCTACCCT 542

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||||||    |||    ||||||||||||||||||||
Db        543 TACAATTATAATACTACCGCTAGTGACCAAATTTTGATTGAGAATGCGGCCGGCCACCGT 602

Qy        468 ValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaVal 487
              ||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||
Db        603 GTCGCTATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACCTCGATCTCTGCGGTC 662

Qy        488 AlaValLeuAlaPro 492
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Db        663 GGTGTACTAGCTCCA 677

RESULT 77
BD077228
LOCUS       BD077228                678 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077228
VERSION     BD077228.1  GI:22622831
KEYWORDS    JP 2001520384-A/107.
SOURCE      unidentified
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  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 678)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 107 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/107
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   us2-667
            FH   Key             Location/Qualifiers
            FT   source          1. .678
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                        virus)'.
FEATURES             Location/Qualifiers
     source          1. .678
                     /organism="unidentified"
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                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              72.6          Length:        678
Score:                  212.00        Matches:       212
Percent Similarity:     94.22%        Conservative:  0
Best Local Similarity:  94.22%        Mismatches:    13
Query Match:            38.62%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x BD077228 (1-678)

Qy        268 LeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSer 287
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Db          3 CTTCTTGGTGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGCCAACTGTTTTACTCC 62

Qy        288 ArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsn 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATATACATCTGTTGAGAAT 122

Qy        308 AlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSerArgVal 327
              |||||||||||||||||||  |||||||||||||||||||||||||  |||||||||
Db        123 GCGCAGCAAGACAAGGGCATCACCATTCCACATGATATAGACCTGGGTGACTCCCGTGTG 182

Qy        328 ValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaPro 347
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GTTATCCAGGATTATGATAACCAGCAYGAGCAAGACCGACCTACTCCGTCACCTGCCCCC 242

Qy        348 SerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAla 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 TCTCGCCCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTTTCCCTCACTGCCGCT 302

Qy        368 GluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerVal 387
              ||||||||||||  ||||||||||||||||||  |||  ||||||||||  |||
Db        303 GAGTATGACCAGACTACGTATGGGTCGTCCACCAACCCTATGTATGTCTCTGACACAGTT 362

Qy        388 ThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLys 407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        363 ACGCTTGTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCCCTTGATTGGTCTAAA 422

Qy        408 ValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheVal 427
              ||||||||||||||||||||||  ||||||||||||||||||||||||||  |||
Db        423 GTTACTCTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCTAAGACATTTTATGTT 482

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 CTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACTAAGGCCGGCTACCCT 542

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||||||  |||  ||||||||||||||||||||||
Db        543 TACAATTATAATACTACCGCTAGTGACCAAATTTTGATTGAGAATGCGGCCGGCCACCGT 602

Qy        468 ValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaVal 487
              ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        603 GTCGCTATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACCTCGATCTCTGCGGTC 662

Qy        488 AlaValLeuAlaPro 492
              |||||||||||||
Db        663 GGTGTACTAGCTCCA 677

RESULT 78
AF170450
LOCUS       AF170450                617 bp    RNA     linear   VRL 09-AUG-1999
DEFINITION  Hepatitis E virus structural protein 2 gene, partial cds.
ACCESSION   AF170450
VERSION     AF170450.1  GI:5713199
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 617)
  AUTHORS   Nguyen,T.N., Nguyen,T.V., Hoang,T.N., Meng,J.H., Purdy,M.A.,
            Khudyakov,Y. and Fields,H.W.
  TITLE     Partial sequence and phylogenetic analysis HEV isolated from Viet
            Nam
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 617)
  AUTHORS   Nguyen,T.N., Nguyen,T.V., Hoang,T.N., Meng,J.H., Purdy,M.A.,
            Khudyakov,Y. and Fields,H.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-1999) Hepatitis Laboratory, National Institute of
            Hygiene and Epidemiology, 1 Yersin, Hanoi 10000, Viet Nam
FEATURES             Location/Qualifiers
     source          1. .617
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:12461"
                     /map="ORF2"
                     /country="Viet Nam"
     CDS             <1. .>617
                     /note="ORF2"
                     /codon_start=1
                     /product="structural protein 2"
                     /protein_id="AAD47842.1"
                     /db_xref="GI:5713200"
                     /translation="GLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTN
                     TRVSRYSSTARHRLRRSADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNL
                     ADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDL
                     GESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAA"

Alignment Scores:
Pred. No.:              81.9          Length:        617
Score:                  203.00        Matches:       203
Percent Similarity:     99.02%        Conservative:  0
Best Local Similarity:  99.02%        Mismatches:    2
Query Match:            36.98%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AF170450 (1-617)

Qy        163 GlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyr 182
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db          1 GGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAATACACCCTAT 60

Qy        183 ThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrPro 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGTAACCTTACCCCT 120
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Qy        203 GlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArg 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTAACACTAATACGCGGGTCTCCCGCTATTCCAGCACTGCTCGCCACCGCCTTCGCCGC 180

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGTGCGGACGGGACTGCTGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTC 240

Qy        243 TyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPhe 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TATTTTACTAGTACTAATGGTGTCGGTGAAATCGGCCGCGGGATAGCCCTCACCCTGTTC 300

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAATTGATTTCGTCGGCTGGCGGC 360

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGCTGTTCTACTCTCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGCTGTAT 420

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACATCTGTAGAGAATGCTCAGCAAGATAAGGGTATTGCAATCCCGCATGACATTGACCTC 480

Qy        323 GlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGGGAATCTCGTGTGGTTATCCAGGATTATGATAACCAACATGAACAAGACCGGCCGACA 540

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCTTCTCCAGCCCCATCGCGCCCTTTTTCTGTCCTTCGGGCTAATGATGTGCTCTGGCTC 600

Qy        363 SerLeuThrAlaAla 367
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Db        601 TCTCTCACCGCCGCC 615

RESULT 79
HEU62654
LOCUS       HEU62654                 506 bp    mRNA    linear   VRL 26-JAN-1999
DEFINITION  Hepatitis E virus structural protein 2 mRNA, partial cds.
ACCESSION   U62654
VERSION     U62654.1  GI:4097490
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 506)
  AUTHORS   Van Cuyck-Gandre,H., Zhang,H., Clements,N., Caudill,J., Cohen,S.,
            Coursaget,P., Buisson,Y. and Longer,C.
  TITLE     Partial sequences of HEV from Algerian and Chad isolates
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 506)
  AUTHORS   Van Cuyck-Gandre,H., Zhang,H., Clements,N., Caudill,J., Cohen,S.,
            Coursaget,P., Buisson,Y. and Longer,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-1996) Virus Diseases, WRAIR, Bld. 40, Washington,
            D.C. 20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .506
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Chad T5"
                     /db_xref="taxon:12461"
                     /note="isolated from the stools of infected patients from
                     Chad, 1981 outbreak"
     CDS             <1. .>506
                     /note="ORF2; capsid protein; polyprotein"
                     /codon_start=1
                     /product="structural protein 2"
                     /protein_id="AAD09495.1"
                     /db_xref="GI:4097491"
                     /translation="NTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNG
                     VGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVEN
                     AQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLT
                     AAEYDQST"

Alignment Scores:
Pred. No.:              131          Length:        506
Score:                  168.00       Matches:       168
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0
Query Match:            30.60%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x HEU62654 (1-506)

Qy        206 AsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAsp 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATACGCGGGTCTCGCGTTACTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGAC 60

Qy        226 GlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThr 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGGACTGCCGAGCTCACCACCACGGCTGCTACCCGTTTTATGAAGGACCTCTATTTCACT 120

Qy        246 SerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAla 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGTACCAATGGTGTCGGTGAGATCGGCCGCGGGATAGCTCTCACCCTGTTCAACCTTGCT 180

Qy        266 AspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPhe 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACACTCTGCTTGGTGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTC 240

Qy        286 TyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerVal 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAGCTGTATACATCTGTA 300

Qy        306 GluAsnAlaGlnGlnAspLysGlyIleAlaIleProHisAspIleAspLeuGlyGluSer 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGGGAATCT 360

Qy        326 ArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerPro 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGTGGTTATTCAGGACTATGATAACCAACATGAACAGGACCGGCCGACGCCTTCGCCA 420

Qy        346 AlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThr 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCTCCATCGCGCCCTTTTTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTCTCTCTCACC 480

Qy        366 AlaAlaGluTyrAspGlnSerThr 373
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Db        481 GCTGCCGAGTATGACCAGTCCACC 504

RESULT 80
AF332620
LOCUS       AF332620                 476 bp ss-RNA     linear   VRL 02-FEB-2002
DEFINITION  Swine hepatitis E virus NLSW15 structural protein gene, partial
            cds.
ACCESSION   AF332620
VERSION     AF332620.1  GI:18478362
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine in the Netherlands are closely
            related to human hepatitis E virus sequences
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
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  JOURNAL   Submitted (20-DEC-2000) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
     source          1. .476
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="NLSW15"
                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAL73138.1"
                     /db_xref="GI:18478363"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPT
                     ELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGDSRVVIQ"

Alignment Scores:
Pred. No.:                162             Length:         476
Score:                    152.00          Matches:        152
Percent Similarity:       96.82%          Conservative:   0
Best Local Similarity:    96.82%          Mismatches:     5
Query Match:              27.69%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AF332620 (1-476)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTTAACTCCTACACCAATACACCCTATACCGGGGCATTGGGGCTCCTCGACTTTGCACTC 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGCTACACT 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCACAGCCCGGCACCGTCTGCGTCGTGGTGCCGATGGGACGGCTGAGCTTACGACCACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||
Db        186 GCAGCCACACGTTTTATGAAGGACTTGCATTTCACCGGGACAAACGGCGTTGGTGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGTATAGCCCTAACGTTGTTTAATCTTGCTGACACACTTCTCGGCGGGCTACCG 305

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ACAGAATTRATTTCGTCGGCTGGAGGTCAGTTGTTTTACTCCCGCCCGGTCGTCTCAGCC 365

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 AATGGCGAGCCGACTGTTAAGCTATACACCTCTGTCGAGAATGCACAGCAGGACAAGGGC 425

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGln 330
              |||||||||||||||||||||||||||  ||||||||||||||||||||
Db        426 ATTGCTATACCGCATGATATAGACTTAGGGGACTCCCGTGTGGTCATACAA 476

RESULT 81
AF336290
LOCUS       AF336290                476 bp ss-RNA     linear   VRL 05-MAR-2002
DEFINITION  Swine hepatitis E virus isolate NLSW20 structural protein gene,
            partial cds.
ACCESSION   AF336290
VERSION     AF336290.1  GI:18478608
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I.,
            Vivo,A., Kooreman,M. and de Roda Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine related to sequences in
            humans, The Netherlands
  JOURNAL   Emerging Infect. Dis. 7 (6), 970-976 (2001)
  MEDLINE   21614760
   PUBMED   11747723
REFERENCE   2  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
     source          1. .476
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW20"
                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAL73215.1"
                     /db_xref="GI:18478609"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPT
                     ELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGDSRVVIQ"

Alignment Scores:
Pred. No.:                162             Length:         476
Score:                    152.00          Matches:        152
Percent Similarity:       96.82%          Conservative:   0
Best Local Similarity:    96.82%          Mismatches:     5
Query Match:              27.69%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AF336290 (1-476)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTTAATTCTTACACCAACACCCCCTACACTGGGGCGCTTGGGCTTCTTGATTTTGCTTTA 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTAGGAACTTGACACCCGGGAACACCAACACCCGTGTTTCACGGTACACA 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGTACAGCCCGTCACCGGCTGCGCCGCGGTGCTGATGGCACCGCCGAACTCACCACTACA 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||
Db        186 GCGGCCACGCGTTTTATGAAGGACCTGCACTTCACCGGTACGAATGGGGTTGGTGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGTCGTGGTATCGCCCTTACACTCTTTAATCTTGCTGACACGCTTCTCGGTGGTTTGCCG 305

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ACAGAATTRATTTCGTCGGCTGGAGGCCAGCTATTTTACTCCCGTCCGGTTGTCTCAGCC 365

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 AATGGCGAGCCGACTGTTAAGTTATACACCTCCGTCGAGAATGCACAGCAGGATAAGGGC 425

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGln 330
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Db        426 ATTGCTATACCGCATGATATAGATTTGGGAGATTCCCGTGTGGTTATTCAG 476

RESULT 82
AF336292
LOCUS       AF336292                476 bp ss-RNA     linear   VRL 05-MAR-2002
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DEFINITION  Swine hepatitis E virus isolate NLSW28 structural protein gene,
            partial cds.
ACCESSION   AF336292
VERSION     AF336292.1  GI:18478614
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I.,
            Vivo,A., Kooreman,M. and de Roda Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine related to sequences in
            humans, The Netherlands
  JOURNAL   Emerging Infect. Dis. 7 (6), 970-976 (2001)
  MEDLINE   21614760
   PUBMED   11747723
REFERENCE   2  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
     source          1. .476
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW28"
                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAL73217.1"
                     /db_xref="GI:18478615"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPT
                     ELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGDSRVVIQ"

Alignment Scores:
Pred. No.:              162          Length:        476
Score:                  152.00       Matches:       152
Percent Similarity:     96.82%       Conservative:  0
Best Local Similarity:  96.82%       Mismatches:    5
Query Match:            27.69%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AF336292 (1-476)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTCAACTCTTACACTAACACACCCTATACCGGGGCATTAGGGCTCCTCGATTTTGCACTC 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
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Db         66 GAGCTTGAATTTAGGAACTTGACCCCCGGGAACACAAACACCCGTGTGTCCCGTTACACT 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCACAGCTCGACATCGTTTGCGTCGTGGCGCCGATGGGACAGCCGAGCTCACGACCACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
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Db        186 GCAGCCACACGTTTCATGAAGGACTTGCATTTCACCGGGACAAACGGCGTTGGTGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
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Db        246 GGCCGTGGTATAGCCCTAACGTTATTTAATCTTGCTGATACACTTCTCGGTGGGCTACCG 305

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
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Db        306 ACAGAATTRATTTCGTCGGCTGGAGGTCAGTTGTTCTACTCCCGCCCGGTCGTCTCAGCC 365

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
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Db        366 AATGGCGAGCCGACTGTTAAGTTATACACCTCTGTCGAGAATGCACAGCAGGACAAGGGC 425

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGln 330
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Db        426 ATTGCTATACCACACGATATAGACTTAGGGGACTCCCGTGTGGTTATACAA 476

RESULT 83
AF336293
LOCUS       AF336293                476 bp ss-RNA     linear   VRL 05-MAR-2002
DEFINITION  Swine hepatitis E virus isolate NLSW36 structural protein gene,
            partial cds.
ACCESSION   AF336293
VERSION     AF336293.1  GI:18478617
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I.,
            Vivo,A., Kooreman,M. and de Roda Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine related to sequences in
            humans, The Netherlands
  JOURNAL   Emerging Infect. Dis. 7 (6), 970-976 (2001)
  MEDLINE   21614760
   PUBMED   11747723
REFERENCE   2  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
     source          1. .476
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW36"
                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAL73218.1"
                     /db_xref="GI:18478618"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPT
                     ELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGDSRVVIQ"

Alignment Scores:
Pred. No.:              162          Length:        476
Score:                  152.00       Matches:       152
Percent Similarity:     96.82%       Conservative:  0
Best Local Similarity:  96.82%       Mismatches:    5
Query Match:            27.69%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AF336293 (1-476)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
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Db          6 GTTAATTCTTATACCAATACCCCCTATACCGGGGCGCTTGGGCTCCTTGATTTTGCTTTA 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
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Db         66 GAACTTGAGTTCAGGAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACA 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGTACAGCCCGTCATCGGCTGCGTCGCGGTGCTGATGGCACCGCCGAACTTACTACTACA 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
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                ||||||||||||||||||||||||||  ||||||  ||||||||||||||||||
Db        186 GCAGCTACACGTTTCATGAAGGACCTGCACTTCACCGGCACGAATGGGGTCGGCGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
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Db        246 GGCCGTGGTATCGCTCTCACACTCTTTAATCTTGCTGATACGCTCCTCGGTGGGTTACCG 305

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
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Db        306 ACAGAATTRATTTCGTCGGCTGGGGGACAGTTGTTCTACTCCCGCCCCGTCGTCTCAGCC 365

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
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Db        366 AATGGCGAACCGACTGTTAAGTTGTATACATCTGTGGAGAATGCACAGCAAGATAAAGGG 425

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGln 330
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Db        426 ATTGCCATTCCACATGACATAGATCTGGGCGACTCTCGTGTTGTCATTCAG 476

RESULT 84
AF336294
LOCUS       AF336294                476 bp ss-RNA     linear   VRL 05-MAR-2002
DEFINITION  Swine hepatitis E virus isolate NLSW82 structural protein gene,
            partial cds.
ACCESSION   AF336294
VERSION     AF336294.1  GI:18478620
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I.,
            Vivo,A., Kooreman,M. and de Roda Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine related to sequences in
            humans, The Netherlands
  JOURNAL   Emerging Infect. Dis. 7 (6), 970-976 (2001)
  MEDLINE   21614760
   PUBMED   11747723
REFERENCE   2  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
     source          1. .476
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW82"
                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAL73219.1"
                     /db_xref="GI:18478621"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPT
                     ELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGDSRVVIQ"

Alignment Scores:
Pred. No.:              162             Length:         476
Score:                  152.00          Matches:        152
Percent Similarity:     96.82%          Conservative:   0
Best Local Similarity:  96.82%          Mismatches:     5
Query Match:            27.69%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF336294 (1-476)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          6 GTCAATTCCTATACCAACACGCCCTATACTGGGGCATTGGGGCTCCTCGACTTTGCACTC 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAATTTAGAAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGTTACACT 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCACAGCCCGACATCGTTTACGTCGTGGCGCCGATGGGACAGCCGAGCTCACAACCACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
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Db        186 GCAGCCACACGTTTTATGAAGGACTTGCACTTCACCGGGACAAATGGCGTTGGTGAGGTA 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGCATAGCTCTAACTCTATTTAATCTTGCTGATACACTTCTCGGTGGGTTGCCG 305

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
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Db        306 ACAGAATTGATTTCGTCGGCTGGAGGTCAACTGTTCTACTCCCGCCCGGTTGTCTCAGCC 365

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
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Db        366 AATGGCGAGCCGACTGTTAAGTTATACACCTCTGTCGAGAATGCACAGCAGGACAAGGGC 425

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGln 330
              ||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        426 ATTGCTATACCACACGATATAGACCTAGGGGATTCCCGTGTGGTTATACAA 476

RESULT 85
AF336295
LOCUS       AF336295                476 bp ss-RNA     linear   VRL 05-MAR-2002
DEFINITION  Swine hepatitis E virus isolate NLSW85 structural protein gene,
            partial cds.
ACCESSION   AF336295
VERSION     AF336295.1  GI:18478622
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I.,
            Vivo,A., Kooreman,M. and de Roda Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine related to sequences in
            humans, The Netherlands
  JOURNAL   Emerging Infect. Dis. 7 (6), 970-976 (2001)
  MEDLINE   21614760
   PUBMED   11747723
REFERENCE   2  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
     source          1. .476
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW85"
                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /note="ORF2"
                     /codon_start=3
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                     /db_xref="GI:18478623"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPT
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Alignment Scores:
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Pred. No.:              162           Length:        476
Score:                  152.00        Matches:       152
Percent Similarity:     96.82%        Conservative:  0
Best Local Similarity:  96.82%        Mismatches:    5
Query Match:            27.69%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AF336295 (1-476)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
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Db          6 GTTAATTCCTATACCAACACGCCCTATACCGGGGCACTGGGGCTTCTCGACTTTGCACTC 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
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Db         66 GAGCTTGAATTTAGAAATTTGACCCCTGGGAACACCAACACCCGTGTGTCCCGTTATACC 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
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Db        126 AGCACAGCCCGACACCGTTTGCGTCGCGGTGCTGATGGTACAGCCGAGCTTACGACCACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
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Db        186 GCAGCCACACGTTTTATGAAGGACTTGCATTTCACCGGGACAAATGGTGTTGGCGAGGTA 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGAATCGCCCTAACGCTATTTAATCTTGCTGATACACTTCTCGGCGGGCTGCCG 305

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ACAGAATTRATTTCGTCGGCTGGAGGTCAACTGTTCTACTCCCGCCCGGTTGTCTCAGCC 365

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
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Db        366 AATGGCGAGCCGACTGTTAAGTTATACACCTCTGTCGAGAATGCACAGCAGGACAAGGGC 425

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGln 330
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Db        426 ATTGCCATACCACACGATATAGACTTAGGGGATTCTCGTGTGGTTATACAA 476

RESULT 86
AF336296
LOCUS       AF336296                476 bp ss-RNA     linear   VRL 05-MAR-2002
DEFINITION  Swine hepatitis E virus isolate NLSW97 structural protein gene,
            partial cds.
ACCESSION   AF336296
VERSION     AF336296.1  GI:18478625
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I.,
            Vivo,A., Kooreman,M. and de Roda Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine related to sequences in
            humans, The Netherlands
  JOURNAL   Emerging Infect. Dis. 7 (6), 970-976 (2001)
  MEDLINE   21614760
   PUBMED   11747723
REFERENCE   2  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
     source          1. .476
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW97"
                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAL73221.1"
                     /db_xref="GI:18478626"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPT
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Alignment Scores:
Pred. No.:              162           Length:        476
Score:                  152.00        Matches:       152
Percent Similarity:     96.82%        Conservative:  0
Best Local Similarity:  96.82%        Mismatches:    5
Query Match:            27.69%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AF336296 (1-476)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
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Db          6 GTTAATTCCTATACTAATACACCCTATACCGGGGCTTTGGGGCTCCTCGACTTTGCGCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
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Db         66 GAGCTTGAATTTAGAAATTTGACCCCTGGGAACACTAACACCCGTGTTTCCCGTTACACT 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
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Db        126 AGTACAGCCCGGCACCGTTTGCGTCGTGGTGCCGATGGGACAGCTGAGCTTACAACCACC 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
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Db        186 GCAGCCACACGTTTTATGAAGGACTTACATTTCACCGGGACAAATGGTGTTGGCGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGTATAGCCCTAACGCTATTCAATCTTGCTGATACACTTCTCGGTGGCCTGCCG 305

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ACAGAATTRATTTCGTCGGCTGGAGGTCAATTGTTTTACTCCCGCCCGGTTGTCTCAGCC 365

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
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Db        366 AATGGCGAGCCGACTGTTAAGTTGTACACCTCTGTCGAGAATGCACAGCAGGACAAGGGC 425

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGln 330
              ||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        426 ATTGCTATACCACACGATATAGATCTAGGGGATTCTCGTGTGGTTATACAA 476

RESULT 87
AF336298
LOCUS       AF336298                476 bp ss-RNA     linear   VRL 05-MAR-2002
DEFINITION  Swine hepatitis E virus isolate NLSW105 structural protein gene,
            partial cds.
ACCESSION   AF336298
VERSION     AF336298.1  GI:18478631
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I.,
            Vivo,A., Kooreman,M. and de Roda Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine related to sequences in
            humans, The Netherlands
  JOURNAL   Emerging Infect. Dis. 7 (6), 970-976 (2001)
  MEDLINE   21614760
   PUBMED   11747723
REFERENCE   2  (bases 1 to 476)
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  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
     source          1. .476
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                     /mol_type="genomic RNA"
                     /isolate="NLSW105"
                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAL73223.1"
                     /db_xref="GI:18478632"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPT
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Alignment Scores:
Pred. No.:              162          Length:         476
Score:                  152.00       Matches:        152
Percent Similarity:     96.82%       Conservative:   0
Best Local Similarity:  96.82%       Mismatches:     5
Query Match:            27.69%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AF336298 (1-476)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTTAATTCTTATACCAATACTCCTTACACCGGGGCGCTTGGACTTCTCGACTTTGCCCTA 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
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Db         66 GAGCTTGAGTTTAGGAACCTGACACCTGGGAACACTAACACCCGTGTTTCCCGGTATACA 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCACAGCCCGCCATCGGCTGCGCCGCGGTGCTGATGGCACCGCCGAGCTTACCACCACG 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||||    ||||||    ||||||||||||||||||||
Db        186 GCGGCCACTCGCTTTATGAAGGACCTGCACTTCACCGGTACGAATGGGGTCGGTGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGTCGAGGTATTGCTCTCACACTCTTTAATCTTGCTGATACGCTTCTCGGTGGTTTGCCG 305

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ACAGAATTRATTTCGTCGGCTGGGGGACAGCTGTTCTACTCCCGCCCCGTCGTCTCAGCC 365

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 AATGGCGAGCCGACCGTTAAGTTATATACATCTGTAGAGAATGCGCAGCAGGATAAAGGG 425

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGln 330
              ||||||||||||||||||||||||||||||    ||||||||||||||||||
Db        426 ATTGCTATCCCACATGACATAGATCTGGGTGACTCTCGAGTGGTCATTCAA 476

RESULT 88
AF336297
LOCUS       AF336297                476 bp ss-RNA     linear   VRL 05-MAR-2002
DEFINITION  Swine hepatitis E virus isolate NLSW99 structural protein gene,
            partial cds.
ACCESSION   AF336297
VERSION     AF336297.1  GI:18478628
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I.,
            Vivo,A., Kooreman,M. and de Roda Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine related to sequences in
            humans, The Netherlands
  JOURNAL   Emerging Infect. Dis. 7 (6), 970-976 (2001)
  MEDLINE   21614760
   PUBMED   11747723
REFERENCE   2  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
     source          1. .476
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW99"
                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAL73222.1"
                     /db_xref="GI:18478629"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGMNGVGEVGRGIALTLFNLADTLLGGLPT
                     ELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGDSRVVIQ"

Alignment Scores:
Pred. No.:              165          Length:         476
Score:                  151.00       Matches:        151
Percent Similarity:     96.18%       Conservative:   0
Best Local Similarity:  96.18%       Mismatches:     6
Query Match:            27.50%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AF336297 (1-476)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
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Db          6 GTTAATTCTTATACCAATACCCCCTACACCGGGGCACTTGGACTCCTTGACTTTGCCCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTAGGAACCTGACACCCGGGAACACTAACACCCGTGTCTCCCGGTATACG 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGCACCGCCGAGCTTACCACCACG 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||||    ||||||    ||||||||||||||||||||
Db        186 GCGGCCACTCGCTTCATGAAGGACCTGCACTTCACCGGTATGAATGGGGTCGGTGAAGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGTCGAGGTATTGCTCTCACACTCTTTAATCTCGCTGATACGCTTCTCGGTGGTCTGCCG 305

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ACAGAATTRATTTCGTCGGCTGGAGGTCAACTGTTTTACTCCCGCCCGGTTGTCTCAGCC 365

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 AATGGCGAGCCGACTGTTAAGTTATACACCTCTGTCGAGAATGCACAGCAAGACAAGGGC 425

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGln 330
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Db        426 ATTGCCATACCACACGATATAGATTTAGGGGATTCCCGAGTGGTCATACAA 476
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RESULT 89
AF336299
LOCUS       AF336299                476 bp ss-RNA     linear   VRL 05-MAR-2002
DEFINITION  Swine hepatitis E virus isolate NLSW122 structural protein gene,
            partial cds.
ACCESSION   AF336299
VERSION     AF336299.1  GI:18478634
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I.,
            Vivo,A., Kooreman,M. and de Roda Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine related to sequences in
            humans, The Netherlands
  JOURNAL   Emerging Infect. Dis. 7 (6), 970-976 (2001)
  MEDLINE   21614760
   PUBMED   11747723
REFERENCE   2  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
     source          1. .476
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW122"
                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAL73224.1"
                     /db_xref="GI:18478635"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGMNGVGEVGRGIALTLFNLADTLLGGLPT
                     ELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGDSRVVIQ"

Alignment Scores:
Pred. No.:              165           Length:        476
Score:                  151.00        Matches:       151
Percent Similarity:     96.18%        Conservative:  0
Best Local Similarity:  96.18%        Mismatches:    6
Query Match:            27.50%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AF336299 (1-476)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTTAATTCCTATACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGATTTTGCACTA 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAATTTAGAAACCTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACC 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCACAGCCCGCCACCGGCTGCGCCGCGGCGCTGATGGTACTGCTGAGCTTACTACCACA 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||   ||||||     ||||||||||||||||
Db        186 GCAGCCACACGTTTCATGAAAGATTTGCACTTTACTGGCATGAATGGTGTCGGTGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGTATCGCTCTGACATTGTTTAATCTTGCTGATACGCTTCTCGGTGGTTTACCG 305

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
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Db        306 ACAGAATTRATTTCGTCGGCTGGGGGTCAATTGTTTTACTCCCGCCCTGTTGTCTCGGCC 365

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 AATGGCGAGCCAACAGTAAAGTTATACACATCTGTTGAGAATGCGCAGCAAGATAAGGGC 425

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGln 330
              |||||||||||||||||||||||||||||   ||||||||||||||||||
Db        426 ATCGCCATCCCGCATGATATAGACCTCGGTGACTCCCGTGTGGTTATTCAG 476

RESULT 90
AF503511
LOCUS       AF503511                473 bp ss-RNA     linear   VRL 01-DEC-2003
DEFINITION  Swine hepatitis E virus isolate P354/1/02 capsid gene, partial cds.
ACCESSION   AF503511
VERSION     AF503511.1  GI:33323622
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 473)
  AUTHORS   Banks,M., Heath,G., Grierson,S.S., King,D.P., Girones,R.,
            Harrison,T. and Emerson,S.
  TITLE     Hepatitis E virus in pigs in the UK, Sweden and Holland
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 473)
  AUTHORS   Grierson,S.S., King,D.P. and Banks,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-APR-2002) Virology, Veterinary Laboratories Agency,
            Woodham Lane, Addlestone, Surrey KT15 3NB, UK
FEATURES             Location/Qualifiers
     source          1. .473
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="P354/1/02"
                     /isolation_source="swine fecal material"
                     /db_xref="taxon:63421"
                     /country="United Kingdom"
     CDS             <1. .>473
                     /note="ORF2"
                     /codon_start=3
                     /product="capsid"
                     /protein_id="AAQ07590.1"
                     /db_xref="GI:33323623"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPT
                     ELISSAGGQLFYSRPVVSANGEPAVKLYTSVENAQQDKGIAIPHDIDLGDSRVVI"

Alignment Scores:
Pred. No.:              167           Length:        473
Score:                  150.00        Matches:       150
Percent Similarity:     96.15%        Conservative:  0
Best Local Similarity:  96.15%        Mismatches:    6
Query Match:            27.32%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AF503511 (1-473)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTTAATTCCTACACTAATACGCCCTATACTGGGGCGTTGGGGCTTCTCGACTTTGCACTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTAGGAACTTGACCCCTGGGAATACCAACACCCGTGTGTCCCGGTACACT 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCACGGCTCGCCACCGTTTACGCCGTGGTGCCGACGGGACTGCTGAGCTCACGACTACT 185
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Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||  ||||||  ||||||||||||||||||
Db        186 GCTGCCACGCGTTTCATGAAGGACCTGCACTTCACCGGGACGAATGGCGTTGGTGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGCATAGCCTTAACTCTATTCAATCTTGCTGATACACTTCTCGGCGGTTTGCCG 305

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ACAGAATTGATTTCGTCGGCCGGAGGTCAGCTCTTTTACTCCCGCCCAGTTGTCTCGGCC 365

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        366 AATGGCGAGCCGGCTGTTAAATTATATACATCCGTTGAGAATGCACAGCAGGATAAGGGC 425

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIle 329
              |||||||||||||||||||||||||||||  ||||||||||||||||
Db        426 ATTGCCATACCGCATGATATAGATCTAGGGGATTCCCGTGTGGTTATC 473
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RESULT 91
AF503512
LOCUS       AF503512                473 bp ss-RNA     linear   VRL 01-DEC-2003
DEFINITION  Swine hepatitis E virus isolate P143/11/02 capsid gene, partial
            cds.
ACCESSION   AF503512
VERSION     AF503512.1  GI:33323624
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 473)
  AUTHORS   Banks,M., Heath,G., Grierson,S.S., King,D.P., Girones,R.,
            Harrison,T. and Emerson,S.
  TITLE     Hepatitis E virus in pigs in the UK, Sweden and Holland
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 473)
  AUTHORS   Grierson,S.S., King,D.P. and Banks,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-APR-2002) Virology, Veterinary Laboratories Agency,
            Woodham Lane, Addlestone, Surrey KT15 3NB, UK
FEATURES             Location/Qualifiers
     source          1. .473
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="P143/11/02"
                     /isolation_source="swine fecal material"
                     /db_xref="taxon:63421"
                     /country="United Kingdom"
     CDS             <1. .>473
                     /note="ORF2"
                     /codon_start=3
                     /product="capsid"
                     /protein_id="AAQ07591.1"
                     /db_xref="GI:33323625"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPT
                     ELISSAGGQLFYSRPVVSANGEPAVKLYTSVENAQQDKGIAIPHDIDLGDSRVVI"

Alignment Scores:
Pred. No.:              167          Length:         473
Score:                  150.00       Matches:        150
Percent Similarity:     96.15%       Conservative:   0
Best Local Similarity:  96.15%       Mismatches:     6
Query Match:            27.32%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AF503512 (1-473)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTAAACTCTTATACCAATACGCCCTATACTGGGGCATTGGGCCTTCTTGACTTCGCACTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAATTTAGAAACTTGACCCCTGGGAACACTAACACCCGTGTTTCCCGGTACACT 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCACGGCTCGTCACCGCTTGCGCCGTGGTGCTGATGGAACTGCCGAGCTCACGACCACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||  ||||||  ||||||||||||||||||
Db        186 GCGGCCACGCGCTTCATGAAGGACCTGCACTTTACTGGGACGAACGGCGTCGGTGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGCATAGCCCTAACATTATTCAACCTTGCTGACACACTTCTCGGCGGCTTGCCG 305

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
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Db        306 ACAGAATTGATTTCGTCGGCCGGAGGTCAGCTCTTTTACTCCCGCCCAGTCGTCTCGGCC 365

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        366 AATGGCGAGCCGGCTGTTAAATTATATACTTCCGTCGAGAATGCACAGCAGGATAAGGGC 425

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIle 329
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Db        426 ATTGCCATACCTCACGATATAGACCTAGGGGATTCCCGCGTGGTTATC 473
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RESULT 92
AF020492
LOCUS       AF020492                448 bp ss-RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus strain TK5/95/Nepal capsid gene, partial cds.
ACCESSION   AF020492
VERSION     AF020492.1  GI:2731791
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 448)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 448)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th and Dahlia St. Bldg. 40, Washington, DC
            20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .448
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TK5/95/Nepal"
                     /db_xref="taxon:12461"
                     /note="from RT-PCR amplified virus in human serum"
     CDS             <1. .>448
                     /codon_start=1
                     /product="capsid"
                     /protein_id="AAB93548.1"
                     /db_xref="GI:2731792"
                     /translation="VATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLS
                     FWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPH
                     SALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK"

Alignment Scores:
Pred. No.:              168          Length:         448
Score:                  149.00       Matches:        149
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Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            27.14%         Indels:        0
DB:                     1              Gaps:          0

US-09-769-066-15 (1-549) x AF020492 (1-448)

Qy        392 ValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeuAsp 411
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Db          1 GTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGAT 60

Qy        412 GlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeuArg 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGTCGCCCTCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGC 120

Qy        432 GlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsn 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCAAGCTCTCTTTCTGGGAGGCAGGCACAACTAAGGCCGGGTACCCTTATAATTACAAC 180

Qy        452 ThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSer 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTTGCTATCTCC 240

Qy        472 ThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAla 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACTTACACCACTAGCCTAGGTGCTGGCCCCGTCTCCATTTCTGCGGTTGCCGTCTTAGCC 300

Qy        492 ProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThr 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCACACTCTGCGCTAGCATTGCTTGAGGATACCTTGGATTACCCTGCCCGCGCCCATACT 360

Qy        512 PheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSer 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGATGATTTCTGCCCAGAGTGCCGCCCCCTTGGCCTCCAGGGCTGCGCTTTCCAATCT 420

Qy        532 ThrValAlaGluLeuGlnArgLeuLys 540
              |||||||||||||||||||||||||||
Db        421 ACTGTCGCTGAGCTTCAGCGCCTTAAG 447

RESULT 93
AF020493
LOCUS       AF020493                448 bp ss-RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus strain TK104/91/Nepal capsid gene, partial cds.
ACCESSION   AF020493
VERSION     AF020493.1  GI:2731793
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 448)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 448)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th and Dahlia St. Bldg. 40, Washington, DC
            20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .448
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TK104/91/Nepal"
                     /db_xref="taxon:12461"
                     /note="from RT-PCR amplified virus in human feces"
     CDS             <1. .>448
                     /codon_start=1
                     /product="capsid"
                     /protein_id="AAB93549.1"
                     /db_xref="GI:2731794"
                     /translation="VATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLS
                     FWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPH
                     SALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK"

Alignment Scores:
Pred. No.:              168            Length:        448
Score:                  149.00         Matches:       149
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            27.14%         Indels:        0
DB:                     1              Gaps:          0

US-09-769-066-15 (1-549) x AF020493 (1-448)

Qy        392 ValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeuAsp 411
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Db          1 GTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGAT 60

Qy        412 GlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeuArg 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGTCGCCCTCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGC 120

Qy        432 GlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsn 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCAAGCTCTCTTTCTGGGAGGCAGGCACAACTAAGGCCGGGTACCCTTATAATTACAAC 180

Qy        452 ThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSer 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTTGCTATCTCC 240

Qy        472 ThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAla 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACTTACACCACTAGCCTGGGTGCTGGCCCCGTCTCCATTTCTGCGGTTGCCGTCTTAGCC 300

Qy        492 ProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThr 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGATTACCCTGCCCGCGCCCATACT 360

Qy        512 PheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSer 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGATGATTTCTGCCCAGAGTGCCGCCCCCTTGGCCTCCAGGGCTGCGCTTTCCAATCT 420

Qy        532 ThrValAlaGluLeuGlnArgLeuLys 540
              |||||||||||||||||||||||||||
Db        421 ACTGTCGCTGAGCTTCAGCGCCTTAAA 447

RESULT 94
AF020494
LOCUS       AF020494                448 bp ss-RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus strain TK4/95/Nepal capsid gene, partial cds.
ACCESSION   AF020494
VERSION     AF020494.1  GI:2731795
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 448)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 448)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th and Dahlia St. Bldg. 40, Washington, DC
```

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          20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .448
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TK4/95/Nepal"
                     /db_xref="taxon:12461"
                     /note="from RT-PCR amplified virus in human serum"
     CDS             <1. .>448
                     /codon_start=1
                     /product="capsid"
                     /protein_id="AAB93550.1"
                     /db_xref="GI:2731796"
                     /translation="VATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLS
                     FWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPH
                     SALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK"

Alignment Scores:
Pred. No.:                168             Length:         448
Score:                    149.00          Matches:        149
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              27.14%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AF020494 (1-448)

Qy        392 ValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeuAsp 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGAC 60

Qy        412 GlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeuArg 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGTCGCCCTCTTTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGC 120

Qy        432 GlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsn 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCAAGCTCTCTTTCTGGGAGGCAGGCACAACTAAGGCCGGGTACCCTTATAATTACAAC 180

Qy        452 ThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSer 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTTGCCATCTCC 240

Qy        472 ThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAla 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACTTACACCACTAGCCTGGGTGCTGGCCCCGTCTCCATTTCTGCGGTTGCCGTCTTAGCC 300

Qy        492 ProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThr 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGATTACCCTGCCCGCGCCCATACT 360

Qy        512 PheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSer 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGATGATTTCTGCCCAGAGTGCCGCCCCCTTGGCCTCCAGGGCTGCGCTTTCCAGTCT 420

Qy        532 ThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||
Db        421 ACTGTCGCTGAGCTTCAGCGCCTTAAG 447

RESULT 95
AF020495
LOCUS       AF020495                448 bp ss-RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus strain TK78/87/Nepal capsid gene, partial cds.
ACCESSION   AF020495
VERSION     AF020495.1  GI:2731797
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 448)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 448)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th and Dahlia St. Bldg. 40, Washington, DC
            20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .448
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TK78/87/Nepal"
                     /db_xref="taxon:12461"
                     /note="from RT-PCR amplified virus in human feces"
     CDS             <1. .>448
                     /codon_start=1
                     /product="capsid"
                     /protein_id="AAB93551.1"
                     /db_xref="GI:2731798"
                     /translation="VATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLS
                     FWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPH
                     SALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK"

Alignment Scores:
Pred. No.:                168             Length:         448
Score:                    149.00          Matches:        149
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              27.14%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AF020495 (1-448)

Qy        392 ValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeuAsp 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGAC 60

Qy        412 GlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeuArg 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGTCGCCCTCTCTCCACCATCCAGCAGTATTCGAAGACCTTCTTTGTCCTGCCGCTCCGC 120

Qy        432 GlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsn 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTAAGCTCTCTTTCTGGGAGGCAGGCACAACTAAAGCCGGGTACCCCTATAATTACAAC 180

Qy        452 ThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSer 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTTGCTATTTCC 240

Qy        472 ThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAla 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACTTACACCACCAGCCTGGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCC 300

Qy        492 ProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThr 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGCGCCCATACT 360

Qy        512 PheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSer 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGATGATTTCTGCCCAGAGTGCCGCCCTCTCGGCCTCCAGGGCTGCGCTTTCCAGTCT 420

Qy        532 ThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||
Db        421 ACTGTCGCTGAGCTTCAGCGCCTTAAG 447

RESULT 96
AF020497
LOCUS       AF020497                448 bp ss-RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus strain Nep4/94/Nepal capsid gene, partial cds.
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ACCESSION   AF020497
VERSION     AF020497.1  GI:2731801
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 448)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 448)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th and Dahlia St. Bldg. 40, Washington, DC
            20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .448
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="Nep4/94/Nepal"
                     /db_xref="taxon:12461"
                     /note="from RT-PCR amplified virus in human serum"
     CDS             <1. .>448
                     /codon_start=1
                     /product="capsid"
                     /protein_id="AAB93553.1"
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                     /translation="VATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLS
                     FWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPH
                     SALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLK"

Alignment Scores:
Pred. No.:              168             Length:         448
Score:                  149.00          Matches:        149
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            27.14%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF020497 (1-448)

Qy        392 ValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeuAsp 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGAT 60

Qy        412 GlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeuArg 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCCGCCCTCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGC 120

Qy        432 GlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsn 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCAAGCTCTCTTTCTGGGAGGCAGGCACAACTAAGGCCGGGTACCCTTATAATTACAAC 180

Qy        452 ThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSer 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTTGCTATCTCC 240

Qy        472 ThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAla 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACTTACACCACTAGCCTAGGTGCTGGCCCCGTCTCCATTTCTGCGGTTGCCGTCTTGGCC 300

Qy        492 ProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThr 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCACACTCTGCGCTAGCATTGCTTGAGGATACCTTGGATTACCCTGCCCGCGCCCATACT 360

Qy        512 PheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSer 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGATGATTTCTGCCCAGAGTGCCGCCCCCTCGGCCTCCAGGGCTGCGCTTTCCAGTCT 420

Qy        532 ThrValAlaGluLeuGlnArgLeuLys 540
              |||||||||||||||||||||||||||
Db        421 ACTGTCGCTGAGCTTCAGCGCCTTAAG 447

RESULT 97
HEU40046
LOCUS       HEU40046                453 bp    DNA     linear   VRL 05-JAN-1998
DEFINITION  Hepatitis E virus structural protein 2 (orf2) mRNA, partial cds.
ACCESSION   U40046
VERSION     U40046.1  GI:2745952
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 453)
  AUTHORS   van Cuyck-Gandre,H., Zhang,H.Y., Tsarev,S.A., Clements,N.J.,
            Cohen,S.J., Caudill,J.D., Buisson,Y., Coursaget,P., Warren,R.L. and
            Longer,C.F.
  TITLE     Characterization of hepatitis E virus (HEV) from Algeria and Chad
            by partial genome sequence
  JOURNAL   J. Med. Virol. 53 (4), 340-347 (1997)
  MEDLINE   98071272
   PUBMED   9407381
REFERENCE   2  (bases 1 to 453)
  AUTHORS   Van Cuyck-Gandre,H., Clements,N.J., Zhang,H.Y., Caudill,J.C.,
            Cohen,S.G., Coursaget,P., Buisson,Y., Warren,R.L. and Longer,C.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-NOV-1995) Helene Van Cuyck-Gandre, Virus Disease,
            Walter Reed Army Institute of Research, BLD 40, Washington, DC
            20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .453
                     /organism="Hepatitis E virus"
                     /mol_type="genomic DNA"
                     /strain="M7 Mostaganem, Algeria"
                     /db_xref="taxon:12461"
                     /note="HEV from patient feces"
     CDS             <1. .453
                     /note="orf2; capsid protein"
                     /codon_start=1
                     /product="structural protein 2"
                     /protein_id="AAB94789.1"
                     /db_xref="GI:2745953"
                     /translation="DRSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTK
                     AGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLED
                     TLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTREL"

Alignment Scores:
Pred. No.:              168             Length:         453
Score:                  149.00          Matches:        149
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            27.14%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x HEU40046 (1-453)

Qy        401 ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 CGGTCGCTTGACTGGACTAAGGTCACGCTTGACGGCCGCCCTCTCTCTACTATTCAGCAG 63

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 TACTCGAAGACTTTCTTCGTCCTGCCGCTTCGTGGTAAACTCTCCTTCTGGGAGGCAGGT 123

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuVal 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ACTACTAAGGCCGGGTACCCTTATAATTATAATACTACTGCTAGTGACCAATTGCTCGTA 183

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGly 480
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Db        184 GAGAACGCCGCCGGGCACCGGGTGGCTATTTCCACTTACACCACCAGCTTGGGTGCTGGC 243

Qy        481 ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGlu 500
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CCTGTTTCCATCTCTGCGGTCGCTGTCCTGGCCCCCCACTCCGCGCTAGCACTGCTTGAG 303

Qy        501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GATACCCTGGACTACCCTGCTCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGTCGC 363

Qy        521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTCCAGCGACTTAAG 423

Qy        541 MetLysValGlyLysThrArgGluLeu 549
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Db        424 ATGAAGGTGGGTAAAACTCGGGAGTTA 450

RESULT 98
AF020496
LOCUS       AF020496                448 bp ss-RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus strain TK15/92/Nepal capsid gene, partial cds.
ACCESSION   AF020496
VERSION     AF020496.1  GI:2731799
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 448)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 448)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th and Dahlia St. Bldg. 40, Washington, DC
            20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .448
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TK15/92/Nepal"
                     /db_xref="taxon:12461"
                     /note="from RT-PCR amplified virus in human feces"
     CDS             <1. .>448
                     /codon_start=1
                     /product="capsid"
                     /protein_id="AAB93552.1"
                     /db_xref="GI:2731800"
                     /translation="VATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLS
                     FWEAGTTKAGYPYNYNTTASGQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPH
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Alignment Scores:
Pred. No.:              171           Length:         448
Score:                  148.00        Matches:        148
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Query Match:            26.96%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF020496 (1-448)

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Db          1 GTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGAT 60

Qy        412 GlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeuArg 431
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Db         61 GGCCGCCCTCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGC 120

Qy        432 GlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsn 451
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Db        121 GGCAAGCTCTCTTTCTGGGAGGCAGGCACAACTAAGGCCGGGTACCCTTATAATTACAAC 180

Qy        452 ThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSer 471
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Db        181 ACCACTGCTAGCGGCCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTTGCTATCTCC 240

Qy        472 ThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAla 491
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Qy        492 ProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThr 511
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Db        301 CCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGATTACCCTGCCCGCGCCCATACT 360

Qy        512 PheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSer 531
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Db        361 TTTGATGATTTCTGCCCAGAGTGCCGCCCCCTTGGCCTCCAGGGCTGCGCTTTCCAGTCT 420

Qy        532 ThrValAlaGluLeuGlnArgLeuLys 540
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Db        421 ACTGTCGCTGAGCTCCAGCGCCTTAAG 447

RESULT 99
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LOCUS       AF336291                476 bp ss-RNA     linear   VRL 05-MAR-2002
DEFINITION  Swine hepatitis E virus isolate NLSW22 structural protein gene,
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ACCESSION   AF336291
VERSION     AF336291.1  GI:18478611
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I.,
            Vivo,A., Kooreman,M. and de Roda Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine related to sequences in
            humans, The Netherlands
  JOURNAL   Emerging Infect. Dis. 7 (6), 970-976 (2001)
  MEDLINE   21614760
   PUBMED   11747723
REFERENCE   2  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /note="ORF2"
                     /codon_start=3
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                     /db_xref="GI:18478612"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLDDTLLGGLPT
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Alignment Scores:
Pred. No.:              171           Length:         476
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Score:                  148.00        Matches:       148
Percent Similarity:     94.27%        Conservative:  0
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Query Match:            26.96%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AF336291 (1-476)

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Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
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Db         66 GAGCTTGAATTTAGAAACCTGACACCCGGGAATACCAACACCCGTGTTTCCAGGTATACC 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
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Db        126 AGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGTACCGCTGAGCTTACCACTACA 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        186 GCAGCCACACGTTTTATGAAAGACCTGCATTTTACTGGCACGAACGGTGTTGGTGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
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Db        246 GGCCGCGGTATCGCCCTGACATTGTTTAATCTCGATGATACGCTTCTCGGTGGTTTACCG 305

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
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Db        306 ACAGAATTNATTTCGTCGGCTAGGGGTCAATTGTTTTACTCCCGCCCTGTTGTCTCGGCC 365

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
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Db        366 AATGGCGAGCCAACAGTAAAGTTGTATACATCTGTTGAGAATGCGCAGCAAGATAAGGGC 425

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGln 330
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Db        426 ATCACCATTCCACATGATATAGATCTTGGTGACTCCCGTGTGGTTATTCAG 476

RESULT 100
AF047864
LOCUS       AF047864                448 bp    DNA     linear   VRL 06-MAR-1998
DEFINITION  Hepatitis E virus capsid gene, partial cds.
ACCESSION   AF047864
VERSION     AF047864.1  GI:2935424
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 448)
  AUTHORS   Gouvea,V.S., Innis,B.L., Drabick,J.J., Gambel,J.M., Seriwatana,J.
            and Hoke,C.H. Jr.
  TITLE     Hepatitis E in Bangladeshi soldiers serving in the United Nations
            mission to Haiti (UNMIH)
  JOURNAL   (in) XTH INTERNATIONAL CONGRESS OF VIROLOGY, JERUSALEM ABSTRACTS:
            241-PW54-15;
            (1996)
REFERENCE   2  (bases 1 to 448)
  AUTHORS   Drabick,J.J., Gambel,J.M., Gouvea,V.S., Caudill,J.D., Sun,W.,
            Hoke,C.H. Jr. and Innis,B.L.
  TITLE     A cluster of acute hepatitis E infection in United Nations
            Bangladeshi peacekeepers in Haiti
  JOURNAL   Am. J. Trop. Med. Hyg. 57 (4), 449-454 (1997)
  MEDLINE   98006185
   PUBMED   9347962
REFERENCE   3  (bases 1 to 448)
  AUTHORS   Gouvea,V.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1998) Virus Diseases, Walter Reed Army Institute
            of Research, 14th & Dahlia St. Bldg 40, Washington, DC 20307-5100,
            USA

FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              180           Length:        448
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Best Local Similarity:  96.64%        Mismatches:    5
Query Match:            26.23%        Indels:        0
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US-09-769-066-15 (1-549) x AF047864 (1-448)

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Db          1 GTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGAT 60

Qy        412 GlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeuArg 431
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Db         61 GGTCGCCCCCTCTCCACCATCCAGCAGTATTCGAAGACCTTCTTTGTCCTGCCGCTCCGC 120

Qy        432 GlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsn 451
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Db        121 GGTAAGCTCTCTTTCTGGGAGGCAGGTACTACTAAAGCCGGGTACCCTTATAATTATAAC 180

Qy        452 ThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSer 471
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Db        181 ACCACTGCTAGCGACCAATTGCTCGTTGAGAATGCCGCTGGGCATCGGGTTGCTATTTCC 240

Qy        472 ThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAla 491
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Db        241 ACTTACACCACTAGCCTGGGTGCTGGCCCCGTCTCCATTTCCGCGGTTGCCGTTTTAGCC 300

Qy        492 ProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThr 511
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Qy        512 PheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSer 531
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Qy        532 ThrValAlaGluLeuGlnArgLeuLys 540
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Db        421 CCTGTCGCTGAGCTTCAGCGCCTTAAG 447

RESULT 101
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LOCUS       AY370687                451 bp    RNA     linear   VRL 15-JAN-2004
DEFINITION  Hepatitis E virus isolate Namibia7801 structural protein (ORF2)
            gene, partial cds.
ACCESSION   AY370687
VERSION     AY370687.1  GI:34484264
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 451)
  AUTHORS   Maila,H.T., Bowyer,S.M. and Swanepoel,R.
  TITLE     Identification of a new strain of hepatitis E virus from an
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          outbreak in Namibia in 1995
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 89-95 (2004)
   PUBMED   14718623
REFERENCE   2  (bases 1 to 451)
  AUTHORS   Maila,H.T., Bowyer,S.M. and Swanepoel,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-AUG-2003) Molecular Virology, National Institute for
            Communicable Diseases, Private Bag X4, Sandringham, Johannesburg
            2131, South Africa
FEATURES             Location/Qualifiers
     source          1. .451
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                     DQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTIEQYSKSFFV
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Alignment Scores:
Pred. No.:              187           Length:         451
Score:                  141.00        Matches:        141
Percent Similarity:     94.63%        Conservative:   0
Best Local Similarity:  94.63%        Mismatches:     8
Query Match:            25.68%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AY370687 (1-451)

Qy        326 ArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerPro 345
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Db          3 CGCGTGGTTATTCAGGATTATGACAATCAGCACGAGCAGGACCGCCCCACCCCCTCACCT 62

Qy        346 AlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThr 365
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Db         63 GCACCGTCCCGGCCCTTTTCTGTCCTCCGTGCAAATGATGTGCTTTGGCTGTCTCTTACT 122

Qy        366 AlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAsp 385
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Db        123 GGGGCCGAGTATGACCAATCTACGTACGGGTCGTCCACCGGCCCGGTTTATGTCTCGGAT 182

Qy        386 SerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrp 405
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Db        183 AGTGTGACCTTGGTGAATGTAGCGACCGGCGCGCAGGCCGTAGCCCGGTCGCTCGACTGG 242

Qy        406 ThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhe 425
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Qy        426 PheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGly 445
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Db        303 TTTGTGTTGCCCCTTCGTGGTAAGCTCTCTTTTTGGGAGGCCGGTACAACGAAAGCGGGT 362

Qy        446 TyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGly 465
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Db        363 TACCCCTATAATTACAACACCACTGCTAGTGACCAGATTCTGATCGAGAATGCGGCCGGC 422

Qy        466 HisArgValAlaIleSerThrTyrThr 474
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Db        423 CACCGAGTCTCCATTTCGACCTATACC 449

RESULT 102
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LOCUS       AY370688                451 bp    RNA     linear   VRL 15-JAN-2004
DEFINITION  Hepatitis E virus isolate Namibia7948 structural protein (ORF2)
            gene, partial cds.
ACCESSION   AY370688
VERSION     AY370688.1  GI:34484266
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 451)
  AUTHORS   Maila,H.T., Bowyer,S.M. and Swanepoel,R.
  TITLE     Identification of a new strain of hepatitis E virus from an
            outbreak in Namibia in 1995
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 89-95 (2004)
   PUBMED   14718623
REFERENCE   2  (bases 1 to 451)
  AUTHORS   Maila,H.T., Bowyer,S.M. and Swanepoel,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-AUG-2003) Molecular Virology, National Institute for
            Communicable Diseases, Private Bag X4, Sandringham, Johannesburg
            2131, South Africa
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              187           Length:         451
Score:                  141.00        Matches:        141
Percent Similarity:     94.63%        Conservative:   0
Best Local Similarity:  94.63%        Mismatches:     8
Query Match:            25.68%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AY370688 (1-451)

Qy        326 ArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerPro 345
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Db          3 CGCGTGGTTATTCAGGATTATGACAATCAGCACGAGCAGGACCGCCCCACCCCCTCACCT 62

Qy        346 AlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThr 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 GCACCGTCCCGGCCCTTTTCTGTCCTCCGTGCAAATGATGTGCTTTGGCTGTCTCTTACT 122

Qy        366 AlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAsp 385
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Db        123 GGGGCCGAGTATGACCAGTCTACGTACGGGTCGTCCACCGGCCCGGTTTATGTCTCGGAT 182

Qy        386 SerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrp 405
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Db        243 TCCAAGGTTACTCTTGACGGGCGGCCCTTACCTACTATTGAACAATATTCTAAGTCATTC 302

Qy        426 PheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGly 445
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Qy        446 TyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGly 465
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Db        363 TACCCCTATAATTACAACACCACTGCTAGTGACCAGATTCTGATCGAGAATGCGGCCGGC 422

Qy        466 HisArgValAlaIleSerThrTyrThr 474
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Db        423 CACCGAGTCTCCATTTCGACCTATACC 449

RESULT 103
AY370689
LOCUS       AY370689                451 bp    RNA     linear   VRL 15-JAN-2004
DEFINITION  Hepatitis E virus isolate Namibia8039 structural protein (ORF2)
            gene, partial cds.
ACCESSION   AY370689
VERSION     AY370689.1  GI:34484268
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 451)
  AUTHORS   Maila,H.T., Bowyer,S.M. and Swanepoel,R.
  TITLE     Identification of a new strain of hepatitis E virus from an
            outbreak in Namibia in 1995
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 89-95 (2004)
   PUBMED   14718623
REFERENCE   2  (bases 1 to 451)
  AUTHORS   Maila,H.T., Bowyer,S.M. and Swanepoel,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-AUG-2003) Molecular Virology, National Institute for
            Communicable Diseases, Private Bag X4, Sandringham, Johannesburg
            2131, South Africa
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                     /protein_id="AAQ72768.1"
                     /db_xref="GI:34484269"
                     /translation="RVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTGAEY
                     DQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTIEQYSKSPFV
                     LPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVSISTYTT"

Alignment Scores:
Pred. No.:              187           Length:        451
Score:                  141.00        Matches:       141
Percent Similarity:     94.63%        Conservative:  0
Best Local Similarity:  94.63%        Mismatches:    8
Query Match:            25.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AY370689 (1-451)

Qy        326 ArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerPro 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CGCGTGGTTATTCAGGATTATGACAATCAGCACGAGCAGGACCGCCCCACCCCCTCACCT 62

Qy        346 AlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThr 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 GCACCGTCCCGGCCCTTTTCTGTCCTCCGTGCAAATGATGTGCTTTGGCTGTCTCTTACT 122

Qy        366 AlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAsp 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GGGGCCGAGTATGACCAGTCTACGTACGGGTCGTCCACCGGCCCGGTTTATGTCTCGGAT 182

Qy        386 SerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrp 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AGTGTGACCTTGGTGAATGTAGCGACCGGCGCGCAGGCCGTAGCCCGGTCGCTCGACTGG 242

Qy        406 ThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhe 425
              ||||||||||||||||||||||||||   ||||||   ||||||||||||   |||
Db        243 TCCAAGGTTACTCTTGACGGGCGGCCCTTACCTACTATTGAACAATATTCTAAGTCATTC 302

Qy        426 PheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGly 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TTTGTGTTGCCCCTTCGTGGTAAGCTCTCTTTTTGGGAGGCCGGTACAACGAAAGCGGGT 362

Qy        446 TyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGly 465
              ||||||||||||||||||||||||||||||||||   |||   ||||||||||||||||
Db        363 TACCCCTATAATTACAACACCACTGCTAGTGACCAGATTCTGATCGAGAATGCGGCCGGC 422

Qy        466 HisArgValAlaIleSerThrTyrThr 474
              |||||||||   ||||||||||||||||
Db        423 CACCGAGTCTCCATTTCGACCTATACC 449

RESULT 104
AB080579
LOCUS       AB080579                436 bp    RNA     linear   VRL 23-JUL-2002
DEFINITION  Hepatitis E virus gene for ORF2 protein, partial cds,
            clone:HE-JI3C.
ACCESSION   AB080579
VERSION     AB080579.1  GI:21929140
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Yoshikawa,A., Sato,S., Isoda,N.,
            Ido,K., Sugano,K. and Okamoto,H.
  TITLE     Identification of two distinct genotypes of hepatitis E virus in a
            Japanese patient with acute hepatitis who had not travelled abroad
  JOURNAL   J. Gen. Virol. 83 (Pt 8), 1931-1940 (2002)
   PUBMED   12124457
REFERENCE   2  (bases 1 to 436)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-FEB-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology, Jichi
            Medical School; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun,
            Tochigi-Ken 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp,
            Tel:81-285-58-7404, Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .436
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JI3"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /clone="HE-JI3C"
                     /tissue_type="serum"
                     /country="Japan"
     gene            2. .436
                     /gene="ORF2"
     CDS             <2. .>436
                     /gene="ORF2"
                     /codon_start=1
                     /product="ORF2 protein"
                     /protein_id="BAC05704.1"
                     /db_xref="GI:21929141"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK"

Alignment Scores:
Pred. No.:              190           Length:        436
Score:                  140.00        Matches:       140
Percent Similarity:     96.55%        Conservative:  0
Best Local Similarity:  96.55%        Mismatches:    5
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Query Match:            25.50%      Indels:        0
DB:                     1           Gaps:          0

US-09-769-066-15 (1-549) x AB080579 (1-436)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCCGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATTCACGGCTCCCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTACACTGGTGCACTGGGGCTCCTTGATTTTGCATTGGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAACTTGACACCCGGGAATACCAACACCCGTGTCTCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGTCGCGGTGCTGATGGGACAGCTGAGCTCACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||   ||||||   ||||||||||||||||||||   ||||||
Db        242 ACACGTTTCATGAAAGATCTGCATTTTACTGGCACGAACGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCCCTGACACTGTTTAATCTTGCTGACACGCTTCTTGGCGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGly 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCGGCCAATGGC 421

Qy        296 GluProThrValLys 300
              |||||||||||||||
Db        422 GAGCCAACAGTAAAG 436

RESULT 105
AY160125
LOCUS       AY160125                438 bp    mRNA    linear   VRL 26-DEC-2003
DEFINITION  Hepatitis E virus capsid protein mRNA, partial cds.
ACCESSION   AY160125
VERSION     AY160125.1  GI:37724689
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 438)
  AUTHORS   He,J., Kuschner,R.A., Innis,B.L., Caudill,J.D. and Vaughn,D.W.
  TITLE     Molecular Detection and Sequence Analysis of a New Hepatitis E
            Virus Isolate from Pakistan
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 438)
  AUTHORS   He,J., Kuschner,R.A., Innis,B.L., Caudill,J.D. and Vaughn,D.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-2002) Department of Virus Diseases, Walter Reed
            Army Institute of Research, 504 Scott Street, Silver Spring, MD
            20910, USA
FEATURES             Location/Qualifiers
     source          1. .438
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /db_xref="taxon:12461"
     CDS             <1. .>438
                     /note="ORF-2 structural protein"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAO18364.1"
                     /db_xref="GI:37724690"
                     /translation="LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGY
                     PYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSVLALLEDTMD
                     YPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLKMKVVSPGG"

Alignment Scores:
Pred. No.:              192         Length:        438
Score:                  139.00      Matches:       139
Percent Similarity:     98.58%      Conservative:  0
Best Local Similarity:  98.58%      Mismatches:    2
Query Match:            25.32%      Indels:        0
DB:                     1           Gaps:          0

US-09-769-066-15 (1-549) x AY160125 (1-438)

Qy        403 LeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSer 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAGTATTCA 60

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGAACTACT 120

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTTGAGAAT 180

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCGCTGGGCATCGGGTTGCTATTTCCACCTACACTACTAGCCTGGGTGCTGGCCCCGTC 240

Qy        483 SerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThr 502
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        241 TCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCTGTGCTAGCATTGCTTGAGGATACC 300

Qy        503 LeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArgProLeu 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGCCCCCTT 360

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysMetLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAG 420

Qy        543 Val 543
              |||
Db        421 GTG 423

RESULT 106
AY370686
LOCUS       AY370686                451 bp    RNA     linear   VRL 15-JAN-2004
DEFINITION  Hepatitis E virus isolate Namibia7798 structural protein (ORF2)
            gene, partial cds.
ACCESSION   AY370686
VERSION     AY370686.1  GI:34484262
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 451)
  AUTHORS   Maila,H.T., Bowyer,S.M. and Swanepoel,R.
  TITLE     Identification of a new strain of hepatitis E virus from an
            outbreak in Namibia in 1995
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 89-95 (2004)
   PUBMED   14718623
REFERENCE   2  (bases 1 to 451)
  AUTHORS   Maila,H.T., Bowyer,S.M. and Swanepoel,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-AUG-2003) Molecular Virology, National Institute for
            Communicable Diseases, Private Bag X4, Sandringham, Johannesburg
            2131, South Africa
FEATURES             Location/Qualifiers
     source          1. .451
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="Namibia7798"
                     /db_xref="taxon:12461"
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     gene            <1. .>451
                     /gene="ORF2"
     CDS             <1. .>451
                     /gene="ORF2"
                     /codon_start=3
                     /product="structural protein"
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                     /db_xref="GI:34484263"
                     /translation="RVVIQDYDNQHEQDRPTPSPAPSRSFSVLRANDVLWLSLTGAEY
                     DQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTIEQYSKSFFV
                     LPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAGGHRVSISTYTT"

Alignment Scores:
Pred. No.:                192           Length:         451
Score:                    139.00        Matches:        139
Percent Similarity:       93.29%        Conservative:   0
Best Local Similarity:    93.29%        Mismatches:     10
Query Match:              25.32%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x AY370686 (1-451)

Qy        326 ArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerPro 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CGCGTGGTTATTCAGGATTATGACAATCAGCACGAGCAGGACCGCCCCACCCCCTCACCT 62

Qy        346 AlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThr 365
              |||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db         63 GCACCGTCCCGGTCCTTTTCTGTCCTCCGTGCAAATGATGTGCTTTGGCTGTCTCTCACT 122

Qy        366 AlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAsp 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GGGGCCGAGTATGACCAATCTACGTACGGGTCGTCCACCGGCCCGGTTTATGTCTCGGAT 182

Qy        386 SerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrp 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AGTGTGACCTTGGTGAATGTAGCGACCGGCGCGCAGGCCGTAGCCCGGTCGCTCGACTGG 242

Qy        406 ThrLysValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhe 425
              |||||||||||||||||||||||||   ||||||   ||||||||||||   |||
Db        243 TCCAAGGTTACTCTTGACGGGCGGCCCTTACCTACTATTGAACAATATTCTAAGTCATTC 302

Qy        426 PheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGly 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TTTGTGTTGCCCCTTCGTGGTAAGCTCTCTTTTTGGGAGGCCGGTACAACGAAAGCGGGT 362

Qy        446 TyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGly 465
              |||||||||||||||||||||||||||||||||   |||   |||||||||   |||
Db        363 TACCCCTATAATTACAATACCACTGCTAGTGACCAGATTCTGATCGAGAATGCGGGCGGG 422

Qy        466 HisArgValAlaIleSerThrTyrThr 474
              |||||||||   ||||||||||||||
Db        423 CACCGAGTCTCCATTTCGACCTATACC 449

RESULT 107
AB085949
LOCUS       AB085949                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne014.
ACCESSION   AB085949
VERSION     AB085949.1  GI:27372320
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES              Location/Qualifiers
     source           1. .412
                      /organism="Hepatitis E virus"
                      /virion
                      /mol_type="genomic RNA"
                      /isolate="Ne014"
                      /specific_host="human"
                      /db_xref="taxon:12461"
                      /tissue_type="serum"
                      /country="Nepal: Kathmandu"
                      /note="isolated from a patient with sporadic hepatitis
                      E-subtype 1c"
     CDS              <1. .>412
                      /note="ORF2"
                      /codon_start=2
                      /product="capsid protein"
                      /protein_id="BAC53671.1"
                      /db_xref="GI:27372321"
                      /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                      LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                      ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                199           Length:         412
Score:                    136.00        Matches:        136
Percent Similarity:       99.27%        Conservative:   0
Best Local Similarity:    99.27%        Mismatches:     1
Query Match:              24.77%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x AB085949 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 108
AB085950
LOCUS       AB085950                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne026.
ACCESSION   AB085950
VERSION     AB085950.1  GI:27372322
KEYWORDS    .
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SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /isolate="Ne026"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1a"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53672.1"
                     /db_xref="GI:27372323"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085950 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTTGGGCTGCTGGACTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTTTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 109
AB085951
LOCUS       AB085951                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne037.
ACCESSION   AB085951
VERSION     AB085951.1  GI:27372324
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne037"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1a"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53673.1"
                     /db_xref="GI:27372325"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085951 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAATCTTACCCCTGGCAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCTCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 110
AB085952
LOCUS       AB085952                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne049.
ACCESSION   AB085952
VERSION     AB085952.1  GI:27372326
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne049"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1a"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53674.1"
                     /db_xref="GI:27372327"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085952 (1-412)
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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAATCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 111
AB085953
LOCUS       AB085953                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne063.
ACCESSION   AB085953
VERSION     AB085953.1  GI:27372328
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
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                     /product="capsid protein"
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Alignment Scores:
Pred. No.:                199             Length:         412
Score:                    136.00          Matches:        136
Percent Similarity:       99.27%          Conservative:   0
Best Local Similarity:    99.27%          Mismatches:     1
Query Match:              24.77%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB085953 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 112
AB085954
LOCUS       AB085954                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne064.
ACCESSION   AB085954
VERSION     AB085954.1  GI:27372330
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     E-subtype 1a"
     CDS             <1. .>412
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Alignment Scores:
Pred. No.:                199             Length:         412
Score:                    136.00          Matches:        136
Percent Similarity:       99.27%          Conservative:   0
Best Local Similarity:    99.27%          Mismatches:     1
Query Match:              24.77%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB085954 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAATCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 113
AB085955
LOCUS       AB085955                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne068.
ACCESSION   AB085955
VERSION     AB085955.1  GI:27372332
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
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  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:                199             Length:         412
Score:                    136.00          Matches:        136
Percent Similarity:       99.27%          Conservative:   0
Best Local Similarity:    99.27%          Mismatches:     1
Query Match:              24.77%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB085955 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTC 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTCGCAATCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 114
AB085956
LOCUS       AB085956                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne069,
            clone:Ne069a.
ACCESSION   AB085956
VERSION     AB085956.1  GI:27372334
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne069"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /clone="Ne069a"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1a"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53678.1"
                     /db_xref="GI:27372335"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                199             Length:         412
Score:                    136.00          Matches:        136
Percent Similarity:       99.27%          Conservative:   0
Best Local Similarity:    99.27%          Mismatches:     1
Query Match:              24.77%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB085956 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAATCTTACCCCTGGCAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCTCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 115
AB085957
LOCUS       AB085957                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne069,
            clone:Ne069c.
ACCESSION   AB085957
VERSION     AB085957.1  GI:27372336
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /isolate="Ne069"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /clone="Ne069c"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53679.1"
                     /db_xref="GI:27372337"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085957 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 116
AB085958
LOCUS       AB085958                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne072.
ACCESSION   AB085958
VERSION     AB085958.1  GI:27372338
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /country="Nepal: Kathmandu"
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                     E-subtype 1a"
     CDS             <1. .>412
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
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DB:                 1           Gaps:          0

US-09-769-066-15 (1-549) x AB085958 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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                     /mol_type="genomic RNA"
                     /isolate="Ne080"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1a"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53682.1"
                     /db_xref="GI:27372343"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                199             Length:         412
Score:                    136.00          Matches:        136
Percent Similarity:       99.27%          Conservative:   0
Best Local Similarity:    99.27%          Mismatches:     1
Query Match:              24.77%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB085960 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTTGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAACCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 119
AB085961
LOCUS       AB085961                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne081.
ACCESSION   AB085961
VERSION     AB085961.1  GI:27372344
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES              Location/Qualifiers
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                      /organism="Hepatitis E virus"
                      /virion
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                      /specific_host="human"
                      /db_xref="taxon:12461"
                      /tissue_type="serum"
                      /country="Nepal: Kathmandu"
                      /note="isolated from a patient with sporadic hepatitis
                      E-subtype 1a"
     CDS              <1. .>412
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Alignment Scores:
Pred. No.:                199             Length:         412
Score:                    136.00          Matches:        136
Percent Similarity:       99.27%          Conservative:   0
Best Local Similarity:    99.27%          Mismatches:     1
Query Match:              24.77%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB085961 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAATCTTACCCCTGGCAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 120
AB085962
LOCUS       AB085962                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne086.
ACCESSION   AB085962
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VERSION     AB085962.1  GI:27372346
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
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                     /country="Nepal: Kathmandu"
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                     E-subtype 1c"
     CDS             <1. .>412
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                     /codon_start=2
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                     /db_xref="GI:27372347"
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085962 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 121
AB085963
LOCUS       AB085963                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne087.
ACCESSION   AB085963
VERSION     AB085963.1  GI:27372348
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne087"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53685.1"
                     /db_xref="GI:27372349"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085963 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                 ||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 122
AB085964
LOCUS       AB085964                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne090.
ACCESSION   AB085964
VERSION     AB085964.1  GI:27372350
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne090"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53686.1"
                     /db_xref="GI:27372351"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                199           Length:          412
Score:                    136.00        Matches:         136
Percent Similarity:       99.27%        Conservative:    0
Best Local Similarity:    99.27%        Mismatches:      1
Query Match:              24.77%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x AB085964 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                 ||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 123
AB085965
LOCUS       AB085965                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne091.
ACCESSION   AB085965
VERSION     AB085965.1  GI:27372352
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne091"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53687.1"
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                     /db_xref="GI:27372353"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199           Length:        412
Score:                  136.00        Matches:       136
Percent Similarity:     99.27%        Conservative:  0
Best Local Similarity:  99.27%        Mismatches:    1
Query Match:            24.77%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB085965 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 124
AB085966
LOCUS       AB085966                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne105.
ACCESSION   AB085966
VERSION     AB085966.1  GI:27372354
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES              Location/Qualifiers
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                      /organism="Hepatitis E virus"
                      /virion
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                      /specific_host="human"
                      /db_xref="taxon:12461"
                      /tissue_type="serum"
                      /country="Nepal: Kathmandu"
                      /note="isolated from a patient with sporadic hepatitis
                      E~subtype 1a"
     CDS              <1. .>412
                      /note="ORF2"
                      /codon_start=2
                      /product="capsid protein"
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                      /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                      ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199           Length:        412
Score:                  136.00        Matches:       136
Percent Similarity:     99.27%        Conservative:  0
Best Local Similarity:  99.27%        Mismatches:    1
Query Match:            24.77%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB085966 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAATCTTACCCCTGGCAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 125
AB085967
LOCUS       AB085967                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne112.
ACCESSION   AB085967
VERSION     AB085967.1  GI:27372356
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
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  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="Ne112"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1a"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53689.1"
                     /db_xref="GI:27372357"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                199             Length:         412
Score:                    136.00          Matches:        136
Percent Similarity:       99.27%          Conservative:   0
Best Local Similarity:    99.27%          Mismatches:     1
Query Match:              24.77%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB085967 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAATCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACTACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 126
AB085968
LOCUS       AB085968                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne118.
ACCESSION   AB085968
VERSION     AB085968.1  GI:27372358
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1a"
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                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53690.1"
                     /db_xref="GI:27372359"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:                199             Length:         412
Score:                    136.00          Matches:        136
Percent Similarity:       99.27%          Conservative:   0
Best Local Similarity:    99.27%          Mismatches:     1
Query Match:              24.77%          Indels:         0
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US-09-769-066-15 (1-549) x AB085968 (1-412)

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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTCGCAATCTTACCCCTGGCAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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RESULT 127
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DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne131.
ACCESSION   AB085969
VERSION     AB085969.1  GI:27372360
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     E-subtype 1a"
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                     /db_xref="GI:27372361"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
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US-09-769-066-15 (1-549) x AB085969 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db        122 GAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTCTCCCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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RESULT 128
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LOCUS       AB085970                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne132.
ACCESSION   AB085970
VERSION     AB085970.1  GI:27372362
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0
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US-09-769-066-15 (1-549) x AB085970 (1-412)

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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTCATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTCTCCCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTCACCCTGTTTAACCTTGCTGACACTCTCCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 129
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LOCUS       AB085971                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne133.
ACCESSION   AB085971
VERSION     AB085971.1  GI:27372364
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SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
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US-09-769-066-15 (1-549) x AB085971 (1-412)

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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTCTCCCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGCCTTCGCCGCGGCGCAGACGGGACCGCCGAGCTCACCACCACGGCAGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGCGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTCACCCTGTTTAACCTTGCTGACACTCTCCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 130
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LOCUS       AB085972                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne134.
ACCESSION   AB085972
VERSION     AB085972.1  GI:27372366
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
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Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085972 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTCATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGCCTTCGCCGCGGCGCAGACGGGACCGCCGAGCTCACCACCACGGCAGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGCGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTTAACCTTGCTGACACTCTCCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 131
AB085973
LOCUS       AB085973                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne135.
ACCESSION   AB085973
VERSION     AB085973.1  GI:27372368
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
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            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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                      /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                      LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                      ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085973 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTCATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTCTCCCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGCCTTCGCCGCGGCGCAGACGGGACCGCCGAGCTCACCACCACGGCAGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGCGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTTAACCTTGCTGACACTCTCCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 132
AB085975
LOCUS       AB085975                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne136,
            clone:Ne136c.
ACCESSION   AB085975
VERSION     AB085975.1  GI:27372372
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KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne136"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /clone="Ne136c"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53697.1"
                     /db_xref="GI:27372373"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085975 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACTCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 133
AB085976
LOCUS       AB085976                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne137.
ACCESSION   AB085976
VERSION     AB085976.1  GI:27372374
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne137"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53698.1"
                     /db_xref="GI:27372375"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085976 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235

Db        182 GCTCGCCACCGCCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255

Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275

Db        302 GGGATAGCCCTTACTCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292

Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 134
AB085977
LOCUS       AB085977                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne146.
ACCESSION   AB085977
VERSION     AB085977.1  GI:27372376
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne146"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1a"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53699.1"
                     /db_xref="GI:27372377"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199          Length:        412
Score:                  136.00       Matches:       136
Percent Similarity:     99.27%       Conservative:  0
Best Local Similarity:  99.27%       Mismatches:    1
Query Match:            24.77%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AB085977 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175

Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195

Db         62 TCTTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215

Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235

Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255

Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275

Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292

Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 135
AB085978
LOCUS       AB085978                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne149.
ACCESSION   AB085978
VERSION     AB085978.1  GI:27372378
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne149"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                199           Length:       412
Score:                    136.00        Matches:      136
Percent Similarity:       99.27%        Conservative: 0
Best Local Similarity:    99.27%        Mismatches:   1
Query Match:              24.77%        Indels:       0
DB:                       1             Gaps:         0

US-09-769-066-15 (1-549) x AB085978 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 136
AB085979
LOCUS       AB085979                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne150.
ACCESSION   AB085979
VERSION     AB085979.1  GI:27372380
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne150"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
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                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53701.1"
                     /db_xref="GI:27372381"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                199           Length:       412
Score:                    136.00        Matches:      136
Percent Similarity:       99.27%        Conservative: 0
Best Local Similarity:    99.27%        Mismatches:   1
Query Match:              24.77%        Indels:       0
DB:                       1             Gaps:         0

US-09-769-066-15 (1-549) x AB085979 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 137
AB085980
LOCUS       AB085980                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne151.
ACCESSION   AB085980
VERSION     AB085980.1  GI:27372382
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
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  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne151"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53702.1"
                     /db_xref="GI:27372383"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085980 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 138
AB085982
LOCUS       AB085982                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne154.
ACCESSION   AB085982
VERSION     AB085982.1  GI:27372386
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne154"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53704.1"
                     /db_xref="GI:27372387"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085982 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 139
AB085983
LOCUS       AB085983                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne155.
ACCESSION   AB085983
VERSION     AB085983.1  GI:27372388
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="Ne155"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53705.1"
                     /db_xref="GI:27372389"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085983 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 140
AB085984
LOCUS       AB085984                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne157.
ACCESSION   AB085984
VERSION     AB085984.1  GI:27372390
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /db_xref="GI:27372391"
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0
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US-09-769-066-15 (1-549) x AB085984 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 141
AB085985
LOCUS       AB085985                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne159.
ACCESSION   AB085985
VERSION     AB085985.1  GI:27372392
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="Ne159"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E~subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53707.1"
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085985 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 142
AB085986
LOCUS       AB085986                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne162.
ACCESSION   AB085986
VERSION     AB085986.1  GI:27372394
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /isolate="Ne162"
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                     /specific_host="human"
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                     /note="isolated from a patient with sporadic hepatitis
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     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
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                     /db_xref="GI:27372395"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                199             Length:         412
Score:                    136.00          Matches:        136
Percent Similarity:       99.27%          Conservative:   0
Best Local Similarity:    99.27%          Mismatches:     1
Query Match:              24.77%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB085986 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 143
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DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne164.
ACCESSION   AB085987
VERSION     AB085987.1  GI:27372396
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES              Location/Qualifiers
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                      /tissue_type="serum"
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                      /note="isolated from a patient with sporadic hepatitis
                      E-subtype 1c"
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Alignment Scores:
Pred. No.:                199             Length:         412
Score:                    136.00          Matches:        136
Percent Similarity:       99.27%          Conservative:   0
Best Local Similarity:    99.27%          Mismatches:     1
Query Match:              24.77%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB085987 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 144
AB085988
LOCUS       AB085988                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne165.
ACCESSION   AB085988
VERSION     AB085988.1  GI:27372398
KEYWORDS    .
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SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              199           Length:        412
Score:                  136.00        Matches:       136
Percent Similarity:     99.27%        Conservative:  0
Best Local Similarity:  99.27%        Mismatches:    1
Query Match:            24.77%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB085988 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 145
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LOCUS       AB085989                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne166.
ACCESSION   AB085989
VERSION     AB085989.1  GI:27372400
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              199           Length:        412
Score:                  136.00        Matches:       136
Percent Similarity:     99.27%        Conservative:  0
Best Local Similarity:  99.27%        Mismatches:    1
Query Match:            24.77%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB085989 (1-412)

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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 146
AB085990
LOCUS       AB085990                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne169.
ACCESSION   AB085990
VERSION     AB085990.1  GI:27372402
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              199          Length:         412
Score:                  136.00       Matches:        136
Percent Similarity:     99.27%       Conservative:   0
Best Local Similarity:  99.27%       Mismatches:     1
Query Match:            24.77%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AB085990 (1-412)
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 147
AB085991
LOCUS       AB085991                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne172.
ACCESSION   AB085991
VERSION     AB085991.1  GI:27372404
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085991 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 148
AB085992
LOCUS       AB085992                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne174.
ACCESSION   AB085992
VERSION     AB085992.1  GI:27372406
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES              Location/Qualifiers
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                      /organism="Hepatitis E virus"
                      /virion
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                      /isolate="Ne174"
                      /specific_host="human"
                      /db_xref="taxon:12461"
                      /tissue_type="serum"
                      /country="Nepal: Kathmandu"
                      /note="isolated from a patient with sporadic hepatitis
                      E~subtype 1c"
     CDS              <1. .>412
                      /note="ORF2"
                      /codon_start=2
                      /product="capsid protein"
                      /protein_id="BAC53714.1"
                      /db_xref="GI:27372407"
                      /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
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Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085992 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 149
AB085993
LOCUS       AB085993                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne177.
ACCESSION   AB085993
VERSION     AB085993.1  GI:27372408
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
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  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /virion
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                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
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                     /product="capsid protein"
                     /protein_id="BAC53715.1"
                     /db_xref="GI:27372409"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085993 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 150
AB085994
LOCUS       AB085994                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne181.
ACCESSION   AB085994
VERSION     AB085994.1  GI:27372410
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
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                     E-subtype 1c"
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085994 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361
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Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 151
AB085995
LOCUS       AB085995                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne182.
ACCESSION   AB085995
VERSION     AB085995.1  GI:27372412
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     E~subtype 1c"
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085995 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 152
AB085996
LOCUS       AB085996                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne183.
ACCESSION   AB085996
VERSION     AB085996.1  GI:27372414
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /note="isolated from a patient with sporadic hepatitis
                     E~subtype 1c"
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB085996 (1-412)
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412
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RESULT 153
AB085997
LOCUS AB085997 412 bp RNA linear VRL 25-DEC-2002
DEFINITION Hepatitis E virus for capsid protein, partial cds, isolate:Ne185.
ACCESSION AB085997
VERSION AB085997.1 GI:27372416
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y., Takeda,N. and Okamoto,H.
TITLE Molecular investigation of hepatitis E virus infection in patients with acute hepatitis in Kathmandu, Nepal
JOURNAL J. Med. Virol. 69, 207-214 (2003)
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School, Immunology Division and Division of Molecular Virology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
FEATURES Location/Qualifiers
source 1. .412
/organism="Hepatitis E virus"
/virion
/mol_type="genomic RNA"
/isolate="Ne185"
/specific_host="human"
/db_xref="taxon:12461"
/tissue_type="serum"
/country="Nepal: Kathmandu"
/note="isolated from a patient with sporadic hepatitis E-subtype 1c"
CDS <1. .>412
/note="ORF2"
/codon_start=2
/product="capsid protein"
/protein_id="BAC53719.1"
/db_xref="GI:27372417"
/translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

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Alignment Scores:
Pred. No.:                199             Length:          412
Score:                    136.00          Matches:         136
Percent Similarity:       99.27%          Conservative:    0
Best Local Similarity:    99.27%          Mismatches:      1
Query Match:              24.77%          Indels:          0
DB:                       1               Gaps:            0

US-09-769-066-15 (1-549) x AB085997 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412
```

RESULT 154
AB085998
LOCUS AB085998 412 bp RNA linear VRL 25-DEC-2002
DEFINITION Hepatitis E virus for capsid protein, partial cds, isolate:Ne186.
ACCESSION AB085998
VERSION AB085998.1 GI:27372418
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y., Takeda,N. and Okamoto,H.
TITLE Molecular investigation of hepatitis E virus infection in patients with acute hepatitis in Kathmandu, Nepal
JOURNAL J. Med. Virol. 69, 207-214 (2003)
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School, Immunology Division and Division of Molecular Virology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
FEATURES Location/Qualifiers
source 1. .412
/organism="Hepatitis E virus"
/virion
/mol_type="genomic RNA"
/isolate="Ne186"
/specific_host="human"
/db_xref="taxon:12461"

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                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E~subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53720.1"
                     /db_xref="GI:27372419"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                199           Length:        412
Score:                    136.00        Matches:       136
Percent Similarity:       99.27%        Conservative:  0
Best Local Similarity:    99.27%        Mismatches:    1
Query Match:              24.77%        Indels:        0
DB:                       1             Gaps:          0

US-09-769-066-15 (1-549) x AB085998 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 155
AB085999
LOCUS       AB085999                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne-A2.
ACCESSION   AB085999
VERSION     AB085999.1  GI:27372420
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES              Location/Qualifiers
     source           1. .412
                      /organism="Hepatitis E virus"
                      /virion
                      /mol_type="genomic RNA"
                      /isolate="Ne-A2"
                      /specific_host="human"
                      /db_xref="taxon:12461"
                      /tissue_type="stool"
                      /country="Nepal: Kathmandu"
                      /note="isolated from a patient with sporadic hepatitis
                      E~subtype 1a"
     CDS              <1. .>412
                      /note="ORF2"
                      /codon_start=2
                      /product="capsid protein"
                      /protein_id="BAC53721.1"
                      /db_xref="GI:27372421"
                      /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                      LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                      ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                199           Length:        412
Score:                    136.00        Matches:       136
Percent Similarity:       99.27%        Conservative:  0
Best Local Similarity:    99.27%        Mismatches:    1
Query Match:              24.77%        Indels:        0
DB:                       1             Gaps:          0

US-09-769-066-15 (1-549) x AB085999 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTACACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 156
AB086000
LOCUS       AB086000                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds,
            isolate:Ne-A312.
ACCESSION   AB086000
VERSION     AB086000.1  GI:27372422
KEYWORDS    .
SOURCE      Hepatitis E virus
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  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne-A312"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="stool"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1a"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53722.1"
                     /db_xref="GI:27372423"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:                199           Length:          412
Score:                    136.00        Matches:         136
Percent Similarity:       99.27%        Conservative:    0
Best Local Similarity:    99.27%        Mismatches:      1
Query Match:              24.77%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x AB086000 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTACACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 157
AB116160
LOCUS       AB116160                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne015-1999.
ACCESSION   AB116160
VERSION     AB116160.1  GI:40809770
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne015-1999"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07300.1"
                     /db_xref="GI:40809771"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                199           Length:          412
Score:                    136.00        Matches:         136
Percent Similarity:       99.27%        Conservative:    0
Best Local Similarity:    99.27%        Mismatches:      1
Query Match:              24.77%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-15 (1-549) x AB116160 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTTTCCCGTTATTCCAGCACT 181
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 158
AB116161
LOCUS       AB116161                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne018-1999.
ACCESSION   AB116161
VERSION     AB116161.1  GI:40809772
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
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Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116161 (1-412)
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        182 GCTCGCCACCGCCTTCGCCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 159
AB116162
LOCUS       AB116162                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne020-1999.
ACCESSION   AB116162
VERSION     AB116162.1  GI:40809774
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
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                     /isolate="Ne020-1999"
                     /isolation_source="serum"
                     /specific_host="human"
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                     /country="Nepal:Kathmandu"
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Alignment Scores:

Pred. No.:	199	Length:	412
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DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AB116162 (1-412)

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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGTATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTCGCAACCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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RESULT 160
AB116163
LOCUS AB116163 412 bp RNA linear VRL 14-JAN-2004
DEFINITION Hepatitis E virus gene for capsid protein, partial cds, isolate: Ne025-1999.
ACCESSION AB116163
VERSION AB116163.1 GI:40809776
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M., Gotanda,Y. and Okamoto,H.
TITLE Genetic changes in hepatitis E virus of subtype 1a in patients with sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
JOURNAL J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
PUBMED 14718624
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School, Division of Virology, Department of Infection and Immunity; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
FEATURES Location/Qualifiers
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/organism="Hepatitis E virus"
/virion
/mol_type="genomic RNA"
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Alignment Scores:

Pred. No.:	199	Length:	412
Score:	136.00	Matches:	136
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Query Match:	24.77%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AB116163 (1-412)

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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGTATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTCGCAACCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGCCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412
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RESULT 161
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LOCUS AB116164 412 bp RNA linear VRL 14-JAN-2004
DEFINITION Hepatitis E virus gene for capsid protein, partial cds, isolate: Ne026-1999.
ACCESSION AB116164
VERSION AB116164.1 GI:40809778
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M., Gotanda,Y. and Okamoto,H.
TITLE Genetic changes in hepatitis E virus of subtype 1a in patients with sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
JOURNAL J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
PUBMED 14718624
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.

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  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116164 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTCGCAACCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGCCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 162
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LOCUS       AB116165                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116165
VERSION     AB116165.1  GI:40809780
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116165 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGTATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGCCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 163
AB116166
LOCUS       AB116166                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne031-1999.
ACCESSION   AB116166
VERSION     AB116166.1  GI:40809782
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116166 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGTATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAACCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGCCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 164
AB116167
LOCUS       AB116167                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne032-1999.
ACCESSION   AB116167
VERSION     AB116167.1  GI:40809784
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne032-1999"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07307.1"
                     /db_xref="GI:40809785"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116167 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07309.1"
                     /db_xref="GI:40809789"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                199             Length:         412
Score:                    136.00          Matches:        136
Percent Similarity:       99.27%          Conservative:   0
Best Local Similarity:    99.27%          Mismatches:     1
Query Match:              24.77%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB116169 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 167
AB116170
LOCUS       AB116170                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne035-1999.
ACCESSION   AB116170
VERSION     AB116170.1  GI:40809790
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne035-1999"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07310.1"
                     /db_xref="GI:40809791"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                199             Length:         412
Score:                    136.00          Matches:        136
Percent Similarity:       99.27%          Conservative:   0
Best Local Similarity:    99.27%          Mismatches:     1
Query Match:              24.77%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB116170 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 168
AB116171
LOCUS       AB116171                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne036-1999.
ACCESSION   AB116171
VERSION     AB116171.1  GI:40809792
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
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          Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
          Hepevirus.
REFERENCE 1
  AUTHORS Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
          Gotanda,Y. and Okamoto,H.
  TITLE   Genetic changes in hepatitis E virus of subtype 1a in patients with
          sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED 14718624
REFERENCE 2  (bases 1 to 412)
  AUTHORS Okamoto,H.
  TITLE   Direct Submission
  JOURNAL Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
          Division of Virology, Department of Infection and Immunity; 3311-1
          Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
          Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
          Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="Ne036-1999"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /db_xref="GI:40809793"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199           Length:        412
Score:                  136.00        Matches:       136
Percent Similarity:     99.27%        Conservative:  0
Best Local Similarity:  99.27%        Mismatches:    1
Query Match:            24.77%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB116171 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 169
AB116172
LOCUS       AB116172                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne037-1999.
ACCESSION   AB116172
VERSION     AB116172.1  GI:40809794
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne037-1999"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07312.1"
                     /db_xref="GI:40809795"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199           Length:        412
Score:                  136.00        Matches:       136
Percent Similarity:     99.27%        Conservative:  0
Best Local Similarity:  99.27%        Mismatches:    1
Query Match:            24.77%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB116172 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 170
AB116173
LOCUS       AB116173                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne038-1999.
ACCESSION   AB116173
VERSION     AB116173.1  GI:40809796
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /country="Nepal:Kathmandu"
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                     /codon_start=2
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
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US-09-769-066-15 (1-549) x AB116173 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAATACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 171
AB116174
LOCUS       AB116174                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne040-1999.
ACCESSION   AB116174
VERSION     AB116174.1  GI:40809798
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne040-1999"
                     /isolation_source="serum"
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                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
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                     /db_xref="GI:40809799"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"
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Alignment Scores:
Pred. No.:              199           Length:         412
Score:                  136.00        Matches:        136
Percent Similarity:     99.27%        Conservative:   0
Best Local Similarity:  99.27%        Mismatches:     1
Query Match:            24.77%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AB116174 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 172
AB116175
LOCUS       AB116175                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne045-1999.
ACCESSION   AB116175
VERSION     AB116175.1  GI:40809800
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
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                     /isolation_source="serum"
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                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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                     /db_xref="GI:40809801"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              199           Length:         412
Score:                  136.00        Matches:        136
Percent Similarity:     99.27%        Conservative:   0
Best Local Similarity:  99.27%        Mismatches:     1
Query Match:            24.77%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AB116175 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412

RESULT 173
AB116176
LOCUS       AB116176                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne008-2000.
ACCESSION   AB116176
VERSION     AB116176.1  GI:40809802
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
```

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          Division of Virology, Department of Infection and Immunity; 3311-1
          Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
          Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
          Fax:81-285-44-1557)
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                     /isolate="Ne008-2000"
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                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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Alignment Scores:
Pred. No.:              199           Length:         412
Score:                  136.00        Matches:        136
Percent Similarity:     99.27%        Conservative:   0
Best Local Similarity:  99.27%        Mismatches:     1
Query Match:            24.77%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AB116176 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCTCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAACACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 174
AB116177
LOCUS       AB116177                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne032-2000.
ACCESSION   AB116177
VERSION     AB116177.1  GI:40809804
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /country="Nepal:Kathmandu"
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                     /codon_start=2
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Alignment Scores:
Pred. No.:              199           Length:         412
Score:                  136.00        Matches:        136
Percent Similarity:     99.27%        Conservative:   0
Best Local Similarity:  99.27%        Mismatches:     1
Query Match:            24.77%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AB116177 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCTCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCG 412
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RESULT 175
AB116178
LOCUS       AB116178                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne036-2000.
ACCESSION   AB116178
VERSION     AB116178.1  GI:40809806
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /db_xref="GI:40809807"
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Alignment Scores:
Pred. No.:              199           Length:        412
Score:                  136.00        Matches:       136
Percent Similarity:     99.27%        Conservative:  0
Best Local Similarity:  99.27%        Mismatches:    1
Query Match:            24.77%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB116178 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCTCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGTGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 176
AB116179
LOCUS       AB116179                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne037-2000.
ACCESSION   AB116179
VERSION     AB116179.1  GI:40809808
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne037-2000"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07319.1"
                     /db_xref="GI:40809809"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199           Length:        412
Score:                  136.00        Matches:       136
Percent Similarity:     99.27%        Conservative:  0
Best Local Similarity:  99.27%        Mismatches:    1
Query Match:            24.77%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB116179 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACAYGGTTCACCCGTAAAT 61
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAAYACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCTCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCYCGCCACCGCCTTCGTCGTGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412
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RESULT 177
AB116180
LOCUS AB116180 412 bp RNA linear VRL 14-JAN-2004
DEFINITION Hepatitis E virus gene for capsid protein, partial cds, isolate: Ne045-2000.
ACCESSION AB116180
VERSION AB116180.1 GI:40809810
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M., Gotanda,Y. and Okamoto,H.
TITLE Genetic changes in hepatitis E virus of subtype 1a in patients with sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
JOURNAL J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
PUBMED 14718624
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School, Division of Virology, Department of Infection and Immunity; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)

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FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne045-2000"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07320.1"
                     /db_xref="GI:40809811"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"
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Alignment Scores:

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Pred. No.:              199          Length:          412
Score:                  136.00       Matches:         136
Percent Similarity:     99.27%       Conservative:    0
Best Local Similarity:  99.27%       Mismatches:      1
Query Match:            24.77%       Indels:          0
DB:                     1            Gaps:            0

US-09-769-066-15 (1-549) x AB116180 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCTCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGTGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412
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RESULT 178
AB116181
LOCUS AB116181 412 bp RNA linear VRL 14-JAN-2004
DEFINITION Hepatitis E virus gene for capsid protein, partial cds, isolate: Ne052-2000.
ACCESSION AB116181
VERSION AB116181.1 GI:40809812
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M., Gotanda,Y. and Okamoto,H.
TITLE Genetic changes in hepatitis E virus of subtype 1a in patients with sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
JOURNAL J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
PUBMED 14718624
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School, Division of Virology, Department of Infection and Immunity; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)

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FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne052-2000"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
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                /country="Nepal:Kathmandu"
     CDS        <1. .>412
                /note="ORF2"
                /codon_start=2
                /product="capsid protein"
                /protein_id="BAD07321.1"
                /db_xref="GI:40809813"
                /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116181 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCTCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACTCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 179
AB116182
LOCUS       AB116182                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne053-2000.
ACCESSION   AB116182
VERSION     AB116182.1  GI:40809814
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES            Location/Qualifiers
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                    /virion
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                    /isolate="Ne053-2000"
                    /isolation_source="serum"
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                    /country="Nepal:Kathmandu"
     CDS            <1. .>412
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116182 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCTCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACTCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 180
AB116183
LOCUS       AB116183                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne054-2000.
ACCESSION   AB116183
VERSION     AB116183.1  GI:40809816
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
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REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
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                     /protein_id="BAD07323.1"
                     /db_xref="GI:40809817"
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116183 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412
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RESULT 181
AB116184
LOCUS       AB116184                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne055-2000.
ACCESSION   AB116184
VERSION     AB116184.1  GI:40809818
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne055-2000"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07324.1"
                     /db_xref="GI:40809819"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116184 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241
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Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 182
AB116185
LOCUS       AB116185                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne057-2000.
ACCESSION   AB116185
VERSION     AB116185.1  GI:40809820
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne057-2000"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /db_xref="GI:40809821"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116185 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 183
AB116186
LOCUS       AB116186                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne059-2000.
ACCESSION   AB116186
VERSION     AB116186.1  GI:40809822
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne059-2000"
                     /isolation_source="serum"
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                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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Alignment Scores:
Pred. No.:              199             Length:         412
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Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116186 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATTCACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTTTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCAGACGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTTATGAAGGATCTTTATTTTACTAGTACTAATGGCGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTCGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 184
AB116187
LOCUS       AB116187                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne060-2000.
ACCESSION   AB116187
VERSION     AB116187.1  GI:40809825
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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                     /note="ORF2"
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116187 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATTCACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTTTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCAGACGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAGGATCTTTATTTTACTAGTACTAATGGCGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTCGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 185
AB116188
LOCUS       AB116188                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne068-2000.
ACCESSION   AB116188
VERSION     AB116188.1  GI:40809829
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
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           Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
           Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116188 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACCAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 186
AB116189
LOCUS       AB116189                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne078-2000.
ACCESSION   AB116189
VERSION     AB116189.1  GI:40809831
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
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            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
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                     /mol_type="genomic RNA"
                     /isolate="Ne078-2000"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07329.1"
                     /db_xref="GI:40809832"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116189 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTCCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 187
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AB116190
LOCUS       AB116190                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne013-2002.
ACCESSION   AB116190
VERSION     AB116190.1  GI:40809834
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne013-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /protein_id="BAD07330.1"
                     /db_xref="GI:40809835"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116190 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAATACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCAGACGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTTATGAAGGATCTTTATTTTACTAGTACTAATGGCGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTCGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 188
AB116197
LOCUS       AB116197                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne032-2002.
ACCESSION   AB116197
VERSION     AB116197.1  GI:40809853
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
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                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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                     /codon_start=2
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                     /protein_id="BAD07337.1"
                     /db_xref="GI:40809854"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116197 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy         196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy         216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db         182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy         236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy         256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy         276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412

RESULT 189
AB116201
LOCUS       AB116201                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne039-2002.
ACCESSION   AB116201
VERSION     AB116201.1  GI:40809868
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /isolate="Ne039-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
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                     /db_xref="GI:40809869"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              199          Length:       412
Score:                  136.00       Matches:      136
Percent Similarity:     99.27%       Conservative: 0
Best Local Similarity:  99.27%       Mismatches:   1
Query Match:            24.77%       Indels:       0
DB:                     1            Gaps:         0

US-09-769-066-15 (1-549) x AB116201 (1-412)

Qy         156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db           2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGCTCACCCGTAAAT 61

Qy         176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy         196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy         216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db         182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy         236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db         242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy         256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy         276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412

RESULT 190
AB116204
LOCUS       AB116204                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne049-2002.
ACCESSION   AB116204
VERSION     AB116204.1  GI:40809874
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /isolation_source="serum"
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                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
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Alignment Scores:
Pred. No.:                199             Length:         412
Score:                    136.00          Matches:        136
Percent Similarity:       99.27%          Conservative:   0
Best Local Similarity:    99.27%          Mismatches:     1
Query Match:              24.77%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB116204 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412

RESULT 191
AB116214
LOCUS       AB116214                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne093-2002.
ACCESSION   AB116214
VERSION     AB116214.1  GI:40809896
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:                199             Length:         412
Score:                    136.00          Matches:        136
Percent Similarity:       99.27%          Conservative:   0
Best Local Similarity:    99.27%          Mismatches:     1
Query Match:              24.77%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB116214 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412

RESULT 192
AB116217
LOCUS       AB116217                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne105-2002.
ACCESSION   AB116217
VERSION     AB116217.1  GI:40809902
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
```

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            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne105-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07357.1"
                     /db_xref="GI:40809903"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116217 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412

RESULT 193
AB116218
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LOCUS       AB116218                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne107-2002.
ACCESSION   AB116218
VERSION     AB116218.1  GI:40809904
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /virion
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                     /isolate="Ne107-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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                     /codon_start=2
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                     /protein_id="BAD07358.1"
                     /db_xref="GI:40809905"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116218 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412

RESULT 194
AB116219
LOCUS       AB116219                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne117-2002.
ACCESSION   AB116219
VERSION     AB116219.1  GI:40809906
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116219 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         62 TCTTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTCCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412

RESULT 195
AB116221
LOCUS       AB116221                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne122-2002.
ACCESSION   AB116221
VERSION     AB116221.1  GI:40809910
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /virion
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                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
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Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116221 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAATCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412

RESULT 196
AB116224
LOCUS       AB116224                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne134-2002.
ACCESSION   AB116224
VERSION     AB116224.1  GI:40809916
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
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Alignment Scores:
Pred. No.:              199             Length:         412
Score:                  136.00          Matches:        136
Percent Similarity:     99.27%          Conservative:   0
Best Local Similarity:  99.27%          Mismatches:     1
Query Match:            24.77%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116224 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412

RESULT 197
AB085974
LOCUS       AB085974                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne136,
            clone:Ne136a.
ACCESSION   AB085974
VERSION     AB085974.1  GI:27372370
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne136"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /clone="Ne136a"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1a"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53696.1"
                     /db_xref="GI:27372371"
                     /translation="AEEEATSGLVKLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                202             Length:         412
Score:                    135.00          Matches:        135
Percent Similarity:       98.54%          Conservative:   0
Best Local Similarity:    98.54%          Mismatches:     2
Query Match:              24.59%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB085974 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTCAAGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTCTCCCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGCCTTCGCCGCGGCGCAGACGGGACCGCCGAGCTCACCACCACGGCAGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGCGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTCACCCTGTTTAACCTTGCTGACACTCTCCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 198
AB085981
LOCUS       AB085981                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne153.
ACCESSION   AB085981
VERSION     AB085981.1  GI:27372384
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES              Location/Qualifiers
     source           1. .412
                      /organism="Hepatitis E virus"
                      /virion
                      /mol_type="genomic RNA"
                      /isolate="Ne153"
                      /specific_host="human"
                      /db_xref="taxon:12461"
                      /tissue_type="serum"
                      /country="Nepal: Kathmandu"
                      /note="isolated from a patient with sporadic hepatitis
                      E-subtype 1c"
     CDS              <1. .>412
                      /note="ORF2"
                      /codon_start=2
                      /product="capsid protein"
                      /protein_id="BAC53703.1"
                      /db_xref="GI:27372385"
                      /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                      LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTSGVGEIGRGI
                      ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                202             Length:         412
Score:                    135.00          Matches:        135
Percent Similarity:       98.54%          Conservative:   0
Best Local Similarity:    98.54%          Mismatches:     2
Query Match:              24.59%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB085981 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAGTGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 199
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AB116191
LOCUS       AB116191                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne014-2002.
ACCESSION   AB116191
VERSION     AB116191.1  GI:40809839
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne014-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07331.1"
                     /db_xref="GI:40809840"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              202           Length:         412
Score:                  135.00        Matches:        135
Percent Similarity:     98.54%        Conservative:   0
Best Local Similarity:  98.54%        Mismatches:     2
Query Match:            24.59%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AB116191 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTGCTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTCGTCTCA 412

RESULT 200
AB116192
LOCUS       AB116192                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne016-2002.
ACCESSION   AB116192
VERSION     AB116192.1  GI:40809843
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne016-2002"
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                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07332.1"
                     /db_xref="GI:40809844"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              202           Length:         412
Score:                  135.00        Matches:        135
Percent Similarity:     98.54%        Conservative:   0
Best Local Similarity:  98.54%        Mismatches:     2
Query Match:            24.59%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AB116192 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
                 |||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTGCTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTCGTCTCA 412
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RESULT 201
AB116193
LOCUS AB116193 412 bp RNA linear VRL 14-JAN-2004
DEFINITION Hepatitis E virus gene for capsid protein, partial cds, isolate: Ne021-2002.
ACCESSION AB116193
VERSION AB116193.1 GI:40809845
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M., Gotanda,Y. and Okamoto,H.
TITLE Genetic changes in hepatitis E virus of subtype 1a in patients with sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
JOURNAL J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
PUBMED 14718624
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School, Division of Virology, Department of Infection and Immunity; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)

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                     /virion
                     /mol_type="genomic RNA"
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                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07333.1"
                     /db_xref="GI:40809846"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"
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Alignment Scores:
Pred. No.: 202 Length: 412
Score: 135.00 Matches: 135
Percent Similarity: 98.54% Conservative: 0
Best Local Similarity: 98.54% Mismatches: 2
Query Match: 24.59% Indels: 0
DB: 1 Gaps: 0

US-09-769-066-15 (1-549) x AB116193 (1-412)

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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
                 |||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                 ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412
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RESULT 202
AB116194
LOCUS AB116194 412 bp RNA linear VRL 14-JAN-2004
DEFINITION Hepatitis E virus gene for capsid protein, partial cds, isolate: Ne023-2002.
ACCESSION AB116194
VERSION AB116194.1 GI:40809847
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M., Gotanda,Y. and Okamoto,H.
TITLE Genetic changes in hepatitis E virus of subtype 1a in patients with sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
JOURNAL J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
PUBMED 14718624
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School, Division of Virology, Department of Infection and Immunity; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)

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                     /virion
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                     /isolate="Ne023-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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                     /codon_start=2
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:                202           Length:         412
Score:                    135.00        Matches:        135
Percent Similarity:       98.54%        Conservative:   0
Best Local Similarity:    98.54%        Mismatches:     2
Query Match:              24.59%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x AB116194 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCTGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 203
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LOCUS       AB116195                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne028-2002.
ACCESSION   AB116195
VERSION     AB116195.1  GI:40809849
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /isolate="Ne028-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
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                     /db_xref="GI:40809850"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                202           Length:         412
Score:                    135.00        Matches:        135
Percent Similarity:       98.54%        Conservative:   0
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Query Match:              24.59%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x AB116195 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 204
AB116196
LOCUS       AB116196                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116196
VERSION     AB116196.1  GI:40809851
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
```

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            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
    PUBMED  14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              202             Length:         412
Score:                  135.00          Matches:        135
Percent Similarity:     98.54%          Conservative:   0
Best Local Similarity:  98.54%          Mismatches:     2
Query Match:            24.59%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116196 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGYTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGYAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGKTATTCYAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTYTATTTTTWCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCYGTTGTCTCA 412

RESULT 205
AB116198
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LOCUS       AB116198                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116198
VERSION     AB116198.1  GI:40809860
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
    PUBMED  14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              202             Length:         412
Score:                  135.00          Matches:        135
Percent Similarity:     98.54%          Conservative:   0
Best Local Similarity:  98.54%          Mismatches:     2
Query Match:            24.59%          Indels:         0
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US-09-769-066-15 (1-549) x AB116198 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 206
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LOCUS       AB116200                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116200
VERSION     AB116200.1  GI:40809866
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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Alignment Scores:
Pred. No.:              202             Length:         412
Score:                  135.00          Matches:        135
Percent Similarity:     98.54%          Conservative:   0
Best Local Similarity:  98.54%          Mismatches:     2
Query Match:            24.59%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116200 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 207
AB116202
LOCUS       AB116202                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116202
VERSION     AB116202.1  GI:40809870
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
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            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
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                     /product="capsid protein"
                     /protein_id="BAD07342.1"
                     /db_xref="GI:40809871"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFSSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              202             Length:         412
Score:                  135.00          Matches:        135
Percent Similarity:     98.54%          Conservative:   0
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Best Local Similarity:  98.54%          Mismatches:     2
Query Match:            24.59%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116202 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 208
AB116203
LOCUS       AB116203                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne046-2002.
ACCESSION   AB116203
VERSION     AB116203.1  GI:40809872
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne046-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
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                     /db_xref="GI:40809873"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              202             Length:         412
Score:                  135.00          Matches:        135
Percent Similarity:     98.54%          Conservative:   0
Best Local Similarity:  98.54%          Mismatches:     2
Query Match:            24.59%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116203 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 209
AB116205
LOCUS       AB116205                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne050-2002.
ACCESSION   AB116205
VERSION     AB116205.1  GI:40809877
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="Ne050-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07345.1"
                     /db_xref="GI:40809878"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:                202             Length:         412
Score:                    135.00          Matches:        135
Percent Similarity:       98.54%          Conservative:   0
Best Local Similarity:    98.54%          Mismatches:     2
Query Match:              24.59%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB116205 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 210
AB116206
LOCUS       AB116206                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne054-2002.
ACCESSION   AB116206
VERSION     AB116206.1  GI:40809879
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
  PUBMED    14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
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                     /product="capsid protein"
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                     /db_xref="GI:40809880"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                202             Length:         412
Score:                    135.00          Matches:        135
Percent Similarity:       98.54%          Conservative:   0
Best Local Similarity:    98.54%          Mismatches:     2
Query Match:              24.59%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB116206 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 211
AB116208
LOCUS       AB116208                412 bp    RNA     linear   VRL 14-JAN-2004
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DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne066-2002.
ACCESSION   AB116208
VERSION     AB116208.1  GI:40809884
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /isolate="Ne066-2002"
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                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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                     /codon_start=2
                     /product="capsid protein"
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                     /db_xref="GI:40809885"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:                202             Length:         412
Score:                    135.00          Matches:        135
Percent Similarity:       98.54%          Conservative:   0
Best Local Similarity:    98.54%          Mismatches:     2
Query Match:              24.59%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB116208 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 212
AB116209
LOCUS       AB116209                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne073-2002.
ACCESSION   AB116209
VERSION     AB116209.1  GI:40809886
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /country="Nepal:Kathmandu"
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                     /codon_start=2
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                     /protein_id="BAD07349.1"
                     /db_xref="GI:40809887"
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Alignment Scores:
Pred. No.:                202             Length:         412
Score:                    135.00          Matches:        135
Percent Similarity:       98.54%          Conservative:   0
Best Local Similarity:    98.54%          Mismatches:     2
Query Match:              24.59%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB116209 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121
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Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 213
AB116210
LOCUS       AB116210                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne075-2002.
ACCESSION   AB116210
VERSION     AB116210.1  GI:40809888
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne075-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07350.1"
                     /db_xref="GI:40809889"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFSSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              202          Length:        412
Score:                  135.00       Matches:       135
Percent Similarity:     98.54%       Conservative:  0
Best Local Similarity:  98.54%       Mismatches:    2

Query Match:            24.59%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AB116210 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||||||    |||||||||||||||||||||||||||||||
Db        242 ACCCGCTTTATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 214
AB116211
LOCUS       AB116211                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne080-2002.
ACCESSION   AB116211
VERSION     AB116211.1  GI:40809890
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne080-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /product="capsid protein"
                     /protein_id="BAD07351.1"
                     /db_xref="GI:40809891"
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                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFSSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                202             Length:         412
Score:                    135.00          Matches:        135
Percent Similarity:       98.54%          Conservative:   0
Best Local Similarity:    98.54%          Mismatches:     2
Query Match:              24.59%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB116211 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 215
AB116212
LOCUS       AB116212                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne082-2002.
ACCESSION   AB116212
VERSION     AB116212.1  GI:40809892
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
  PUBMED    14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="Ne082-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /db_xref="GI:40809893"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                202             Length:         412
Score:                    135.00          Matches:        135
Percent Similarity:       98.54%          Conservative:   0
Best Local Similarity:    98.54%          Mismatches:     2
Query Match:              24.59%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB116212 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 216
AB116213
LOCUS       AB116213                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne092-2002.
ACCESSION   AB116213
VERSION     AB116213.1  GI:40809894
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
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            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /isolate="Ne092-2002"
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                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /protein_id="BAD07353.1"
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              202             Length:         412
Score:                  135.00          Matches:        135
Percent Similarity:     98.54%          Conservative:   0
Best Local Similarity:  98.54%          Mismatches:     2
Query Match:            24.59%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116213 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 217
AB116215
LOCUS       AB116215                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne095-2002.
ACCESSION   AB116215
VERSION     AB116215.1  GI:40809898
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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                     /isolate="Ne095-2002"
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                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
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                     /db_xref="GI:40809899"
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Alignment Scores:
Pred. No.:              202             Length:         412
Score:                  135.00          Matches:        135
Percent Similarity:     98.54%          Conservative:   0
Best Local Similarity:  98.54%          Mismatches:     2
Query Match:            24.59%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116215 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301
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Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 218
AB116216
LOCUS       AB116216                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne098-2002.
ACCESSION   AB116216
VERSION     AB116216.1  GI:40809900
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne098-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07356.1"
                     /db_xref="GI:40809901"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFSSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              202             Length:         412
Score:                  135.00          Matches:        135
Percent Similarity:     98.54%          Conservative:   0
Best Local Similarity:  98.54%          Mismatches:     2
Query Match:            24.59%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116216 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 219
AB116220
LOCUS       AB116220                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne118-2002.
ACCESSION   AB116220
VERSION     AB116220.1  GI:40809908
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne118-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07360.1"
                     /db_xref="GI:40809909"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              202             Length:         412
Score:                  135.00          Matches:        135
Percent Similarity:     98.54%          Conservative:   0
Best Local Similarity:  98.54%          Mismatches:     2
Query Match:            24.59%          Indels:         0
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DB:                 1           Gaps:          0

US-09-769-066-15 (1-549) x AB116220 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 220
AB116222
LOCUS       AB116222                 412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne131-2002.
ACCESSION   AB116222
VERSION     AB116222.1  GI:40809912
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne131-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
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                     /db_xref="GI:40809913"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              202           Length:         412
Score:                  135.00        Matches:        135
Percent Similarity:     98.54%        Conservative:   0
Best Local Similarity:  98.54%        Mismatches:     2
Query Match:            24.59%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AB116222 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 221
AB116223
LOCUS       AB116223                 412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne133-2002.
ACCESSION   AB116223
VERSION     AB116223.1  GI:40809914
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
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                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
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                     /db_xref="GI:40809915"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                202             Length:         412
Score:                    135.00          Matches:        135
Percent Similarity:       98.54%          Conservative:   0
Best Local Similarity:    98.54%          Mismatches:     2
Query Match:              24.59%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB116223 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 222
AB116225
LOCUS       AB116225                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne135-2002.
ACCESSION   AB116225
VERSION     AB116225.1  GI:40809918
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
  PUBMED    14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
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                     /product="capsid protein"
                     /protein_id="BAD07365.1"
                     /db_xref="GI:40809919"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                202             Length:         412
Score:                    135.00          Matches:        135
Percent Similarity:       98.54%          Conservative:   0
Best Local Similarity:    98.54%          Mismatches:     2
Query Match:              24.59%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB116225 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 223
AB116226
LOCUS       AB116226                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne138-2002.
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ACCESSION   AB116226
VERSION     AB116226.1  GI:40809920
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne138-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07366.1"
                     /db_xref="GI:40809921"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFSSTNGVGEIGRGI
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Alignment Scores:
Pred. No.:              202             Length:         412
Score:                  135.00          Matches:        135
Percent Similarity:     98.54%          Conservative:   0
Best Local Similarity:  98.54%          Mismatches:     2
Query Match:            24.59%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB116226 (1-412)

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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||||||    |||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 224
AB116227
LOCUS       AB116227                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne139-2002.
ACCESSION   AB116227
VERSION     AB116227.1  GI:40809922
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="Ne139-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07367.1"
                     /db_xref="GI:40809923"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              202             Length:         412
Score:                  135.00          Matches:        135
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US-09-769-066-15 (1-549) x AB116227 (1-412)

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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTCACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 225
AB073911
LOCUS       AB073911                421 bp    RNA     linear   VRL 15-DEC-2001
DEFINITION  Swine hepatitis E virus gene for capsid protein, partial cds,
            strain:swJ791.
ACCESSION   AB073911
VERSION     AB073911.1  GI:17826982
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Okamoto,H., Takahashi,M., Nishizawa,T., Fukai,K., Muramatsu,U. and
            Yoshikawa,A.
  TITLE     Analysis of the complete genome of indigenous swine hepatitis E
            virus isolated in Japan
  JOURNAL   Biochem. Biophys. Res. Commun. 289 (5), 929-936 (2001)
  MEDLINE   21616952
   PUBMED   11741279
REFERENCE   2  (bases 1 to 421)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-NOV-2001) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /virion
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                     /isolate="No. 791"
                     /specific_host="pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     gene            1. .421
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                     /gene="ORF2"
                     /codon_start=2
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                     /protein_id="BAB79303.1"
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                     /translation="SGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELE
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Alignment Scores:
Pred. No.:              202          Length:        421
Score:                  135.00       Matches:       135
Percent Similarity:     96.43%       Conservative:  0
Best Local Similarity:  96.43%       Mismatches:    5
Query Match:            24.59%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AB073911 (1-421)

Qy        153 SerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySer 172
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Db          2 TCGGGCGTGGCCGAGGAAGAGGCAACATCGGGTCTTGTCATGCTTTGTATACATGGTTCC 61

Qy        173 LeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCCGTTAATTCTTACACCAATACGCCCTACACTGGGGCGTTGGGGCTTCTTGACTTTGCA 121

Qy        193 LeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyr 212
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CTCGAGCTTGAATTCAGGAATTTGACCCCTGGGAACACCAATACTCGTGTGTCCCGGTAC 181

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
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Db        182 ACCAGTACGGCTCGCCACCGTTTACGCCGTGGCGCCGACGGAACCGCTGAGCTCACGACC 241

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGlu 252
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Db        242 ACTGCCGCCACGCGCTTCATGAAGGACCTACATTTCACCGGGACGAATGGCGTTGGTGAG 301

Qy        253 IleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GTGGGCCGTGGCATAGCCCTAACTCTATTTAATCTTGCTGATACACTTCTCGGCGGCTTG 361

Qy        273 ProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 CCGACAGAATTGATTTCGTCGGCTGGAGGTCAGCTCTTTTATTCCCGCCCAGTTGTCTCG 421

RESULT 226
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LOCUS       AB116199                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116199
VERSION     AB116199.1  GI:40809864
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    134.00          Matches:        134
Percent Similarity:       97.81%          Conservative:   0
Best Local Similarity:    97.81%          Mismatches:     3
Query Match:              24.41%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB116199 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTCTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGAATGCCGAGCTCACCACCACGGCTACT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATTGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCTCTCACCCTTTTCAATCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 227
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LOCUS       AB116207                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116207
VERSION     AB116207.1  GI:40809882
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
    PUBMED  14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)

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Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    134.00          Matches:        134
Percent Similarity:       97.81%          Conservative:   0
Best Local Similarity:    97.81%          Mismatches:     3
Query Match:              24.41%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB116207 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTCATCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 228
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LOCUS       AB073909                421 bp    RNA     linear   VRL 15-DEC-2001
DEFINITION  Swine hepatitis E virus gene for capsid protein, partial cds,
            strain:swJ570.
ACCESSION   AB073909
VERSION     AB073909.1  GI:17826977
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Okamoto,H., Takahashi,M., Nishizawa,T., Fukai,K., Muramatsu,U. and
            Yoshikawa,A.
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  TITLE     Analysis of the complete genome of indigenous swine hepatitis E
            virus isolated in Japan
  JOURNAL   Biochem. Biophys. Res. Commun. 289 (5), 929-936 (2001)
  MEDLINE   21616952
   PUBMED   11741279
REFERENCE   2  (bases 1 to 421)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-NOV-2001) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /strain="swJ570"
                     /isolate="No. 570"
                     /specific_host="pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     gene            1. .421
                     /gene="ORF2"
     CDS             <1. .>421
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAB79301.1"
                     /db_xref="GI:17826978"
                     /translation="TGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELE
                     FRNLTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVG
                     RGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                  205          Length:         421
Score:                      134.00       Matches:        134
Percent Similarity:         96.40%       Conservative:   0
Best Local Similarity:      96.40%       Mismatches:     5
Query Match:                24.41%       Indels:         0
DB:                         1            Gaps:           0

US-09-769-066-15 (1-549) x AB073909 (1-421)

Qy        154 GlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeu 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GGCGTGGCTGAAGAGGAGGCTACTTCCGGCCTAGTAATGCTCTGCATTCATGGCTCCCCT 64

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GTCAATTCTTATACTAATACACCCTACACAGGAGCACTGGGGCTTCTTGATTTTGCATTG 124

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 GAGCTTGAATTTAGGAATTTGACACCTGGGAATACTAACACCCGTGTATCCCGATATACC 184

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 AGCACAGCCCGCCATCGGCTGCGCCGCGGTGCCGACGGGACTGCCGAGCTTACTACTACG 244

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||
Db        245 GCGGCCACTCGATTTATGAAAGATCTGCACTTCACTGGTACGAATGGAGTTGGAGAGGTG 304

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 GGCCGTGGTATTGCTCTGACCTTGTTTAATCTTGCTGATACGCTTCTCGGTGGCCTGCCG 364

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 ACAGAATTGATTTCGTCGGCTGGGGGTCAGCTCTTCTACTCCCGCCCTGTCGTCTCG 421
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RESULT 229
AB073910
LOCUS       AB073910                421 bp    RNA     linear   VRL 15-DEC-2001
DEFINITION  Swine hepatitis E virus gene for capsid protein, partial cds,
            strain:swJ681.
ACCESSION   AB073910
VERSION     AB073910.1  GI:17826980
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Okamoto,H., Takahashi,M., Nishizawa,T., Fukai,K., Muramatsu,U. and
            Yoshikawa,A.
  TITLE     Analysis of the complete genome of indigenous swine hepatitis E
            virus isolated in Japan
  JOURNAL   Biochem. Biophys. Res. Commun. 289 (5), 929-936 (2001)
  MEDLINE   21616952
   PUBMED   11741279
REFERENCE   2  (bases 1 to 421)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-NOV-2001) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .421
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /strain="swJ681"
                     /isolate="No. 681"
                     /specific_host="pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     gene            1. .421
                     /gene="ORF2"
     CDS             <1. .>421
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAB79302.1"
                     /db_xref="GI:17826981"
                     /translation="TGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELE
                     FRNLTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVG
                     RGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                  205          Length:         421
Score:                      134.00       Matches:        134
Percent Similarity:         96.40%       Conservative:   0
Best Local Similarity:      96.40%       Mismatches:     5
Query Match:                24.41%       Indels:         0
DB:                         1            Gaps:           0

US-09-769-066-15 (1-549) x AB073910 (1-421)

Qy        154 GlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeu 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GGTGTCGCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTCTGTATTCATGGTTCCCCT 64

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GTCAATTCTTACACTAATACACCTTATACCGGTGCACTTGGGCTTCTTGATTTTGCACTA 124

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 GAACTTGAATTCAGGAACCTGACACCCGGGAACACCAATACCCGTGTGTCCCGGTATACT 184

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 AGTACAGCCCGTCATAGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACTACTACG 244

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
                ||||||||||||||||||||||||||||  ||||||  ||||||||||||||||||
Db        245 GCGGCCACGCGTTTTATGAAGGATTTGCATTTCACTGGCACGAATGGAGTTGGTGAAGTG 304

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 GGCCGAGGCATCGCTTTGACACTGTTCAACCTTGCTGACACGCTTCTCGGTGGTCTGCCG 364

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 ACAGAATTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 421
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RESULT 230
AF396860

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LOCUS       AF396860                405 bp    RNA     linear   VRL 03-DEC-2002
DEFINITION  Hepatitis E virus isolate 96-Nepalese structural protein 2 gene,
            partial cds.
ACCESSION   AF396860
VERSION     AF396860.1  GI:15088672
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 405)
  AUTHORS   He,J., Innis,B.L., Shrestha,M.P., Clayson,E.T., Scoot,R.M.,
            Linthicum,K.J., Musser,G.G., Gigliotti,S.C., Binn,L.N.,
            Kuschner,R.A. and Vaughn,D.W.
  TITLE     Evidence that Rodents Are a Reservoir of Hepatitis E Virus for
            Humans in Nepal
  JOURNAL   J. Clin. Microbiol. 40 (12), 4493-4498 (2002)
   PUBMED   12454141
REFERENCE   2  (bases 1 to 405)
  AUTHORS   He,J., Shrestha,M.P., Innis,B.L., Scoot,R.M., Linthicum,K.J.,
            Mussert,G.G., Clayson,E.T., Gigliotti,S.C., Binn,L.N.,
            Kuschner,R.A. and Vaughn,D.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUL-2001) Virus Diseases, Walter Reed Army Institute
            of Research, 503 Robert Grant Avenue, Silver Spring, MD 20910, USA
FEATURES             Location/Qualifiers
     source          1. .405
                     /organism="Hepatitis E virus"
                     /virion
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                     /db_xref="taxon:12461"
                     /country="Nepal"
                     /note="RT-PCR amplified from rodent serum"
     CDS             <1. .>405
                     /codon_start=1
                     /product="structural protein 2"
                     /protein_id="AAK84155.1"
                     /db_xref="GI:15088673"
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Pred. No.:              207             Length:         405
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Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            24.23%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF396860 (1-405)

Qy        396 AlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeu 415
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGACGGCCGCCCCCTC 60

Qy        416 SerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSer 435
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCT 120

Qy        436 PheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSer 455
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCTGGGAGGCAGGCACAACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGC 180

Qy        456 AspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThr 475
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACCAACTGCTCGTCGAGAATGCCGCCGGGCACCGGGTTGCTATTTCCACTTACACCACT 240

Qy        476 SerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAla 495
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGCCTGGGTGCTGGACCCGTTTCCATTTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCG 300

Qy        496 LeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPhe 515
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTAGCATTGCTTGAGGATACCTTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTC 360

Qy        516 CysProGluCysArgProLeuGlyLeuGlnGlyCysAla 528
                ||||||||||||||||||||||||||||||||||||||
Db        361 TGCCCAGAGTGCCGCCCCCTTGGCCTCCAGGGCTGTGCT 399
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RESULT 231
AB079763

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LOCUS       AB079763                412 bp    RNA     linear   VRL 06-NOV-2002
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JF2.
ACCESSION   AB079763
VERSION     AB079763.1  GI:24636299
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Suzuki,K., Aikawa,T. and Okamoto,H.
  TITLE     Fulminant hepatitis E in Japan
  JOURNAL   N. Engl. J. Med. 347 (18), 1456 (2002)
  MEDLINE   22297680
   PUBMED   12409557
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-FEB-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi, Tochigi 329-0498, Japan
            (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
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                     /db_xref="taxon:12461"
                     /country="Japan"
                     /note="HE-JF2 was isolated from a Japanese patient
                     (Patient 2) with fulminant hepatitis of unknown
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     CDS             <1. .>412
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ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:

Pred. No.:	210	Length:	412
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Percent Similarity:	96.35%	Conservative:	0
Best Local Similarity:	96.35%	Mismatches:	5
Query Match:	24.04%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AB079763 (1-412)

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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGCCTGGTAATGCTTTGCATTCATGGCTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACAAATACACCTTATACTGGAGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTCAGGAACTTGACACCTGGGAACACTAATACCCGTGTATCCCGATACACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGAGTTGGTGAGGTAGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCCCTGACACTGTTCAATCTTGCTGATACACTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGCTGTTCTACTCCCGCCCCGTCGTCTCA 412
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RESULT 232
AB082560
LOCUS AB082560 412 bp RNA linear VRL 03-SEP-2002
DEFINITION Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA4.
ACCESSION AB082560
VERSION AB082560.1 GI:22759616
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y., Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
TITLE Polyphyletic Strains of Hepatitis E Virus Are Responsible for Sporadic Cases of Acute Hepatitis in Japan
JOURNAL J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
PUBMED 12202555
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School, Immunology Division and Division of Molecular Virology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
FEATURES Location/Qualifiers
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/organism="Hepatitis E virus"
/virion
/mol_type="genomic RNA"
/isolate="HE-JA4"
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/specific_host="human"
/db_xref="taxon:12461"
/clone="HE-JA4-2"
/country="Japan:Hokkaido, Sapporo"
gene 1. .412
/gene="ORF2"
CDS <1. .>412
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ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:

Pred. No.:	210	Length:	412
Score:	132.00	Matches:	132
Percent Similarity:	96.35%	Conservative:	0
Best Local Similarity:	96.35%	Mismatches:	5
Query Match:	24.04%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AB082560 (1-412)

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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTGGTAATGCTTTGTATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGAAATCTGACACCCGGGAACACAAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCACCGGCTGCGCCGCGGTGCTGATGGGACTGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGTTTCATGAAGGATTTACATTTTACTGGCACGAACGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATCGCTCTGACATTGTTTAATCTCGCTGACACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCG 412
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RESULT 233
AB082561
LOCUS AB082561 412 bp RNA linear VRL 03-SEP-2002
DEFINITION Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA5.
ACCESSION AB082561
VERSION AB082561.1 GI:22759618
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y., Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
TITLE Polyphyletic Strains of Hepatitis E Virus Are Responsible for Sporadic Cases of Acute Hepatitis in Japan
JOURNAL J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
PUBMED 12202555
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.

```
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /db_xref="taxon:12461"
                     /clone="HE-JA5-2"
                     /country="Japan:Iwate, Morioka"
     gene            1. .412
                     /gene="ORF2"
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                     /protein_id="BAC10960.1"
                     /db_xref="GI:22759619"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:                210           Length:         412
Score:                    132.00        Matches:        132
Percent Similarity:       96.35%        Conservative:   0
Best Local Similarity:    96.35%        Mismatches:     5
Query Match:              24.04%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x AB082561 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTGATGCTCTGTATTCATGGCTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATTTGACACCTGGGAATACCAACACTCGTGTATCTCGATACACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCCGAGCTCACTACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGTTTTATGAAGGACTTGCATTTCACTGGCACGAATGGAGTTGGTGAAGTRGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACACTGTTTAATCTTGCTGATACGCTTCTCGGTGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCCGTCGTCTCA 412

RESULT 234
AB082562
LOCUS       AB082562                412 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA6.
ACCESSION   AB082562
VERSION     AB082562.1  GI:22759620
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JA6"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /clone="HE-JA6-2"
                     /country="Japan:Iwate, Morioka"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /protein_id="BAC10961.1"
                     /db_xref="GI:22759621"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210           Length:         412
Score:                    132.00        Matches:        132
Percent Similarity:       96.35%        Conservative:   0
Best Local Similarity:    96.35%        Mismatches:     5
Query Match:              24.04%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x AB082562 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTAATGCTCTGTATTCACGGCTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTCGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACACCCGGGAATACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGCCGCGGTGCCGACGGGACCGCTGAACTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGTTTTATGAAAGACCTGCATTTTACTGGCACGAATGGGGTCGGCGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATTGCTCTGACATTGTTCAACCTTGCTGATACGCTTCTCGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTAATTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCG 412

RESULT 235
AB082563
LOCUS       AB082563                412 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA7.
ACCESSION   AB082563
VERSION     AB082563.1  GI:22759622
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae,
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JA7"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /clone="HE-JA7-2"
                     /country="Japan:Iwate, Morioka"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /protein_id="BAC10962.1"
                     /db_xref="GI:22759623"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AB082563 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTGGTAATGCTTTGTATCCACGGCTCCCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTATACTGGTGCTTTGGGGCTTCTTGATTTTGCATTAGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGAAACCTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGCCGCGGCGCTGATGGGACCGCTGAGCTCACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACACGTTTTATGAAGGATTTGCATTTTACTGGCACGAATGGCGTTGGAGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCCCTGACACTGTTTAATCTTGCTGATACGCTTCTTGGTGGCTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAATTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 236
AB082564
LOCUS       AB082564                412 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA8.
ACCESSION   AB082564
VERSION     AB082564.1  GI:22759624
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /clone="HE-JA8-2"
                     /country="Japan:Iwate, Morioka"
     gene            1. .412
                     /gene="ORF2"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
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DB:                    1             Gaps:          0

US-09-769-066-15 (1-549) x AB082564 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCCGAGGAGGAGGCTACCTCCGGCCTGGTAATGCTTTGTATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAACTA 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTCACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACACGTTTTATGAAGGATTTGCATTTTACTGGCACGAATGGTGTTGGTGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATCGCTCTGACATTGTTTAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 237
AB082565
LOCUS       AB082565                412 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA9.
ACCESSION   AB082565
VERSION     AB082565.1  GI:22759626
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
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                     /virion
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                     /clone="HE-JA9-2"
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                     /gene="ORF2"
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                     /db_xref="GI:22759627"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB082565 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCATGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCCGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACGCGTTTTATGAAGGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTTCTCGGTGGCTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 238
AB082566
LOCUS       AB082566                412 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA10.
ACCESSION   AB082566
VERSION     AB082566.1  GI:22759628
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
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                     /country="Japan:Tokyo"
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Alignment Scores:
Pred. No.:                210          Length:          412
Score:                    132.00       Matches:         132
Percent Similarity:       96.35%       Conservative:    0
Best Local Similarity:    96.35%       Mismatches:      5
Query Match:              24.04%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-15 (1-549) x AB082566 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db          2 GCCGAGGAGGAGGCTACCTCCGGCCTGGTAATGCTTTGTATCCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||  ||||||  ||||||||||||||||||||  ||||||
Db        242 ACACGTTTCATGAAGGATTTGCATTTTACTGGCACGAACGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATCGCTCTGACATTGTTTAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 239
AB088418
LOCUS       AB088418                412 bp    RNA     linear   VRL 31-OCT-2002
DEFINITION  Hepatitis E virus gene for capsid, partial cds.
ACCESSION   AB088418
VERSION     AB088418.1  GI:24430384
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Aikawa,T., Kojima,M., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Identification of indigenous hepatitis E virus from a Japanese
            patient who contracted sporadic acute hepatitis in 1982
  JOURNAL   J. Infect. Dis. 186 (10), 1535-1536 (2002)
  MEDLINE   22292015
   PUBMED   12404177
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JUL-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JO-1982"
                     /db_xref="taxon:12461"
                     /country="Japan:Mito"
                     /note="An HEV strain (genotype III) isolated from serum of
                     a Japanese patient who developed sporadic acute hepatitis
                     in 1982."
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid"
                     /protein_id="BAC22593.1"
                     /db_xref="GI:24430385"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210          Length:          412
Score:                    132.00       Matches:         132
Percent Similarity:       96.35%       Conservative:    0
Best Local Similarity:    96.35%       Mismatches:      5
Query Match:              24.04%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-15 (1-549) x AB088418 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGCCTGGTAATGCTTTGCATTCATGGTTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACAAATACACCTTATACTGGAGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        122 GAATTTAGGAATTTGACACCTGGGAACACCAATACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAACTCACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||  ||||||  ||||||||||||||||||||  ||||||
Db        242 ACGCGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTTAATCTTGCTGATACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTTTCA 412

RESULT 240
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AB093535
LOCUS       AB093535                412 bp    RNA     linear   VRL 12-APR-2003
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds.
ACCESSION   AB093535
VERSION     AB093535.1  GI:29824080
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yajima,Y., Takahashi,N., Yamagishi,H., Kodama,A., Miyazaki,A.,
            Sugiyama,K., Eda,Y. and Okamoto,H.
  TITLE     An acute hepatitis case domestically infected with a hepatitis E
            virus whose nucleotode sequence showed a high similarity to that
            from a domestic swine in Japan
  JOURNAL   Jpn. J. Gastroenterol. 100, 454-458 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HEV-Sendai"
                     /isolation_source="human serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Japan:Sendai"
                     /note="genotype III"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /note="The HEV-Sendai isolate is 98.3% similar to a swine
                     HEV isolate of Japan origin (swJ791: accession no.
                     AB073911), in the 412-nt sequence of ORF2."
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC75540.1"
                     /db_xref="GI:29824081"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB093535 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAAGAGGCAACATCGGGTCTTGTCATGCTTTGTATACATGGCTCCCCCGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACCAATACGCCCTACACTGGGGCGTTGGGGCTTCTTGACTTTGCACTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTCAGGAATTTGACCCCTGGGAACACCAATACCCGTGTGTCCCGGTACACCAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGTCACCGTTTACGCCGTGGCGCTGACGGAACCGCTGAGCTCACGACCACTGCCGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACGCGCTTCATGAAGGACCTACATTTCACCGGGACGAATGGCGTTGGTGAGGTGGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTCTATTTAATCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTCTTTTATTCCCGCCCAGTTGTCTCG 412

RESULT 241
AB094203
LOCUS       AB094203                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ1-1.
ACCESSION   AB094203
VERSION     AB094203.1  GI:29292661
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ1-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66226.1"
                     /db_xref="GI:29292662"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB094203 (1-412)
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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ1-4"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66229.1"
                     /db_xref="GI:29292668"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210           Length:        412
Score:                    132.00        Matches:       132
Percent Similarity:       96.35%        Conservative:  0
Best Local Similarity:    96.35%        Mismatches:    5
Query Match:              24.04%        Indels:        0
DB:                       1             Gaps:          0

US-09-769-066-15 (1-549) x AB094206 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db          2 GCGGAGGAGGAGGCTACTTCCGGTCTCGTAATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        122 GAGTTTAGAAATTTGACACCCGGGAACACCAACACCCGCGTTTCCAGGTACACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||    ||||||    ||||||||||||||||||||    ||||||
Db        242 ACACGTTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTAGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCTCTTACACTGTTTAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATATCGTCGGCTGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 244
AB094207
LOCUS       AB094207                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ2-1.
ACCESSION   AB094207
VERSION     AB094207.1  GI:29292669
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ2-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66230.1"
                     /db_xref="GI:29292670"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210           Length:        412
Score:                    132.00        Matches:       132
Percent Similarity:       96.35%        Conservative:  0
Best Local Similarity:    96.35%        Mismatches:    5
Query Match:              24.04%        Indels:        0
DB:                       1             Gaps:          0

US-09-769-066-15 (1-549) x AB094207 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTTGTAATGCTTTGCATTCATGGCTCGCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        122 GAGTTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTGTCCAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||    ||||||    ||||||||||||||||||||    ||||||
Db        242 ACACGTTTCATGAAGGATCTGCATTTTACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCTCTTACACTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 245
AB094208
LOCUS       AB094208                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ2-2.
```

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ACCESSION   AB094208
VERSION     AB094208.1  GI:29292671
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ2-2"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66231.1"
                     /db_xref="GI:29292672"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094208 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTTGTAATGCTTTGCATTCATGGCTCGCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        122 GAGTTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTGTCCAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||| |||||| |||||||||||||||||| ||||||
Db        242 ACACGTTTCATGAAGGATCTGCATTTTACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCTCTTACACTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 246
AB094209
LOCUS       AB094209                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ2-3.
ACCESSION   AB094209
VERSION     AB094209.1  GI:29292673
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ2-3"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
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                     /db_xref="GI:29292674"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094209 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTTGTAATGCTTTGCATTCATGGCTCGCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121
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Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACACGTTTCATGAAGGATCTGCATTTTACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCTCTTACACTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412
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RESULT 247
AB094210
LOCUS AB094210 412 bp RNA linear VRL 27-MAR-2003
DEFINITION Swine hepatitis E virus ORF2 gene for capsid protein, partial cds, isolate:swJ2-4.
ACCESSION AB094210
VERSION AB094210.1 GI:29292675
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T., Tsuda,F. and Okamoto,H.
TITLE Swine hepatitis E virus strains in Japan form four phylogenetic clusters comparable with those of Japanese isolates of human hepatitis E virus
JOURNAL J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
PUBMED 12655086
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School, Immunology Division and Division of Molecular Virology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
FEATURES Location/Qualifiers
source 1. .412
/organism="Swine hepatitis E virus"
/virion
/mol_type="genomic RNA"
/isolate="swJ2-4"
/isolation_source="swine serum"
/specific_host="farm pig"
/db_xref="taxon:63421"
/country="Japan"
CDS <1. .>412
/note="ORF2"
/codon_start=2
/product="capsid protein"
/protein_id="BAC66233.1"
/db_xref="GI:29292676"
/translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.: 210 Length: 412
Score: 132.00 Matches: 132
Percent Similarity: 96.35% Conservative: 0
Best Local Similarity: 96.35% Mismatches: 5
Query Match: 24.04% Indels: 0
DB: 1 Gaps: 0

US-09-769-066-15 (1-549) x AB094210 (1-412)

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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTTGTAATGCTTTGCATTCATGGCTCGCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        122 GAGTTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTGTCTAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACACGTTTCATGAAGGATCTGCATTTTACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCTCTTACACTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412
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RESULT 248
AB094211
LOCUS AB094211 412 bp RNA linear VRL 27-MAR-2003
DEFINITION Swine hepatitis E virus ORF2 gene for capsid protein, partial cds, isolate:swJ2-5.
ACCESSION AB094211
VERSION AB094211.1 GI:29292677
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T., Tsuda,F. and Okamoto,H.
TITLE Swine hepatitis E virus strains in Japan form four phylogenetic clusters comparable with those of Japanese isolates of human hepatitis E virus
JOURNAL J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
PUBMED 12655086
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School, Immunology Division and Division of Molecular Virology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
FEATURES Location/Qualifiers
source 1. .412
/organism="Swine hepatitis E virus"
/virion
/mol_type="genomic RNA"
/isolate="swJ2-5"
/isolation_source="swine serum"
/specific_host="farm pig"
/db_xref="taxon:63421"
/country="Japan"
CDS <1. .>412

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                     /protein_id="BAC66234.1"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094211 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTTGTAATGCTTTGTATTCATGGCTCGCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTGTCCAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACACGTTTCATGAAGGATCTGCATTTTACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATCGCTCTTACACTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 249
AB094212
LOCUS       AB094212                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ3-1.
ACCESSION   AB094212
VERSION     AB094212.1  GI:29292679
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094212 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAAGAGGCTACTTCCGGTCTCGTAATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAACACACCTTACACTGGGGCATTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGGAACTTGACGCCCGGGAACACTAACACCCGTGTTTCCAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACACGTTTCATGAAGGATTTGCATTTTACCGGCACGAACGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCTCTGACACTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 250
AB094213
LOCUS       AB094213                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ3-2.
ACCESSION   AB094213
VERSION     AB094213.1  GI:29292681
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
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  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /db_xref="GI:29292682"
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Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094213 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAAGAGGCTACTTCCGGTCTCGTAATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAACACACCTTACACTGGGGCATTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGGAACTTGACGCCCGGGAACACTAACACCCGTGTTTCCAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACACGTTTCATGAAGGATTTGCATTTTACCGGCACGAACGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCTCTGACACTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412
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RESULT 251
AB094214
LOCUS       AB094214                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ3-3.
ACCESSION   AB094214
VERSION     AB094214.1  GI:29292683
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ3-3"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66237.1"
                     /db_xref="GI:29292684"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094214 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCCGGTCTTGTAATGCTTTGCATTCACGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTACACTGGGGCATTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGGAACCTGACGCCCGGGAACACTAACACCCGTGTCTCCAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCC 241
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Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGTTTCATGAAGGATTTGCATTTTACCGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCTCTGACACTGTTCAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 252
AB094215
LOCUS       AB094215                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ4-1.
ACCESSION   AB094215
VERSION     AB094215.1  GI:29292685
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ4-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66238.1"
                     /db_xref="GI:29292686"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AB094215 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCCACTTCCGGTCTTGTGATGCTTTGTATTCATGGTTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGAAATCTGACACCCGGGAACACTAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACAGGTTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACACGTTTTATGAAAGATCTGCATTTTACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTTAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CTGATTTCGTCGGCTGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 253
AB094216
LOCUS       AB094216                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ5-1.
ACCESSION   AB094216
VERSION     AB094216.1  GI:29292687
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ5-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
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Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094216 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCGACATCGGGGCTGGTCATGCTTTGTATTCATGGTTCCCCTGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACCAACACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTCAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCTTGCGCCGTGGCGCCGACGGAACCGCCGAGCTTACGACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACTAATGGCGTTGGTGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCTCTGACTTTATTCAACCTTGCTGATACACTTCTCGGCGGCTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGCCAGCTCTTTTACTCCCGTCCAGTCGTCTCG 412

RESULT 254
AB094217
LOCUS       AB094217                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ6-1.
ACCESSION   AB094217
VERSION     AB094217.1  GI:29292689
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
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Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094217 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACTTCCGGTCTGGTAATGCTTTGTATTCACGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGCGCATTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAATCTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTCACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACACGATTCATGAAGGACTTGCACTTTACTGGCACAAACGGTGTTGGTGAGGTGGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACGCTATTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 255
AB094218
LOCUS       AB094218                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ6-2.
ACCESSION   AB094218
VERSION     AB094218.1  GI:29292691
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
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  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094218 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          2 GCTGAGGAGGAAGCTACTTCCGGTCTGGTAATGCTTTGTATTCACGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGCGCATTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAATCTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTCACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||| |||||| |||||||||||||||||| ||||||
Db        242 ACACGATTCATGAAGGACTTGCACTTTACTGGCACAAACGGTGTTGGTGAGGTGGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACGCTATTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 256
AB094238
LOCUS       AB094238                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ10-1.
ACCESSION   AB094238
VERSION     AB094238.1  GI:29292731
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
  PUBMED    12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /virion
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                     /isolate="swJ10-1"
                     /isolation_source="swine serum"
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                     /db_xref="taxon:63421"
                     /country="Japan"
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Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
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Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094238 (1-412)

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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCTTACACTGGCGCATTGGGGCTCCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAATCTGACACCTGGGAACACTAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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RESULT 257
AB094239
LOCUS       AB094239                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ10-2.
ACCESSION   AB094239
VERSION     AB094239.1  GI:29292733
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ10-2"
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                     /country="Japan"
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Alignment Scores:
Pred. No.:              210           Length:         412
Score:                  132.00        Matches:        132
Percent Similarity:     96.35%        Conservative:   0
Best Local Similarity:  96.35%        Mismatches:     5
Query Match:            24.04%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AB094239 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAAGCTACTTCCGGTCTGGTAATGCTTTGTATTCATGGCTCCCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGCCGCGGTGCCGATGGGACCGCTGAGCTCACCACCACAGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATTGCTCTGACGCTATTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAATTGTTCTACTCCCGCCCTGTTGTCTCG 412

RESULT 258
AB094240
LOCUS       AB094240                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ11-1.
ACCESSION   AB094240
VERSION     AB094240.1  GI:29292735
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              210           Length:         412
Score:                  132.00        Matches:        132
Percent Similarity:     96.35%        Conservative:   0
Best Local Similarity:  96.35%        Mismatches:     5
Query Match:            24.04%        Indels:         0
DB:                     1             Gaps:           0
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US-09-769-066-15 (1-549) x AB094240 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCYCCCGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAACACACCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATCGCCCTGACATTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 259
AB094241
LOCUS       AB094241                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ11-2.
ACCESSION   AB094241
VERSION     AB094241.1  GI:29292737
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210             Length:          412
Score:                    132.00          Matches:         132
Percent Similarity:       96.35%          Conservative:    0
Best Local Similarity:    96.35%          Mismatches:      5
Query Match:              24.04%          Indels:          0
DB:                       1               Gaps:            0

US-09-769-066-15 (1-549) x AB094241 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCTCCYGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAACACACCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGCTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATCGCCCTGACATTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 260
AB094242
LOCUS       AB094242                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ11-3.
ACCESSION   AB094242
VERSION     AB094242.1  GI:29292739
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:                210          Length:         412
Score:                    132.00       Matches:        132
Percent Similarity:       96.35%       Conservative:   0
Best Local Similarity:    96.35%       Mismatches:     5
Query Match:              24.04%       Indels:         0
DB:                       1            Gaps:           0

US-09-769-066-15 (1-549) x AB094242 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAACACACCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGCTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCCCTGACATTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 261
AB094243
LOCUS       AB094243                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ11-4.
ACCESSION   AB094243
VERSION     AB094243.1  GI:29292741
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
  PUBMED    12655086
REFERENCE   2  (bases 1 to 412)
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            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
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                      /db_xref="GI:29292742"
                      /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                      LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                      ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210          Length:         412
Score:                    132.00       Matches:        132
Percent Similarity:       96.35%       Conservative:   0
Best Local Similarity:    96.35%       Mismatches:     5
Query Match:              24.04%       Indels:         0
DB:                       1            Gaps:           0

US-09-769-066-15 (1-549) x AB094243 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCTCCCGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAACACACCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||   ||||||   ||||||||||||||||||||   ||||||
Db        242 ACACGCTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCCCTGACATTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 262
AB094244
LOCUS       AB094244                412 bp    RNA     linear   VRL 27-MAR-2003
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DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ11-5.
ACCESSION   AB094244
VERSION     AB094244.1  GI:29292743
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ11-5"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66267.1"
                     /db_xref="GI:29292744"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AB094244 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCTCCCGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAACACACCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||    ||||||    ||||||||||||||||||    ||||||
Db        242 ACACGCTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCCCTGACATTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 263
AB094245
LOCUS       AB094245                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ11-6.
ACCESSION   AB094245
VERSION     AB094245.1  GI:29292745
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ11-6"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66268.1"
                     /db_xref="GI:29292746"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AB094245 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCTCCCGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 TCCTATACTAACACACCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy         196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db         122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy         216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db         182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy         236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
                ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db         242 ACACGCTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTGGGTCGT 301

Qy         256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         302 GGTATCGCCCTGACATTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy         276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 264
AB094246
LOCUS       AB094246                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ11-7.
ACCESSION   AB094246
VERSION     AB094246.1  GI:29292747
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ11-7"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210             Length:        412
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Score:                  132.00          Matches:       132
Percent Similarity:     96.35%          Conservative:  0
Best Local Similarity:  96.35%          Mismatches:    5
Query Match:            24.04%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-15 (1-549) x AB094246 (1-412)

Qy         156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db           2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCTCCCGTTAAT 61

Qy         176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 TCCTATACTAACACACCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy         196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db         122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy         216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db         182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy         236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
                ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db         242 ACACGCTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTGGGTCGT 301

Qy         256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         302 GGTATCGCCCTGACATTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy         276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 265
AB094247
LOCUS       AB094247                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ11-8.
ACCESSION   AB094247
VERSION     AB094247.1  GI:29292749
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                /country="Japan"
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                ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB094247 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCTCCCGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAACACACCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACACGCTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCCCTGACATTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 266
AB094248
LOCUS       AB094248                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ11-9.
ACCESSION   AB094248
VERSION     AB094248.1  GI:29292751
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES            Location/Qualifiers
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                    /db_xref="taxon:63421"
                    /country="Japan"
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                    /note="ORF2"
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                    ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB094248 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCTCCCGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAACACACCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGCTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCCCTGACATTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCTCGCCCTGTTGTCTCG 412

RESULT 267
AB094249
LOCUS       AB094249                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ11-10.
ACCESSION   AB094249
VERSION     AB094249.1  GI:29292753
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
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          Hepevirus.
REFERENCE 1
  AUTHORS Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
          Tsuda,F. and Okamoto,H.
  TITLE   Swine hepatitis E virus strains in Japan form four phylogenetic
          clusters comparable with those of Japanese isolates of human
          hepatitis E virus
  JOURNAL J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED 12655086
REFERENCE 2  (bases 1 to 412)
  AUTHORS Okamoto,H.
  TITLE   Direct Submission
  JOURNAL Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
          Immunology Division and Division of Molecular Virology; 3311-1
          Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
          Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
          Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ11-10"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66272.1"
                     /db_xref="GI:29292754"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:        412
Score:                  132.00       Matches:       132
Percent Similarity:     96.35%       Conservative:  0
Best Local Similarity:  96.35%       Mismatches:    5
Query Match:            24.04%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AB094249 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCTCCCGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAAYACACCTTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACACGCTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCCCTGACATTGTTTAATCTCGCTGAYACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 268
AB094256
LOCUS       AB094256                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-1.
ACCESSION   AB094256
VERSION     AB094256.1  GI:29292767
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ15-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66279.1"
                     /db_xref="GI:29292768"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:        412
Score:                  132.00       Matches:       132
Percent Similarity:     96.35%       Conservative:  0
Best Local Similarity:  96.35%       Mismatches:    5
Query Match:            24.04%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AB094256 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCCCTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGTCGTGGRGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
                ||||||||||||||||||||    ||||||    ||||||||||||||||||    ||||||
Db        242 ACGCGTTTCATGAAGGACCTGCACTTTACTGGCACGAAYGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAACCTTGCTGATACACTTCTCGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CTGATTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 269
AB094257
LOCUS       AB094257                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-2.
ACCESSION   AB094257
VERSION     AB094257.1  GI:29292769
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
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                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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Alignment Scores:
Pred. No.:              210             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB094257 (1-412)
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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCCCTGGGGCTTCTTGATTTTGCAYTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
                ||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGTCGTGGAGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
                ||||||||||||||||||||    ||||||    ||||||||||||||||||    ||||||
Db        242 ACGCGTTTCATGAAGGACCTGCACTTTACTGGCACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAACCTTGCTGATACACTTCTCGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CTGATTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 270
AB094259
LOCUS       AB094259                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-4.
ACCESSION   AB094259
VERSION     AB094259.1  GI:29292773
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /country="Japan"
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Alignment Scores:
Pred. No.:              210           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB094259 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCTCTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGTCGTGGAGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACGCGTTTCATGAAGGACCTGCACTTTACTGGCACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAACCTAGCTGATACACTTCTCGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CTGATTTCGTCGGCCGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 271
AB094260
LOCUS       AB094260                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-5.
ACCESSION   AB094260
VERSION     AB094260.1  GI:29292775
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:63421"
                     /country="Japan"
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Alignment Scores:
Pred. No.:              210           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB094260 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCCCTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGTCGTGGAGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACGCGTTTCATGAAGGACCTGCACTTTACTGGCACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAACCTTGCTGATACACTTCTCGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CTGATTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 272
AB094261
LOCUS       AB094261                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-6.
ACCESSION   AB094261
VERSION     AB094261.1  GI:29292777
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
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   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Pax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ15-6"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66284.1"
                     /db_xref="GI:29292778"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210          Length:          412
Score:                    132.00       Matches:         132
Percent Similarity:       96.35%       Conservative:    0
Best Local Similarity:    96.35%       Mismatches:      5
Query Match:              24.04%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-15 (1-549) x AB094261 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCCCTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGTCGTGGAGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||    ||||||    ||||||||||||||||||    ||||||
Db        242 ACGCGTTTCATGAAGGACCTGCACTTTACTGGCACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAACCTTGCTGATACACTTCTCGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CTGATTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 273
AB094262
LOCUS       AB094262                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-7.
ACCESSION   AB094262
VERSION     AB094262.1  GI:29292779
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ15-7"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66285.1"
                     /db_xref="GI:29292780"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210          Length:          412
Score:                    132.00       Matches:         132
Percent Similarity:       96.35%       Conservative:    0
Best Local Similarity:    96.35%       Mismatches:      5
Query Match:              24.04%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-15 (1-549) x AB094262 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCCCTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGTCGTGGAGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||    ||||||    ||||||||||||||||||    ||||||
Db        242 ACGCGTTTCATGAAGGACCTGCACTTTACTGGCACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAACCTTGCTGATACACTTCTCGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CTGATTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 274
AB094263
LOCUS       AB094263                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-8.
ACCESSION   AB094263
VERSION     AB094263.1  GI:29292781
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ15-8"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /protein_id="BAC66286.1"
                     /db_xref="GI:29292782"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB094263 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACACCCGTGTGTCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGTCGTGGTGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACGCGATTCATGAAGGACCTGCACTTTACTGGCACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAACCTAGCTGATACGCTTCTCGGCGGACTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CTGATTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCG 412

RESULT 275
AB094264
LOCUS       AB094264                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-9.
ACCESSION   AB094264
VERSION     AB094264.1  GI:29292783
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
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                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /note="ORF2"
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                     /db_xref="GI:29292784"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
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Query Match:            24.04%      Indels:        0
DB:                     1           Gaps:          0

US-09-769-066-15 (1-549) x AB094264 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTAYACTGGTGCYCTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGTCGTGGAGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACGCGTTTCATGAAGGACCTGCACTTTACTGGCACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAACCTAGCTGATACACTTCTCGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CTGATTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGYCCTGTCGTCTCA 412

RESULT 276
AB094265
LOCUS       AB094265                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-10.
ACCESSION   AB094265
VERSION     AB094265.1  GI:29292785
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
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                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /protein_id="BAC66288.1"
                     /db_xref="GI:29292786"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210         Length:        412
Score:                  132.00      Matches:       132
Percent Similarity:     96.35%      Conservative:  0
Best Local Similarity:  96.35%      Mismatches:    5
Query Match:            24.04%      Indels:        0
DB:                     1           Gaps:          0

US-09-769-066-15 (1-549) x AB094265 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCCCTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGTCGTGGAGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACGCGTTTCATGAAGGACCTGCACTTTACTGGCACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAACCTAGCTGATACACTTCTCGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CTGATTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 277
AB094266
LOCUS       AB094266                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-11.
ACCESSION   AB094266
VERSION     AB094266.1  GI:29292787
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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US-09-769-066-15 (1-549) x AB094266 (1-412)

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LOCUS       AB094267                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ16-1.
ACCESSION   AB094267
VERSION     AB094267.1  GI:29292789
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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US-09-769-066-15 (1-549) x AB094267 (1-412)

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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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RESULT 279
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DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
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ACCESSION   AB094268
VERSION     AB094268.1  GI:29292791
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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Alignment Scores:
Pred. No.:              210             Length:         412
Score:                  132.00          Matches:        132
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Best Local Similarity:  96.35%          Mismatches:     5
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US-09-769-066-15 (1-549) x AB094268 (1-412)

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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTACACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        302 GGTATCGCTCTGACACTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

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Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTCTACTCCCGCCCTGTTGTCTCG 412

RESULT 280
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LOCUS       AB094269                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
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ACCESSION   AB094269
VERSION     AB094269.1  GI:29292793
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
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Alignment Scores:
Pred. No.:              210             Length:         412
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US-09-769-066-15 (1-549) x AB094269 (1-412)

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Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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RESULT 281
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LOCUS       AB094270                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
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VERSION     AB094270.1  GI:29292795
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
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Alignment Scores:
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Percent Similarity:       96.35%          Conservative:    0
Best Local Similarity:    96.35%          Mismatches:      5
Query Match:              24.04%          Indels:          0
DB:                       1               Gaps:            0

US-09-769-066-15 (1-549) x AB094270 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCCGGTCTCGTCATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTCTACTCCCGCCCTGTTGTCTCG 412

RESULT 282
AB094271
LOCUS       AB094271                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
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ACCESSION   AB094271
VERSION     AB094271.1  GI:29292797
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
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            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
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                     /protein_id="BAC66294.1"
                     /db_xref="GI:29292798"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094271 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCCGGTCTCGTAATGCTTTGCATCCACGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGCCGTGGTGCTGATGGGACTGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGTTTCATGAAGGATCTGCATTTCACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATCGCTCTGACACTGTTCAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 CTGATTTCGTCGGCTGGGGGTCAACTATTCTACTCCCGCCCTGTTGTCTCG 412

RESULT 283
AB094272
LOCUS       AB094272                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ17-1.
ACCESSION   AB094272
VERSION     AB094272.1  GI:29292799
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES              Location/Qualifiers
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                      /organism="Swine hepatitis E virus"
                      /virion
                      /mol_type="genomic RNA"
                      /isolate="swJ17-1"
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                      /db_xref="taxon:63421"
                      /country="Japan"
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                      /db_xref="GI:29292800"
                      /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                      ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094272 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTCGTTATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAACTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTACACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGTTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGTTTCATGAAGGATCTGCATTTCACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATTGCTCTGACACTGTTTAATCTTGCTGATACGCTCCTTGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 284
AB094273
LOCUS       AB094273                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ17-2.
ACCESSION   AB094273
VERSION     AB094273.1  GI:29292801
KEYWORDS    .
SOURCE      Swine hepatitis E virus
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  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
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                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210           Length:        412
Score:                    132.00        Matches:       132
Percent Similarity:       96.35%        Conservative:  0
Best Local Similarity:    96.35%        Mismatches:    5
Query Match:              24.04%        Indels:        0
DB:                       1             Gaps:          0

US-09-769-066-15 (1-549) x AB094273 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTCGTTATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAACTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTACACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGTTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGTTTCATGAAGGATCTGCATTTCACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATTGCTCTGACACTGTTTAATCTTGCTGATACGCTCCTTGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 285
AB094274
LOCUS       AB094274                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ17-3.
ACCESSION   AB094274
VERSION     AB094274.1  GI:29292803
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /db_xref="taxon:63421"
                     /country="Japan"
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Alignment Scores:
Pred. No.:                210           Length:        412
Score:                    132.00        Matches:       132
Percent Similarity:       96.35%        Conservative:  0
Best Local Similarity:    96.35%        Mismatches:    5
Query Match:              24.04%        Indels:        0
DB:                       1             Gaps:          0

US-09-769-066-15 (1-549) x AB094274 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTCGTTATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAACTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTACACCAGTACA 181
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGTTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGTTTCATGAAGGATCTGCATTTCACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATTGCTCTGACACTGTTTAATCTTGCTGATACGCTCCTTGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412
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RESULT 286
AB094276
LOCUS       AB094276                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ18-2.
ACCESSION   AB094276
VERSION     AB094276.1  GI:29292807
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              210          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0
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US-09-769-066-15 (1-549) x AB094276 (1-412)

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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGCCGTGGTGCCGACGGGACTGCCGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGTTTTATGAAGGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412
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RESULT 287
AB094277
LOCUS       AB094277                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ18-3.
ACCESSION   AB094277
VERSION     AB094277.1  GI:29292809
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              210          Length:        412
Score:                  132.00       Matches:       132
Percent Similarity:     96.35%       Conservative:  0
Best Local Similarity:  96.35%       Mismatches:    5
Query Match:            24.04%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AB094277 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCCGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGTTTTATGAAGGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 288
AB094278
LOCUS       AB094278                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ18-4.
ACCESSION   AB094278
VERSION     AB094278.1  GI:29292811
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ18-4"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66301.1"
                     /db_xref="GI:29292812"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:        412
Score:                  132.00       Matches:       132
Percent Similarity:     96.35%       Conservative:  0
Best Local Similarity:  96.35%       Mismatches:    5
Query Match:            24.04%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AB094278 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCCGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGTTTTATGAAGGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 289
AB094279
LOCUS       AB094279                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ19-1.
ACCESSION   AB094279
VERSION     AB094279.1  GI:29292813
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
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          hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ19-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /protein_id="BAC66302.1"
                     /db_xref="GI:29292814"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094279 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTTTGGTGATGCTTTGCATCCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTTGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGTCGTGGCGCCGATGGGACAGCTGAGCTTACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACACGTTTCATGAAGGACTTGCATTTTACTGGTACGAATGGGGTTGGTGAGGTGGGTCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTTTGACATTGTTCAATCTTGCTGATACGCTTCTCGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCG 412

RESULT 290
AB094280
LOCUS       AB094280                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ19-2.
ACCESSION   AB094280
VERSION     AB094280.1  GI:29292815
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ19-2"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /note="ORF2"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094280 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTTTGGTGATGCTTTGCATCCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTTGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGTCGTGGCGCCGATGGGACAGCTGAGCTTACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGTTTCATGAAGGACTTGCATTTTACTGGTACGAATGGGGTTGGTGAGGTGGGTCGA 301
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Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTTTGACATTGTTCAATCTTGCTGATACGCTTCTCGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCG 412

RESULT 291
AB094281
LOCUS       AB094281                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ19-3.
ACCESSION   AB094281
VERSION     AB094281.1  GI:29292817
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /country="Japan"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB094281 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTTTGGTGATGCTTTGCATCCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         62 TCTTATACTAATACACCTTACACTGGTGCACTTGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        122 GAGTTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGTCGTGGCGCCGATGGGACAGCTGAGCTTACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACACGTTTCATGAAGGACTTGCATTTTACTGGTACGAATGGGGTTGGTGAGGTGGGTCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTTTGACATTGTTCAATCTTGCTGATACGCTTCTCGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCG 412

RESULT 292
AB094282
LOCUS       AB094282                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ19-4.
ACCESSION   AB094282
VERSION     AB094282.1  GI:29292819
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
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                     /db_xref="taxon:63421"
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Alignment Scores:
Pred. No.:              210           Length:        412
Score:                  132.00        Matches:       132
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Percent Similarity:     96.35%          Conservative:  0
Best Local Similarity:  96.35%          Mismatches:    5
Query Match:            24.04%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-15 (1-549) x AB094282 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTTTGGTGATGCTTTGCATCCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTTGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGTCGTGGCGCCGATGGGACAGCTGAGCTTACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACACGTTTCATGAAGGACTTGCATTTTACTGGTACGAATGGGGTTGGTGAGGTGGGTCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTTTGACATTGTTCAATCTTGCTGATACGCTTCTCGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCG 412

RESULT 293
AB094283
LOCUS       AB094283                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ19-5.
ACCESSION   AB094283
VERSION     AB094283.1  GI:29292821
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ19-5"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66306.1"
                     /db_xref="GI:29292822"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210             Length:        412
Score:                  132.00          Matches:       132
Percent Similarity:     96.35%          Conservative:  0
Best Local Similarity:  96.35%          Mismatches:    5
Query Match:            24.04%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-15 (1-549) x AB094283 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTTTGGTGATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTTGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGTCGTGGCGCTGATGGGACAGCTGAGCTTACCACCACGGCYGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACACGCTTCATGAAGGACTTGCATTTTACTGGTACGAATGGGGTTGGTGAGGTGGGTCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACATTGTTCAATCTTGCTGATACGCTTCTCGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCG 412

RESULT 294
AB094284
LOCUS       AB094284                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ19-6.
ACCESSION   AB094284
VERSION     AB094284.1  GI:29292823
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
```

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           Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
           Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
           Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ19-6"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66307.1"
                     /db_xref="GI:29292824"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AB094284 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTTTGGTGATGCTTTGCATYCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTTGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAGTTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACCAGYACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGTCGTGGCGCYGATGGGACAGCTGAGCTTACCACCACGGCYGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||   ||||||  ||||||||||||||||||||   ||||||
Db        242 ACACGYTTCATGAAGGACTTGCATTTTACTGGTACGAATGGGGTTGGTGAGGTGGGTCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTYTGACATTGTTCAATCTTGCTGATACGCTTCTCGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCG 412

RESULT 295
AB094285
LOCUS       AB094285                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ19-7.
ACCESSION   AB094285
VERSION     AB094285.1  GI:29292825
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ19-7"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /db_xref="GI:29292826"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AB094285 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTTTGGTGATGCTTTGCATCCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTTGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAGTTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGTCGTGGCGCCGATGGGACAGCTGAGCTTACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||   ||||||  ||||||||||||||||||||   ||||||
Db        242 ACACGTTTCATGAAGGACTTGCATTTTACTGGTACGAATGGGGTTGGTGAGGTGGGTCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTTTGACATTGTTCAATCTTGCTGATACGCTTCTCGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCG 412
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RESULT 296
AB094286
LOCUS       AB094286                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ19-8.
ACCESSION   AB094286
VERSION     AB094286.1  GI:29292827
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AB094286 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTTTGGTGATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTTGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGTCGTGGCGCTGATGGGACAGCTGAGCTTACCACCACGGCCGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACACGCTTCATGAAGGACTTGCATTTTACTGGTACGAATGGGGTTGGTGAGGTGGGTCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACATTGTTCAATCTTGCTGATACGCTTCTCGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCG 412

RESULT 297
AB094287
LOCUS       AB094287                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ19-9.
ACCESSION   AB094287
VERSION     AB094287.1  GI:29292829
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /country="Japan"
     CDS             <1. .>412
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AB094287 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66313.1"
                     /db_xref="GI:29292836"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:                210          Length:          412
Score:                    132.00       Matches:         132
Percent Similarity:       96.35%       Conservative:    0
Best Local Similarity:    96.35%       Mismatches:      5
Query Match:              24.04%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-15 (1-549) x AB094290 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCCGGTTTGGTAATGCTTTGCATTCATGGGTCCCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTACGCCGCGGTGCCGACGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACACGTTTTATGAAGGATCTGCACTTTACCGGTACGAATGGCGTTGGTGAGGTGGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCCCTGACACTGTTTAATCTTGCCGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCCGTTGTCTCG 412

RESULT 300
AB094291
LOCUS       AB094291                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ20-2.
ACCESSION   AB094291
VERSION     AB094291.1  GI:29292837
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086

REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ20-2"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66314.1"
                     /db_xref="GI:29292838"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210          Length:          412
Score:                    132.00       Matches:         132
Percent Similarity:       96.35%       Conservative:    0
Best Local Similarity:    96.35%       Mismatches:      5
Query Match:              24.04%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-15 (1-549) x AB094291 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCCGGTTTGGTAATGCTTTGCATTCATGGGTCCCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTACGCCGCGGTGCCGACGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGTTTTATGAAGGATCTGCACTTTACCGGTACGAATGGCGTTGGTGAGGTGGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCCCTGACACTGTTTAATCTTGCCGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCCGTTGTCTCG 412

RESULT 301
AB094292
LOCUS       AB094292                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ20-3.
ACCESSION   AB094292
VERSION     AB094292.1  GI:29292839
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KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
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                     /isolate="swJ20-3"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /protein_id="BAC66315.1"
                     /db_xref="GI:29292840"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210           Length:         412
Score:                  132.00        Matches:        132
Percent Similarity:     96.35%        Conservative:   0
Best Local Similarity:  96.35%        Mismatches:     5
Query Match:            24.04%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AB094292 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAGGCTACCTCCGGTTTGGTAATGCTTTGCATTCATGGGTCCCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTACGCCGCGGTGCCGACGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACACGTTTTATGAAGGATCTGCACTTTACCGGTACGAATGGCGTTGGTGAGGTGGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCCCTGACACTGTTTAATCTTGCCGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCCGTTGTCTCG 412

RESULT 302
AB094293
LOCUS       AB094293                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-1.
ACCESSION   AB094293
VERSION     AB094293.1  GI:29292841
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
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                     /country="Japan"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210           Length:         412
Score:                  132.00        Matches:        132
Percent Similarity:     96.35%        Conservative:   0
Best Local Similarity:  96.35%        Mismatches:     5
Query Match:            24.04%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AB094293 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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                 ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB094295 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATTGCTYTGACATTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 305
AB094296
LOCUS       AB094296                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-4.
ACCESSION   AB094296
VERSION     AB094296.1  GI:29292847
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)

FEATURES             Location/Qualifiers
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                     /virion
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                     /isolate="swJ22-4"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66319.1"
                     /db_xref="GI:29292848"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB094296 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACYGGTGCATTGGGMCTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAATYTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATTGCTCTGACATTGTTCAATCTTGCTGAYACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCA 412

RESULT 306
AB094298
LOCUS       AB094298                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-6.
ACCESSION   AB094298
VERSION     AB094298.1  GI:29292851
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
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  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
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                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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                     /protein_id="BAC66321.1"
                     /db_xref="GI:29292852"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210           Length:         412
Score:                    132.00        Matches:        132
Percent Similarity:       96.35%        Conservative:   0
Best Local Similarity:    96.35%        Mismatches:     5
Query Match:              24.04%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x AB094298 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACATTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 307
AB094299
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LOCUS       AB094299                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-7.
ACCESSION   AB094299
VERSION     AB094299.1  GI:29292853
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ22-7"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66322.1"
                     /db_xref="GI:29292854"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210           Length:         412
Score:                    132.00        Matches:        132
Percent Similarity:       96.35%        Conservative:   0
Best Local Similarity:    96.35%        Mismatches:     5
Query Match:              24.04%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x AB094299 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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                ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACATTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 308
AB094301
LOCUS       AB094301                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-9.
ACCESSION   AB094301
VERSION     AB094301.1  GI:29292857
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ22-9"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66324.1"
                     /db_xref="GI:29292858"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB094301 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
                ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
                ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAATCTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
                ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACATTGTTCAATCTTGCTGACACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCA 412

RESULT 309
AB094302
LOCUS       AB094302                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-10.
ACCESSION   AB094302
VERSION     AB094302.1  GI:29292859
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ22-10"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
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                     /product="capsid protein"
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                     /db_xref="GI:29292860"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
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Pred. No.:              210          Length:          412
Score:                  132.00       Matches:         132
Percent Similarity:     96.35%       Conservative:    0
Best Local Similarity:  96.35%       Mismatches:      5
Query Match:            24.04%       Indels:          0
DB:                     1            Gaps:            0

US-09-769-066-15 (1-549) x AB094302 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACATTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCA 412

RESULT 310
AB094303
LOCUS       AB094303                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-11.
ACCESSION   AB094303
VERSION     AB094303.1  GI:29292861
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
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                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /db_xref="GI:29292862"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:          412
Score:                  132.00       Matches:         132
Percent Similarity:     96.35%       Conservative:    0
Best Local Similarity:  96.35%       Mismatches:      5
Query Match:            24.04%       Indels:          0
DB:                     1            Gaps:            0

US-09-769-066-15 (1-549) x AB094303 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACATTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCA 412

RESULT 311
AB094304
LOCUS       AB094304                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-12.
ACCESSION   AB094304
VERSION     AB094304.1  GI:29292863
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
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  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
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                     /country="Japan"
     CDS             <1. .>412
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                     /codon_start=2
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094304 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||   ||||||   ||||||||||||||||||||   ||||||
Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACATTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCA 412

RESULT 312
AB094305
LOCUS       AB094305                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ23-1.
ACCESSION   AB094305
VERSION     AB094305.1  GI:29292865
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ23-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66328.1"
                     /db_xref="GI:29292866"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094305 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCTCCCGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAATACACCCTACACTGGTGCACTTGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGTCGTGGCGCCGATGGGACCGCTGAGCTCACCACCACGGCGGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACTCGTTTCATGAAGGACCTGCACTTTACCGGCACGAATGGGGTTGGCGAGGTGGGTAGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACATTGTTCAATCTTGCTGATACGCTTCTCGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTATTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 313
AB094306
LOCUS       AB094306                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-1.
ACCESSION   AB094306
VERSION     AB094306.1  GI:29292867
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ24-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66329.1"
                     /db_xref="GI:29292868"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AB094306 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATTCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCACTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACACGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCCTTGACACTTTTAATCTTGCTGACACGCTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 314
AB094307
LOCUS       AB094307                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-2.
ACCESSION   AB094307
VERSION     AB094307.1  GI:29292869
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ24-2"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
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                     /product="capsid protein"
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                     /db_xref="GI:29292870"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AB094307 (1-412)
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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATTCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCACTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACACGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCCTTGACACTTTTTAATCTTGCTGACACGCTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 315
AB094308
LOCUS       AB094308                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-3.
ACCESSION   AB094308
VERSION     AB094308.1  GI:29292871
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
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                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB094308 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATCCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCACTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACACGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCCTTGACACTTTTYAATCTTGCTGACACGCTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 316
AB094309
LOCUS       AB094309                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-4.
ACCESSION   AB094309
VERSION     AB094309.1  GI:29292873
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AB094309 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATTCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCGCTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCCTTGACACTTTTTAATCTTGCTGACACGCTCCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 317
AB094310
LOCUS       AB094310                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-5.
ACCESSION   AB094310
VERSION     AB094310.1  GI:29292875
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
  PUBMED    12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ24-5"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
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                     /db_xref="GI:29292876"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AB094310 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATTCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCRCTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTATCCCGATAYACTAGYACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCCTTGACACTTTTTAATCTTGCTGACACGCTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 318
AB094311
LOCUS       AB094311                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-6.
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ACCESSION   AB094311
VERSION     AB094311.1  GI:29292877
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
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                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
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                     /db_xref="GI:29292878"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210           Length:         412
Score:                  132.00        Matches:        132
Percent Similarity:     96.35%        Conservative:   0
Best Local Similarity:  96.35%        Mismatches:     5
Query Match:            24.04%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AB094311 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATTCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCACTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAAYTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATTGCCTTGACACTTTTTAATCTTGCTGACACGCTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 319
AB094312
LOCUS       AB094312                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-7.
ACCESSION   AB094312
VERSION     AB094312.1  GI:29292879
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
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                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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Alignment Scores:
Pred. No.:              210           Length:         412
Score:                  132.00        Matches:        132
Percent Similarity:     96.35%        Conservative:   0
Best Local Similarity:  96.35%        Mismatches:     5
Query Match:            24.04%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AB094312 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATTCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCACTGGGACTTCTTGATTTTGCATTAGAGCTT 121
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Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||    ||||||    ||||||||||||||||||    ||||||
Db        242 ACACGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCCTTGACACTTTTTAATCTTGCTGACACGCTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412
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RESULT 320
AB094313
LOCUS AB094313 412 bp RNA linear VRL 27-MAR-2003
DEFINITION Swine hepatitis E virus ORF2 gene for capsid protein, partial cds, isolate:swJ24-8.
ACCESSION AB094313
VERSION AB094313.1 GI:29292881
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T., Tsuda,F. and Okamoto,H.
TITLE Swine hepatitis E virus strains in Japan form four phylogenetic clusters comparable with those of Japanese isolates of human hepatitis E virus
JOURNAL J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
PUBMED 12655086
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School, Immunology Division and Division of Molecular Virology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
FEATURES Location/Qualifiers
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CDS <1. .>412
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ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.: 210 Length: 412
Score: 132.00 Matches: 132
Percent Similarity: 96.35% Conservative: 0
Best Local Similarity: 96.35% Mismatches: 5
Query Match: 24.04% Indels: 0
DB: 1 Gaps: 0

US-09-769-066-15 (1-549) x AB094313 (1-412)

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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATTCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCRCTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATYTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGAYGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||    ||||||    ||||||||||||||||||    ||||||
Db        242 ACACGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATTGCCTTGACACTTTTTAATCTTGCTGACACGCTYCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412
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RESULT 321
AB094314
LOCUS AB094314 412 bp RNA linear VRL 27-MAR-2003
DEFINITION Swine hepatitis E virus ORF2 gene for capsid protein, partial cds, isolate:swJ24-9.
ACCESSION AB094314
VERSION AB094314.1 GI:29292883
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T., Tsuda,F. and Okamoto,H.
TITLE Swine hepatitis E virus strains in Japan form four phylogenetic clusters comparable with those of Japanese isolates of human hepatitis E virus
JOURNAL J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
PUBMED 12655086
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School, Immunology Division and Division of Molecular Virology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
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/virion
/mol_type="genomic RNA"
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/isolation_source="swine serum"
/specific_host="farm pig"
/db_xref="taxon:63421"
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CDS <1. .>412

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Alignment Scores:
Pred. No.:                210           Length:        412
Score:                    132.00        Matches:       132
Percent Similarity:       96.35%        Conservative:  0
Best Local Similarity:    96.35%        Mismatches:    5
Query Match:              24.04%        Indels:        0
DB:                       1             Gaps:          0

US-09-769-066-15 (1-549) x AB094314 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATTCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCACTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATTGCCTTGACACTTTTTAATCTTGCTGACACGCTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 322
AB094315
LOCUS       AB094315                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-10.
ACCESSION   AB094315
VERSION     AB094315.1  GI:29292885
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
    PUBMED  12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:63421"
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Alignment Scores:
Pred. No.:                210           Length:        412
Score:                    132.00        Matches:       132
Percent Similarity:       96.35%        Conservative:  0
Best Local Similarity:    96.35%        Mismatches:    5
Query Match:              24.04%        Indels:        0
DB:                       1             Gaps:          0

US-09-769-066-15 (1-549) x AB094315 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATTCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCACTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGRACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACACGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCCTTGACACTTTTTAATCTTGCTGACACGCTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 323
AB094316
LOCUS       AB094316                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-11.
ACCESSION   AB094316
VERSION     AB094316.1  GI:29292887
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
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  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ24-11"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66339.1"
                     /db_xref="GI:29292888"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210          Length:          412
Score:                    132.00       Matches:         132
Percent Similarity:       96.35%       Conservative:    0
Best Local Similarity:    96.35%       Mismatches:      5
Query Match:              24.04%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-15 (1-549) x AB094316 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 325
AB094318
LOCUS       AB094318                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-2.
ACCESSION   AB094318
VERSION     AB094318.1  GI:29292891
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-2"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66341.1"
                     /db_xref="GI:29292892"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AB094318 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||    ||||||   ||||||||||||||||||    ||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 326
AB094319
LOCUS       AB094319                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-3.
ACCESSION   AB094319
VERSION     AB094319.1  GI:29292893
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-3"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66342.1"
                     /db_xref="GI:29292894"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"
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Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094319 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACYAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACRCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 327
AB094321
LOCUS       AB094321                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-5.
ACCESSION   AB094321
VERSION     AB094321.1  GI:29292897
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-5"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /db_xref="GI:29292898"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094321 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCCGTCGTCTCA 412

RESULT 328
AB094322
LOCUS       AB094322                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-6.
ACCESSION   AB094322
VERSION     AB094322.1  GI:29292899
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
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```
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-6"
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                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66345.1"
                     /db_xref="GI:29292900"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210           Length:        412
Score:                    132.00        Matches:       132
Percent Similarity:       96.35%        Conservative:  0
Best Local Similarity:    96.35%        Mismatches:    5
Query Match:              24.04%        Indels:        0
DB:                       1             Gaps:          0

US-09-769-066-15 (1-549) x AB094322 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACAGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||| |||||| |||||||||||||||||| ||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 329
AB094323
LOCUS       AB094323                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-7.
ACCESSION   AB094323
VERSION     AB094323.1  GI:29292901
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
  PUBMED    12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /isolate="swJ25-7"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66346.1"
                     /db_xref="GI:29292902"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210           Length:        412
Score:                    132.00        Matches:       132
Percent Similarity:       96.35%        Conservative:  0
Best Local Similarity:    96.35%        Mismatches:    5
Query Match:              24.04%        Indels:        0
DB:                       1             Gaps:          0

US-09-769-066-15 (1-549) x AB094323 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        122 GAATTYAGGAATTTAACYCCCGGGAACACTAACACCCGTGTATCCCGATATACYAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACRCTACTCGGTGGTTTGCCGACAGAA 361
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Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 330
AB094324
LOCUS       AB094324                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-8.
ACCESSION   AB094324
VERSION     AB094324.1  GI:29292903
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-8"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66347.1"
                     /db_xref="GI:29292904"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB094324 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACYAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 331
AB094325
LOCUS       AB094325                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-9.
ACCESSION   AB094325
VERSION     AB094325.1  GI:29292905
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
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                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /protein_id="BAC66348.1"
                     /db_xref="GI:29292906"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0
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US-09-769-066-15 (1-549) x AB094325 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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     source          1. .412
                     /organism="Swine hepatitis E virus"
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                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66351.1"
                     /db_xref="GI:29292912"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210          Length:          412
Score:                    132.00       Matches:         132
Percent Similarity:       96.35%       Conservative:    0
Best Local Similarity:    96.35%       Mismatches:      5
Query Match:              24.04%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-15 (1-549) x AB094328 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACAGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 334
AB094329
LOCUS       AB094329                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-13.
ACCESSION   AB094329
VERSION     AB094329.1  GI:29292913
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
  PUBMED    12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
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                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210          Length:          412
Score:                    132.00       Matches:         132
Percent Similarity:       96.35%       Conservative:    0
Best Local Similarity:    96.35%       Mismatches:      5
Query Match:              24.04%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-15 (1-549) x AB094329 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCAYGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAAYACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        122 GAATTCAGGAATTTAACYCCCGGGAACACTAACACCCGTGTATCCCGATATACYAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACRCTACTYGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 335
AB094330
LOCUS       AB094330                412 bp    RNA     linear   VRL 27-MAR-2003
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DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-14.
ACCESSION   AB094330
VERSION     AB094330.1  GI:29292915
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-14"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /db_xref="GI:29292916"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210           Length:        412
Score:                    132.00        Matches:       132
Percent Similarity:       96.35%        Conservative:  0
Best Local Similarity:    96.35%        Mismatches:    5
Query Match:              24.04%        Indels:        0
DB:                       1             Gaps:          0

US-09-769-066-15 (1-549) x AB094330 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAAYACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTCAGGAATTTAACYCCCGGGAACACTAACACCCGTGTATCCCGATATACYAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCAYCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRGCRGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||

Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACRCTACTYGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 336
AB094331
LOCUS       AB094331                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-15.
ACCESSION   AB094331
VERSION     AB094331.1  GI:29292917
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-15"
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                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66354.1"
                     /db_xref="GI:29292918"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210           Length:        412
Score:                    132.00        Matches:       132
Percent Similarity:       96.35%        Conservative:  0
Best Local Similarity:    96.35%        Mismatches:    5
Query Match:              24.04%        Indels:        0
DB:                       1             Gaps:          0

US-09-769-066-15 (1-549) x AB094331 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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                     /note="ORF2"
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:                210           Length:         412
Score:                    132.00        Matches:        132
Percent Similarity:       96.35%        Conservative:   0
Best Local Similarity:    96.35%        Mismatches:     5
Query Match:              24.04%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x AB094333 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAACACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||    ||||||    ||||||||||||||||||    ||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTACTTGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 339
AB094334
LOCUS       AB094334                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-18.
ACCESSION   AB094334
VERSION     AB094334.1  GI:29292923
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES              Location/Qualifiers
     source           1. .412
                      /organism="Swine hepatitis E virus"
                      /virion
                      /mol_type="genomic RNA"
                      /isolate="swJ25-18"
                      /isolation_source="swine serum"
                      /specific_host="farm pig"
                      /db_xref="taxon:63421"
                      /country="Japan"
     CDS              <1. .>412
                      /note="ORF2"
                      /codon_start=2
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                      /db_xref="GI:29292924"
                      /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                      ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210           Length:         412
Score:                    132.00        Matches:        132
Percent Similarity:       96.35%        Conservative:   0
Best Local Similarity:    96.35%        Mismatches:     5
Query Match:              24.04%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x AB094334 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTRTCCCGATATACYAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRCGGCGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||    ||||||    ||||||||||||||||||    ||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACRCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 340
AB094335
LOCUS       AB094335                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-19.
ACCESSION   AB094335
VERSION     AB094335.1  GI:29292925
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
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          Hepevirus.
REFERENCE 1
  AUTHORS Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
          Tsuda,F. and Okamoto,H.
  TITLE   Swine hepatitis E virus strains in Japan form four phylogenetic
          clusters comparable with those of Japanese isolates of human
          hepatitis E virus
  JOURNAL J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED 12655086
REFERENCE 2  (bases 1 to 412)
  AUTHORS Okamoto,H.
  TITLE   Direct Submission
  JOURNAL Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
          Immunology Division and Division of Molecular Virology; 3311-1
          Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
          Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
          Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-19"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66358.1"
                     /db_xref="GI:29292926"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:        412
Score:                  132.00       Matches:       132
Percent Similarity:     96.35%       Conservative:  0
Best Local Similarity:  96.35%       Mismatches:    5
Query Match:            24.04%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AB094335 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTRTCCCGATATACYAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRCGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACRCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 341
AB094336
LOCUS       AB094336                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-20.
ACCESSION   AB094336
VERSION     AB094336.1  GI:29292927
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
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                     /db_xref="taxon:63421"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:        412
Score:                  132.00       Matches:       132
Percent Similarity:     96.35%       Conservative:  0
Best Local Similarity:  96.35%       Mismatches:    5
Query Match:            24.04%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AB094336 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
                ||||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACRCTACTTGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 342
AB094337
LOCUS       AB094337                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-21.
ACCESSION   AB094337
VERSION     AB094337.1  GI:29292929
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB094337 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
                ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCCTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
                ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACAGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGATACGCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 343
AB094338
LOCUS       AB094338                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-22.
ACCESSION   AB094338
VERSION     AB094338.1  GI:29292931
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-22"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66361.1"
                     /db_xref="GI:29292932"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              210           Length:         412
Score:                  132.00        Matches:        132
Percent Similarity:     96.35%        Conservative:   0
Best Local Similarity:  96.35%        Mismatches:     5
Query Match:            24.04%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AB094338 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTRTCCCGATATACYAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACRCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 344
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LOCUS       AB094339                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-23.
ACCESSION   AB094339
VERSION     AB094339.1  GI:29292933
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-23"
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                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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                     /db_xref="GI:29292934"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210           Length:         412
Score:                  132.00        Matches:        132
Percent Similarity:     96.35%        Conservative:   0
Best Local Similarity:  96.35%        Mismatches:     5
Query Match:            24.04%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AB094339 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 345
AB105891
LOCUS       AB105891                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JA15.
ACCESSION   AB105891
VERSION     AB105891.1  GI:34097983
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
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   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
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                     /isolation_source="human serum"
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                     /country="Japan:Hokkaido"
                     /note="genotype III; sporadic acute hepatitis E"
     gene            1. .412
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     CDS             <1. .>412
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                     /codon_start=2
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Alignment Scores:
Pred. No.:              210             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB105891 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTGGTAATGCTTTGYATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAATCTGACACCCGGGAACACAAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCACCGGCTGCGCCGCGGTGCTGATGGGACTGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||   ||||||   ||||||||||||||||||||   ||||||
Db        242 ACACGTTTCATGAAGGATTTACATTTTACTGGCACGAATGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCTYTGACATTGTTTAATCTCGCTGACACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 346
AB105892
LOCUS       AB105892                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JA16.
ACCESSION   AB105892
VERSION     AB105892.1  GI:34097985
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /note="genotype III; sporadic acute hepatitis E"
     gene            1. .412
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     CDS             <1. .>412
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB105892 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCCGAGGAGGAGGCTACTTCTGGTCTGGTAATGCTTTGTATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAATCTGACACCCGGGAACACAAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGTTTCATGAAGGATTTACATTTTACTGGCACGAACGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275

Db        302 GGCATCGCCCTGACATTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292

Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 347
AB105898
LOCUS       AB105898                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJL82.
ACCESSION   AB105898
VERSION     AB105898.1  GI:34097997
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /isolation_source="pig liver"
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                     /db_xref="taxon:63421"
                     /country="Japan:Hokkaido"
                     /note="genotype III"
     gene            1. .412
                     /gene="ORF2"
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                     /protein_id="BAC82175.1"
                     /db_xref="GI:34097998"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AB105898 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175

Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTGATGCTTTGCATTCATGGCTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195

Db         62 TCTTATACTAACACACCTTACACTGGTGCACTGGGGCTTCTCGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215

Db        122 GAGTTTAGGAATTTGACACCCGGGAACACTAATACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235

Db        182 GCCCGCCATCGGCTGCGTCGTGGTGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255

Db        242 ACGCGTTTTATGAAAGATCTGCACTTTACTGGCACAAATGGGGTTGGTGAGGTTGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275

Db        302 GGCATTGCTCTGACATTGTTTAACCTTGCTGATACGCTTCTCGGTGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292

Db        362 TTGATTTCGTCGGCCGGGGGTCAGCTGTTCTACTCCCGCCCTGTCGTCTCG 412

RESULT 348
AB105899
LOCUS       AB105899                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJL97.
ACCESSION   AB105899
VERSION     AB105899.1  GI:34097999
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /db_xref="taxon:63421"
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                     /product="capsid protein"
                     /protein_id="BAC82176.1"
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                     /db_xref="GI:34098000"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:        412
Score:                  132.00       Matches:       132
Percent Similarity:     96.35%       Conservative:  0
Best Local Similarity:  96.35%       Mismatches:    5
Query Match:            24.04%       Indels:        0
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US-09-769-066-15 (1-549) x AB105899 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGCCTGGTGATGCTTTGCATTCATGGCTCCCCCGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAATACGCCCTATACTGGTGCACTAGGGCTTCTTGATTTCGCATTAGAGCTC 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTAACACCCGGGAACACCAACACCCGTGTATCCCGATATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGAGGTGCCGACGGGACCGCTGAGCTCACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGTTTTATGAAGGACCTGCATTTCACCGGCACGAATGGGGTCGGTGAAGTCGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACGCTGTTCAATCTAGCTGACACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 349
AB105900
LOCUS       AB105900                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJL98.
ACCESSION   AB105900
VERSION     AB105900.1  GI:34098001
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJL98"
                     /isolation_source="pig liver"
                     /specific_host="swine"
                     /db_xref="taxon:63421"
                     /country="Japan:Hokkaido"
                     /note="genotype III"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC82177.1"
                     /db_xref="GI:34098002"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:        412
Score:                  132.00       Matches:       132
Percent Similarity:     96.35%       Conservative:  0
Best Local Similarity:  96.35%       Mismatches:    5
Query Match:            24.04%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AB105900 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGCCTGGTGATGCTTTGCATTCATGGCTCCCCCGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACGCCCTATACTGGTGCACTAGGGCTTCTTGATTTCGCATTAGAGCTC 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATTTAACACCCGGGAACACCAACACCCGTGTATCCCGATATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGAGGTGCCGACGGGACCGCTGAGCTCACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGTTTTATGAAGGACCTGCATTTCACCGGCACGAATGGGGTCGGTGAAGTCGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACGCTGTTCAATCTAGCTGACACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 350
AB105901
LOCUS       AB105901                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJL131.
ACCESSION   AB105901
VERSION     AB105901.1  GI:34098003
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
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          Gotanda,Y. and Okamoto,H.
  TITLE   Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
          food-borne, as suggested by the presence of hepatitis E virus in
          pig liver as food
  JOURNAL J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED 12917455
REFERENCE 2  (bases 1 to 412)
  AUTHORS Okamoto,H.
  TITLE   Direct Submission
  JOURNAL Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
          Immunology Division and Division of Molecular Virology; 3311-1
          Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
          Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
          Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJL131"
                     /isolation_source="pig liver"
                     /specific_host="swine"
                     /db_xref="taxon:63421"
                     /country="Japan:Hokkaido"
                     /note="genotype III"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC82178.1"
                     /db_xref="GI:34098004"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB105901 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCCACTTCTGGTTTGGTAATGCTTTGTATTCATGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAATACACCTTACACTGGTGCATTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTGTCCCGGTACACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGTCGTGGTGCTGACGGTACCGCTGAGCTTACTACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGTTTCATGAAGGACTTACACTTTACTGGCACGAATGGGGTTGGTGAGGTTGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCCTTGACACTGTTCAATCTTGCTGATACGCTTCTTGGTGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTAATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTCGTCTCG 412

RESULT 351
AB105903
LOCUS       AB105903                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJL234.
ACCESSION   AB105903
VERSION     AB105903.1  GI:34098007
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
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                     /isolate="swJL234"
                     /isolation_source="pig liver"
                     /specific_host="swine"
                     /db_xref="taxon:63421"
                     /country="Japan:Hokkaido"
                     /note="genotype III"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
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                     /protein_id="BAC82180.1"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB105903 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTGGTAATGCTTTGTATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCYTACACTAATACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAATCTGACACCCGGGAACACAAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCACCGGCTGCGCCGCGGTGCTGATGGGACYGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGTTTCATGAAGGATTTACATTTTACTGGCACGAAYGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATCGCYCTGACATTGTTTAATCTCGCTGAYACGCTTCTCGGTGGTYTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 352
AB105904
LOCUS       AB105904                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJL325.
ACCESSION   AB105904
VERSION     AB105904.1  GI:34098009
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /isolate="swJL325"
                     /isolation_source="pig liver"
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                     /db_xref="taxon:63421"
                     /country="Japan:Hokkaido"
                     /note="genotype III"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC82181.1"
                     /db_xref="GI:34098010"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210          Length:        412
Score:                  132.00       Matches:       132
Percent Similarity:     96.35%       Conservative:  0
Best Local Similarity:  96.35%       Mismatches:    5
Query Match:            24.04%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AB105904 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTGGTAATGCTTTGTATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCYTACACTAATACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAATCTGACACCCGGGAACACAAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCACCGGCTGCGCCGCGGTGCTGATGGGACYGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||    ||||||   ||||||||||||||||||   ||||||
Db        242 ACACGTTTCATGAAGGATTTACATTTTACTGGCACGAAYGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATCGCYCTGACATTGTTTAATCTCGCTGAYACGCTTCTCGGTGGTYTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 353
AB107366
LOCUS       AB107366                412 bp    RNA     linear   VRL 07-APR-2004
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate: HE-JAS1.
ACCESSION   AB107366
VERSION     AB107366.1  GI:46250706
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yamamoto,T., Suzuki,H., Toyota,T., Takahashi,M. and Okamoto,H.
  TITLE     Three male patients with sporadic acute hepatitis E in Sendai, who
            were domestically infected with hepatitis E virus of genotype III
            or IV
  JOURNAL   J. Gastroenterol. 39, 292-298 (2004)
   PUBMED   15065009
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-APR-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
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                     /isolation_source="serum"
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                     /note="genotype III"
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                /db_xref="GI:46250707"
                /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              210             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB107366 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCCGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGTATTCACGGCTCCCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTACACTAATACACCTTATACTGGTGCTTTGGGGCTTCTTGATTTTGCATTAGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAACCTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGCCGCGGCGCTGATGGGACCGCTGAGCTCACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGTTTTATGAAGGATTTGCATTTTACTGGCACGAATGGCGTTGGAGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCCCTGACACTGTTTAATCTTGCTGATACGCTTCTTGGTGGCTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAATTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 354
AB107368
LOCUS       AB107368                412 bp    RNA     linear   VRL 07-APR-2004
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate: HE-JAS3.
ACCESSION   AB107368
VERSION     AB107368.1  GI:46250710
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yamamoto,T., Suzuki,H., Toyota,T., Takahashi,M. and Okamoto,H.
  TITLE     Three male patients with sporadic acute hepatitis E in Sendai, who
            were domestically infected with hepatitis E virus of genotype III
            or IV
  JOURNAL   J. Gastroenterol. 39, 292-298 (2004)
   PUBMED   15065009
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-APR-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES            Location/Qualifiers
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                    /organism="Hepatitis E virus"
                    /virion
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                    /isolate="HE-JAS3"
                    /isolation_source="serum"
                    /specific_host="human"
                    /db_xref="taxon:12461"
                    /country="Japan:Sendai"
                    /note="genotype III"
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     CDS            <1. .>412
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                    /db_xref="GI:46250711"
                    /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              210             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB107368 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCCGAGGAGGAGGCTACCTCCGGCCTGGTAATGCTTTGTATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAACTA 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGTTTTATGAAGGATTTGCATTTTACTGGCACGAACGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATCGCTCTGACATTGTTTAATCTTGCTGATACGCTTCTTGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 355
AB112743
LOCUS       AB112743                412 bp    RNA     linear   VRL 22-JUN-2004
DEFINITION  Hepatitis E virus ORF2 gene for capsid, partial cds,
            isolate:HE-JBD1.
ACCESSION   AB112743
VERSION     AB112743.1  GI:49022381
KEYWORDS    .
SOURCE      Hepatitis E virus
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  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Fukuda,S., Sunaga,J., Saito,N., Fujimura,K., Itoh,Y., Sasaki,M.,
            Tsuda,F., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Prevalence of antibodies to hepatitis E virus among Japanese blood
            donors: identification of three blood donors infected with a
            genotype 3 hepatitis E virus
  JOURNAL   J. Med. Virol. 73, 554-561 (2004)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JUN-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JBD1"
                     /isolation_source="human serum"
                     /db_xref="taxon:12461"
                     /country="Japan: Tochigi"
                     /note="genotype III"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid"
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                     /db_xref="GI:49022382"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              210           Length:         412
Score:                  132.00        Matches:        132
Percent Similarity:     96.35%        Conservative:   0
Best Local Similarity:  96.35%        Mismatches:     5
Query Match:            24.04%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AB112743 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGCCTGGTAATGCTTTGCATTCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACAAATACACCTTATACTGGGGCTTTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGGAATTTGACACCTGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGTGGAGCCGACGGGACCGCTGAGCTCACCACTACAGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGTTTTATGAAGGACTTGCATTTCACCGGTACGAATGGAGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCCCTGACACTGTTTAATCTTGCTGATACGCTTCTCGGTGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 356
AB115541
LOCUS       AB115541                412 bp    RNA     linear   VRL 22-JUL-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds,
            isolate:HE-JA20.
ACCESSION   AB115541
VERSION     AB115541.1  GI:50507839
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Sainokami,S., Abe,K., Kumagai,I., Miyasaka,A., Endo,R.,
            Takikawa,Y., Suzuki,K., Mizuo,H., Sugai,Y., Akahane,Y., Koizumi,Y.,
            Yajima,Y. and Okamoto,H.
  TITLE     Epidemiological and clinical study of sporadic acute hepatitis E
            caused by indigenous strains of hepatitis E virus in Japan compared
            with acute hepatitis A
  JOURNAL   J. Gastroenterol. 39, 640-648 (2004)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /country="Japan:Iwate"
                     /note="Genotype III"
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Alignment Scores:
Pred. No.:              210           Length:         412
Score:                  132.00        Matches:        132
Percent Similarity:     96.35%        Conservative:   0
Best Local Similarity:  96.35%        Mismatches:     5
Query Match:            24.04%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AB115541 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCTACCTCCGGCCTGGTAATGCTTTGTATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAACTA 121
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Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAATTTGACACCCGGGAACACTAACACTCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||    ||||||    ||||||||||||||||||    ||||||
Db        242 ACACGTTTTATGAAGGATTTGCATTTTACTGGCACGAACGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATCGCTCTGACATTGTTTAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGTCCTGTTGTCTCG 412
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RESULT 357
AB115542
LOCUS AB115542 412 bp RNA linear VRL 22-JUL-2004
DEFINITION Hepatitis E virus gene for capsid protein, partial cds, isolate:HE-JA21.
ACCESSION AB115542
VERSION AB115542.1 GI:50507841
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Sainokami,S., Abe,K., Kumagai,I., Miyasaka,A., Endo,R., Takikawa,Y., Suzuki,K., Mizuo,H., Sugai,Y., Akahane,Y., Koizumi,Y., Yajima,Y. and Okamoto,H.
TITLE Epidemiological and clinical study of sporadic acute hepatitis E caused by indigenous strains of hepatitis E virus in Japan compared with acute hepatitis A
JOURNAL J. Gastroenterol. 39, 640-648 (2004)
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (24-JUL-2003) Hiroaki Okamoto, Jichi Medical School, Division of Virology, Department of Infection and Immunity; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
FEATURES Location/Qualifiers
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/virion
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/db_xref="taxon:12461"
/country="Japan:Iwate"
/note="Genotype III"
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CDS <1. .>412
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Alignment Scores:

Pred. No.:	210	Length:	412
Score:	132.00	Matches:	132
Percent Similarity:	96.35%	Conservative:	0
Best Local Similarity:	96.35%	Mismatches:	5
Query Match:	24.04%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AB115542 (1-412)

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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCCGAGGAGGAGGCTACCTCCGGCCTGGTGATGCTTTGCATTCATGGCTCCCCCGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACCGGTGCATTGGGGCTTCTTGATTTTGCACTGGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        122 GAGTTTAGGAACTTGACACCTGGGAACACTAACACCCGTGTATCCCGATATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGCGGTGCCGATGGAACAGCTGAGCTCACTACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGTTTTATGAAAGACCTGCATTTCACTGGCACGAATGGGGTTGGAGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCCCTGACATTATTCAATCTTGCTGATACGCTTCTCGGTGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTCTTTTACTCCCGCCCCGTCGTCTCG 412
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RESULT 358
AB115543
LOCUS AB115543 412 bp RNA linear VRL 22-JUL-2004
DEFINITION Hepatitis E virus gene for capsid protein, partial cds, isolate:HE-JA22.
ACCESSION AB115543
VERSION AB115543.1 GI:50507843
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Sainokami,S., Abe,K., Kumagai,I., Miyasaka,A., Endo,R., Takikawa,Y., Suzuki,K., Mizuo,H., Sugai,Y., Akahane,Y., Koizumi,Y., Yajima,Y. and Okamoto,H.
TITLE Epidemiological and clinical study of sporadic acute hepatitis E caused by indigenous strains of hepatitis E virus in Japan compared with acute hepatitis A
JOURNAL J. Gastroenterol. 39, 640-648 (2004)
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (24-JUL-2003) Hiroaki Okamoto, Jichi Medical School, Division of Virology, Department of Infection and Immunity; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:                210           Length:         412
Score:                    132.00        Matches:        132
Percent Similarity:       96.35%        Conservative:   0
Best Local Similarity:    96.35%        Mismatches:     5
Query Match:              24.04%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x AB115543 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTGGTAATGCTTTGTATCCACGGCTCCCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTATACTGGTGCTTTGGGGCTTCTTGATTTTGCATTAGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAACCTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGCCGCGGCGCTGATGGGACCGCTGAGCTCACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACACGTTTTATGAAGGATTTGCATTTTACTGGCACGAATGGCGTTGGAGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCCCTGACACTGTTTAATCTTGCTGATACGCTTCTTGGTGGCTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAATTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 359
AB115544
LOCUS       AB115544                412 bp    RNA     linear   VRL 22-JUL-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds,
            isolate:HE-JA23.
ACCESSION   AB115544
VERSION     AB115544.1  GI:50507845
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Sainokami,S., Abe,K., Kumagai,I., Miyasaka,A., Endo,R.,
            Takikawa,Y., Suzuki,K., Mizuo,H., Sugai,Y., Akahane,Y., Koizumi,Y.,
            Yajima,Y. and Okamoto,H.
  TITLE     Epidemiological and clinical study of sporadic acute hepatitis E
            caused by indigenous strains of hepatitis E virus in Japan compared
            with acute hepatitis A
  JOURNAL   J. Gastroenterol. 39, 640-648 (2004)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JA23"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Japan:Nagano"
                     /note="Genotype III"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD30097.1"
                     /db_xref="GI:50507846"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210           Length:         412
Score:                    132.00        Matches:        132
Percent Similarity:       96.35%        Conservative:   0
Best Local Similarity:    96.35%        Mismatches:     5
Query Match:              24.04%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x AB115544 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCACGGCTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAACACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACCAATACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACGCGGTTTATGAAAGACCTGCACTTCACTGGCACGAACGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATCGCTCTGACACTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 360
AB154829
LOCUS       AB154829                412 bp    RNA     linear   VRL 22-JUN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds,
```

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           isolate:HE-JBD2.
ACCESSION  AB154829
VERSION    AB154829.1  GI:49022580
KEYWORDS   .
SOURCE     Hepatitis E virus
  ORGANISM Hepatitis E virus
           Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
           Hepevirus.
REFERENCE  1
  AUTHORS  Fukuda,S., Sunaga,J., Saito,N., Fujimura,K., Itoh,Y., Sasaki,M.,
           Tsuda,F., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE    Prevalence of antibodies to hepatitis E virus among Japanese blood
           donors: identification of three blood donors infected with a
           genotype 3 hepatitis E virus
  JOURNAL  J. Med. Virol. 73, 554-561 (2004)
REFERENCE  2  (bases 1 to 412)
  AUTHORS  Okamoto,H.
  TITLE    Direct Submission
  JOURNAL  Submitted (19-DEC-2003) Hiroaki Okamoto, Jichi Medical School,
           Department of Infection and Immunity; 3311-1 Yakushiji,
           Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498, Japan
           (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
           Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JBD2"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Japan:Tochigi"
                     /note="genotype 3"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD23990.1"
                     /db_xref="GI:49022581"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210          Length:         412
Score:                    132.00       Matches:        132
Percent Similarity:       96.35%       Conservative:   0
Best Local Similarity:    96.35%       Mismatches:     5
Query Match:              24.04%       Indels:         0
DB:                       1            Gaps:           0

US-09-769-066-15 (1-549) x AB154829 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGCTTGGTAATGCTCTGCATACATGGTTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACAAATACACCTTATACTGGAGCACTGGGGCTCCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGGAATTTGACACCTGGGAACACTAATACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGTTGCGTCGTGGTGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACACGTTTTATGAAGGATCTGCACTTCACCGGTACGAATGGGGTTGGCGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCCCTGACACTGTTTAATCTTGCTGATACGCTTCTCGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGCTATTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 361
AB154830
LOCUS       AB154830                412 bp    RNA     linear   VRL 22-JUN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds,
            isolate:HE-JBD3.
ACCESSION   AB154830
VERSION     AB154830.1  GI:49022585
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Fukuda,S., Sunaga,J., Saito,N., Fujimura,K., Itoh,Y., Sasaki,M.,
            Tsuda,F., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Prevalence of antibodies to hepatitis E virus among Japanese blood
            donors: identification of three blood donors infected with a
            genotype 3 hepatitis E virus
  JOURNAL   J. Med. Virol. 73, 554-561 (2004)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-DEC-2003) Hiroaki Okamoto, Jichi Medical School,
            Department of Infection and Immunity; 3311-1 Yakushiji,
            Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498, Japan
            (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JBD3"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Japan:Tochigi"
                     /note="genotype 3"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD23991.1"
                     /db_xref="GI:49022586"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                210          Length:         412
Score:                    132.00       Matches:        132
Percent Similarity:       96.35%       Conservative:   0
Best Local Similarity:    96.35%       Mismatches:     5
Query Match:              24.04%       Indels:         0
DB:                       1            Gaps:           0

US-09-769-066-15 (1-549) x AB154830 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCCACTTCCGGCCTTGTAATGCTTTGCATTCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAGCTT 121
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Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTATCCCGATACACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGTCGTGGTGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||   ||||||   |||||||||||||||||||   ||||||
Db        242 ACGCGTTTTATGAAAGACCTGCATTTTACCGGCACAAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACACTGTTTAATCTTGCTGATACGCTCCTTGGCGGCTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCG 412

RESULT 362
AY568359
LOCUS       AY568359                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 I capsid protein mRNA, partial
            cds.
ACCESSION   AY568359
VERSION     AY568359.1  GI:46403184
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 I"
                     /country="Algeria"
                     /note="clinical isolate"
     CDS             <1. .>409
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAS92612.1"
                     /db_xref="GI:46403185"
                     /translation="TVARSLEWTKVTLDGRPLSTIQQYSKTFFDLPLRGKLSFWEAGT
                     TKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALL
                     EDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTV"

Alignment Scores:
Pred. No.:              213           Length:         409
Score:                  131.00        Matches:        131
Percent Similarity:     97.76%        Conservative:   0
Best Local Similarity:  97.76%        Mismatches:     3
Query Match:            23.86%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AY568359 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIle 418
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGTCGCCCTCTTTCTACTATT 65

Qy        419 GlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         66 CAGCAGTACTCTAAGACTTTCTTCGACCTGCCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeu 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGly 478
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CTTATTGAGAACGCCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeu 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCGCTG 305

Qy        499 LeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              ||||||||||||||||||||||||||||||||||||||||||
Db        366 TGCCGACCCCTTGGCCTTCAGGGCTGTGCTTTCCAGTCTACT 407

RESULT 363
AY568365
LOCUS       AY568365                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 A capsid protein mRNA, partial
            cds.
ACCESSION   AY568365
VERSION     AY568365.1  GI:46403196
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 A"
                     /country="Algeria"
                     /note="clinical isolate"
     CDS             <1. .>409
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAS92618.1"
                     /db_xref="GI:46403197"
                     /translation="TVARSLEWTKVTLDGRPLSTIQQYSKTFFDLPLRGKLSFWEAGT
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                     EDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTV"

Alignment Scores:
Pred. No.:              213           Length:         409
Score:                  131.00        Matches:        131
Percent Similarity:     97.76%        Conservative:   0
Best Local Similarity:  97.76%        Mismatches:     3
Query Match:            23.86%        Indels:         0
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DB:                    1              Gaps:          0

US-09-769-066-15 (1-549) x AY568365 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIle 418
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGTCGCCCTCTTTCTACTATT 65

Qy        419 GlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db         66 CAGCAGTACTCTAAGACTTTCTTCGACCTGCCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeu 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGly 478
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CTTATTGAGAACGCCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeu 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCACTG 305

Qy        499 LeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              |||||||||||||||||||||||||||||||||||||||||||
Db        366 TGTCGCCCCCTTGGCCTTCAGGGATGCGCTTTCCAGTCTACT 407

RESULT 364
AY596463
LOCUS       AY596463                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 B capsid protein mRNA, partial
            cds.
ACCESSION   AY596463
VERSION     AY596463.1  GI:46403200
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Teyssou,R. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 B"
                     /country="Algeria"
                     /note="clinical isolate"
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                     /protein_id="AAS92620.1"
                     /db_xref="GI:46403201"
                     /translation="TVARSLEWTKVTLDGRPLSTIQQYSKTFFDLPLRGKLSFWEAGT
                     TKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALL
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Best Local Similarity:  97.76%       Mismatches:      3
Query Match:            23.86%       Indels:          0
DB:                     1            Gaps:            0

US-09-769-066-15 (1-549) x AY596463 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIle 418
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Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGTCGCCCTCTTTCTACTATT 65

Qy        419 GlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db         66 CAGCAGTACTCTAAGACTTTCTTCGACCTGCCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeu 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGly 478
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CTTATTGAGAACGCCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeu 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCACTG 305

Qy        499 LeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
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Db        366 TGCCGGCCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACT 407

RESULT 365
AB082567
LOCUS       AB082567                412 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA11.
ACCESSION   AB082567
VERSION     AB082567.1  GI:22759630
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="HE-JA11"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
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                     /country="Japan:Yamanashi, Kofu"
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                     /db_xref="GI:22759631"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              213             Length:         412
Score:                  131.00          Matches:        131
Percent Similarity:     95.62%          Conservative:   0
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Query Match:            23.86%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB082567 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCCGAGGAGGAGGCTACCTCTGGCCTGGTAATGCTTTGTATTCATGGCTCCCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTCAGGAATTTAACACCCGGGAACACTAACACCCGTGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGCCGTGGTGYCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGTTTCATGAAGGATCTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATTGCTTTGACATTGTTCAATCTTGCTGATACGCTTCTCGGTGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCCGTCGTCTCA 412

RESULT 366
AB094204
LOCUS       AB094204                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ1-2.
ACCESSION   AB094204
VERSION     AB094204.1  GI:29292663
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES              Location/Qualifiers
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                      /organism="Swine hepatitis E virus"
                      /virion
                      /mol_type="genomic RNA"
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                      /db_xref="taxon:63421"
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Alignment Scores:
Pred. No.:              213             Length:         412
Score:                  131.00          Matches:        131
Percent Similarity:     95.62%          Conservative:   0
Best Local Similarity:  95.62%          Mismatches:     6
Query Match:            23.86%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB094204 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAGGAGGAGGCTACTTCCGGTCTCGTAATGCTTTGCATTCATGGTTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAGTTTAGAAATTTGACACCCGGGAACACCAACACCCGCGTTTCCAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGTTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTAGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATCGCTCTTACACWGTTTAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 367
AB094226
LOCUS       AB094226                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-1.
ACCESSION   AB094226
VERSION     AB094226.1  GI:29292707
KEYWORDS    .
SOURCE      Swine hepatitis E virus
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  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:                213             Length:         412
Score:                    131.00          Matches:        131
Percent Similarity:       95.62%          Conservative:   0
Best Local Similarity:    95.62%          Mismatches:     6
Query Match:              23.86%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094226 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCCGAGGAGGAGGCAACATCAGGTCTGGTCATGCTTTGCATTCATGGTTCCCCCGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCCGAACTTACTACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGTGTTGGCGAAGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTTTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 368
AB094227
LOCUS       AB094227                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-2.
ACCESSION   AB094227
VERSION     AB094227.1  GI:29292709
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:                213             Length:         412
Score:                    131.00          Matches:        131
Percent Similarity:       95.62%          Conservative:   0
Best Local Similarity:    95.62%          Mismatches:     6
Query Match:              23.86%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094227 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCCGAGGAGGAGGCAACATCTGGTCTGGTCATGCTTTGCATCCATGGTTCTCCCGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCTGAACTTACCACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTCGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTTTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 369
AB094228
LOCUS       AB094228                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-3.
ACCESSION   AB094228
VERSION     AB094228.1  GI:29292711
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              213           Length:        412
Score:                  131.00        Matches:       131
Percent Similarity:     95.62%        Conservative:  0
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Query Match:            23.86%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB094228 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCCGAGGAGGAGGCAACATCTGGTCTGGTCATGCTTTGCATCCATGGTTCTCCCGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCTGAACTTACCACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTCGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTTTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 370
AB094229
LOCUS       AB094229                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-4.
ACCESSION   AB094229
VERSION     AB094229.1  GI:29292713
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ8-4"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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                     /product="capsid protein"
                     /protein_id="BAC66252.1"
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              213           Length:         412
Score:                  131.00        Matches:        131
Percent Similarity:     95.62%        Conservative:   0
Best Local Similarity:  95.62%        Mismatches:     6
Query Match:            23.86%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AB094229 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCCGAGGAGGAGGCAACATCTGGTCTGGTCATGCTTTGCATCCATGGTTCTCCCGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCTGAACTTACCACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTCGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTTTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 371
AB094230
LOCUS       AB094230                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-5.
ACCESSION   AB094230
VERSION     AB094230.1  GI:29292715
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ8-5"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66253.1"
                     /db_xref="GI:29292716"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              213           Length:         412
Score:                  131.00        Matches:        131
Percent Similarity:     95.62%        Conservative:   0
Best Local Similarity:  95.62%        Mismatches:     6
Query Match:            23.86%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AB094230 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db          2 GCCGAGGAGGAGGCAACATCTGGTCTGGTCATGCTTTGCATTCATGGTTCCCCCGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCCGAACTTACCACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTTGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTTTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 372
AB094231
LOCUS       AB094231                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-6.
ACCESSION   AB094231
VERSION     AB094231.1  GI:29292717
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
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          hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
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                     /isolation_source="swine serum"
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                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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                     /protein_id="BAC66254.1"
                     /db_xref="GI:29292718"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              213           Length:        412
Score:                  131.00        Matches:       131
Percent Similarity:     95.62%        Conservative:  0
Best Local Similarity:  95.62%        Mismatches:    6
Query Match:            23.86%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB094231 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCCGAGGAGGAGGCAACATCTGGTCTGGTCATGCTTTGTATTCATGGTTCTCCCGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGGCTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCTGAACTTACCACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTTGGYGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTGACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTTTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 373
AB094232
LOCUS       AB094232                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-7.
ACCESSION   AB094232
VERSION     AB094232.1  GI:29292719
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /country="Japan"
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Alignment Scores:
Pred. No.:              213           Length:        412
Score:                  131.00        Matches:       131
Percent Similarity:     95.62%        Conservative:  0
Best Local Similarity:  95.62%        Mismatches:    6
Query Match:            23.86%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB094232 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCCGAGGAGGAGGCAACATCTGGTCTGGTCATGCTTTGCATCCATGGTTCTCCCGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCTGAACTTACCACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTCGGCGAGGTGGGCCGT 301
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Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 YTGATTTCGTCGGCTGGAGGTCAGCTTTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 374
AB094233
LOCUS       AB094233                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-8.
ACCESSION   AB094233
VERSION     AB094233.1  GI:29292721
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:63421"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              213           Length:        412
Score:                  131.00        Matches:       131
Percent Similarity:     95.62%        Conservative:  0
Best Local Similarity:  95.62%        Mismatches:    6
Query Match:            23.86%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB094233 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCCGAGGAGGAGGCAACATCAGGTCTGGTCATGCTTTGCATTCATGGTTCCCCCGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTAYACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGYCACCGCCTACGCCGTGGCCCCGACGGAACCGCCGAACTTACTACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTTGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTTTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 375
AB094234
LOCUS       AB094234                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-9.
ACCESSION   AB094234
VERSION     AB094234.1  GI:29292723
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ8-9"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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                     /db_xref="GI:29292724"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              213           Length:        412
Score:                  131.00        Matches:       131
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Percent Similarity:     95.62%          Conservative:  0
Best Local Similarity:  95.62%          Mismatches:    6
Query Match:            23.86%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-15 (1-549) x AB094234 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCCGAGGAAGAGGCAACATCAGGTCTGGTCATGCTTTGCATTCATGGTTCCCCCGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTC 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCCGAACTTACTACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTTGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTTTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 376
AB094235
LOCUS       AB094235                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-10.
ACCESSION   AB094235
VERSION     AB094235.1  GI:29292725
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ8-10"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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                     /codon_start=2
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                     /protein_id="BAC66258.1"
                     /db_xref="GI:29292726"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              213             Length:        412
Score:                  131.00          Matches:       131
Percent Similarity:     95.62%          Conservative:  0
Best Local Similarity:  95.62%          Mismatches:    6
Query Match:            23.86%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-15 (1-549) x AB094235 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCCGAGGAAGAGGCAACTTCAGGTCTGGTCATGCTTTGCATTCATGGTTCCCCTGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCCGAACTTACTACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTTGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTCTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 377
AB094236
LOCUS       AB094236                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-11.
ACCESSION   AB094236
VERSION     AB094236.1  GI:29292727
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
```

Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
Fax:81-285-44-1557)

FEATURES Location/Qualifiers
source 1. .412
/organism="Swine hepatitis E virus"
/virion
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ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:

Pred. No.:	213	Length:	412
Score:	131.00	Matches:	131
Percent Similarity:	95.62%	Conservative:	0
Best Local Similarity:	95.62%	Mismatches:	6
Query Match:	23.86%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AB094236 (1-412)

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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCCGAGGAAGAGGCAACTTCAGGTCTGGTCATGCTTTGCATTCATGGTTCCCCTGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCCGAACTTACTACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||||  ||||||  ||||||||||||||||||||||||||||||||||||||
Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTTGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTCTTCTACTCCCGACCAGTCGTCTCG 412
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RESULT 378
AB094237
LOCUS AB094237 412 bp RNA linear VRL 27-MAR-2003
DEFINITION Swine hepatitis E virus ORF2 gene for capsid protein, partial cds, isolate:swJ8-12.
ACCESSION AB094237
VERSION AB094237.1 GI:29292729
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.

REFERENCE 1
AUTHORS Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T., Tsuda,F. and Okamoto,H.
TITLE Swine hepatitis E virus strains in Japan form four phylogenetic clusters comparable with those of Japanese isolates of human hepatitis E virus
JOURNAL J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
PUBMED 12655086
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School, Immunology Division and Division of Molecular Virology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)

FEATURES Location/Qualifiers
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Alignment Scores:

Pred. No.:	213	Length:	412
Score:	131.00	Matches:	131
Percent Similarity:	95.62%	Conservative:	0
Best Local Similarity:	95.62%	Mismatches:	6
Query Match:	23.86%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AB094237 (1-412)

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Db          2 GCCGAGGAAGAGGCAACTTCAGGTCTGGTCATGCTTTGCATTCATGGTTCCCCTGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCCGAACTTACTACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTTGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTCTTCTACTCCCGACCAGTCGTCTCG 412
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RESULT 379
AB094250
LOCUS       AB094250                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ12-1.
ACCESSION   AB094250
VERSION     AB094250.1  GI:29292755
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              213          Length:        412
Score:                  131.00       Matches:       131
Percent Similarity:     95.62%       Conservative:  0
Best Local Similarity:  95.62%       Mismatches:    6
Query Match:            23.86%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AB094250 (1-412)

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Db          2 GCTGAAGAGGAGGCAACATCGGGTCTGGTCATGCTCTGTATTCATGGTTCTCCCGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTACACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCTTACGTCGTGGCGCCGACGGAACTGCCGAGCTTACGACCACTGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||   ||||||      ||||||||||||||   ||||||
Db        242 ACGCGCTTCATGAAGGATCTGCATTTTACTGGGATGAATGGCGTTGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTCTATTCAACCTTGCTGATACACTTCTTGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGCCAGCTCTTTTACTCCCGCCCAGTCGTCTCG 412

RESULT 380
AB094251
LOCUS       AB094251                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ12-2.
ACCESSION   AB094251
VERSION     AB094251.1  GI:29292757
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ12-2"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66274.1"
                     /db_xref="GI:29292758"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGMNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              213          Length:        412
Score:                  131.00       Matches:       131
Percent Similarity:     95.62%       Conservative:  0
Best Local Similarity:  95.62%       Mismatches:    6
Query Match:            23.86%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AB094251 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAAGAGGAGGCAACATCGGGTCTGGTCATGCTCTGTATTCATGGTTCTCCCGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195

Db         62 TCCTACACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215

Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235

Db        182 GCTCGTCACCGCTTACGTCGTGGCGCCGACGGAACTGCCGAGCTTACGACCACTGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255

Db        242 ACGCGCTTCATGAAGGATCTGCATTTTACTGGGATGAATGGCGTTGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275

Db        302 GGCATAGCCCTAACTCTATTCAACCTTGCTGATACACTTCTTGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292

Db        362 TTGATTTCGTCGGCTGGAGGCCAGCTCTTTTACTCCCGCCCAGTCGTCTCG 412
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RESULT 381
AB094252
LOCUS       AB094252                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ12-3.
ACCESSION   AB094252
VERSION     AB094252.1  GI:29292759
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
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                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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                     /db_xref="GI:29292760"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                213             Length:         412
Score:                    131.00          Matches:        131
Percent Similarity:       95.62%          Conservative:   0
Best Local Similarity:    95.62%          Mismatches:     6
Query Match:              23.86%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094252 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175

Db          2 GCTGAAGAGGAGGCAACATCGGGTCTGGTCATGCTCTGTATTCATGGTTCTCCCGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195

Db         62 TCCTACACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215

Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235

Db        182 GCTCGTCACCGCTTACGTCGTGGCGCCGACGGAACTGCCGAGCTTACGACCACTGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255

Db        242 ACGCGCTTCATGAAGGATTTGCATTTTACTGGGATGAATGGCGTTGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275

Db        302 GGCATAGCCCTAACTCTATTCAACCTTGCTGATACACTTCTTGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292

Db        362 TTGATTTCGTCGGCTGGAGGCCAGCTCTTTTACTCCCGCCCAGTCGTCTCG 412
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RESULT 382
AB094253
LOCUS       AB094253                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ12-4.
ACCESSION   AB094253
VERSION     AB094253.1  GI:29292761
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
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                     /isolate="swJ12-4"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
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                     /db_xref="GI:29292762"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                213           Length:        412
Score:                    131.00        Matches:       131
Percent Similarity:       95.62%        Conservative:  0
Best Local Similarity:    95.62%        Mismatches:    6
Query Match:              23.86%        Indels:        0
DB:                       1             Gaps:          0

US-09-769-066-15 (1-549) x AB094253 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAGGCAACATCGGGTCTGGTCATGCTCTGTATTCATGGTTCTCCCGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCTTACGTCGTGGCGCCGACGGAACTGCCGAGCTTACGACCACTGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||   ||||||      ||||||||||||||   ||||||
Db        242 ACGCGCTTCATGAAGGATCTGCATTTTACTGGGATGAATGGCGTTGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTCTATTCAACCTTGCTGATACACTTCTTGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGCCAGCTCTTTTACTCCCGCCCAGTCGTCTCG 412

RESULT 383
AB094258
LOCUS       AB094258                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-3.
ACCESSION   AB094258
VERSION     AB094258.1  GI:29292771
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086

REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ15-3"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
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Alignment Scores:
Pred. No.:                213           Length:        412
Score:                    131.00        Matches:       131
Percent Similarity:       95.62%        Conservative:  0
Best Local Similarity:    95.62%        Mismatches:    6
Query Match:              23.86%        Indels:        0
DB:                       1             Gaps:          0

US-09-769-066-15 (1-549) x AB094258 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCCCTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGTCGTGGAGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||   ||||||   ||||||||||||||||   ||||||
Db        242 ACGCGTTTCATGAAGGACCTGCACTTTACTGGCACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAACCTTGCTGATACACTTCTCGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              |||   ||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CTGRTTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 384
AB094275
LOCUS       AB094275                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ18-1.
ACCESSION   AB094275
VERSION     AB094275.1  GI:29292805
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KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:63421"
                     /country="Japan"
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Alignment Scores:
Pred. No.:              213             Length:         412
Score:                  131.00          Matches:        131
Percent Similarity:     95.62%          Conservative:   0
Best Local Similarity:  95.62%          Mismatches:     6
Query Match:            23.86%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB094275 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCCGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACGCGTTTTATGAAGGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              |||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGCCGGCTGGTGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 385
AB094289
LOCUS       AB094289                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ19-11.
ACCESSION   AB094289
VERSION     AB094289.1  GI:29292833
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /db_xref="taxon:63421"
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAAXRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              213             Length:         412
Score:                  131.00          Matches:        131
Percent Similarity:     95.62%          Conservative:   0
Best Local Similarity:  95.62%          Mismatches:     6
Query Match:            23.86%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB094289 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTTTGGTGATGCTTTGCATYCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTTGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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/product="capsid protein"
/protein_id="BAC66323.1"
/db_xref="GI:29292856"
/translation="AEEEATSGLVMLCIHGSPVNSYTNXPYTGALGLLDFALELEFRN
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ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:

Pred. No.:	213	Length:	412
Score:	131.00	Matches:	131
Percent Similarity:	95.62%	Conservative:	0
Best Local Similarity:	95.62%	Mismatches:	6
Query Match:	23.86%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AB094300 (1-412)

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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATRCACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATCTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||||||||
Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACATTGTTCAATCTTGCTGACACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCA 412
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RESULT 388
AB094320
LOCUS AB094320 412 bp RNA linear VRL 27-MAR-2003
DEFINITION Swine hepatitis E virus ORF2 gene for capsid protein, partial cds, isolate:swJ25-4.
ACCESSION AB094320
VERSION AB094320.1 GI:29292895
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T., Tsuda,F. and Okamoto,H.
TITLE Swine hepatitis E virus strains in Japan form four phylogenetic clusters comparable with those of Japanese isolates of human hepatitis E virus
JOURNAL J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
PUBMED 12655086
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School, Immunology Division and Division of Molecular Virology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)

FEATURES Location/Qualifiers
source 1. .412
/organism="Swine hepatitis E virus"
/virion
/mol_type="genomic RNA"
/isolate="swJ25-4"
/isolation_source="swine serum"
/specific_host="farm pig"
/db_xref="taxon:63421"
/country="Japan"
CDS <1. .>412
/note="ORF2"
/codon_start=2
/product="capsid protein"
/protein_id="BAC66343.1"
/db_xref="GI:29292896"
/translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
LTPGNTNXRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:

Pred. No.:	213	Length:	412
Score:	131.00	Matches:	131
Percent Similarity:	95.62%	Conservative:	0
Best Local Similarity:	95.62%	Mismatches:	6
Query Match:	23.86%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AB094320 (1-412)

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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTAGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTCAGGAATTTAACTCCCGGGAACACTAACAYCCGTGTATCCCGATATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACACTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412
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RESULT 389
AB094326
LOCUS AB094326 412 bp RNA linear VRL 27-MAR-2003
DEFINITION Swine hepatitis E virus ORF2 gene for capsid protein, partial cds, isolate:swJ25-10.
ACCESSION AB094326
VERSION AB094326.1 GI:29292907
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T., Tsuda,F. and Okamoto,H.

```
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-10"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66349.1"
                     /db_xref="GI:29292908"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADXLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              213           Length:        412
Score:                  131.00        Matches:       131
Percent Similarity:     95.62%        Conservative:  0
Best Local Similarity:  95.62%        Mismatches:    6
Query Match:            23.86%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB094326 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACYAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACRCRCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 390
AB096756
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LOCUS       AB096756                412 bp    RNA     linear   VRL 11-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate: swJC1990.
ACCESSION   AB096756
VERSION     AB096756.1  GI:28971695
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Identification of a Genotype III Swine Hepatitis E Virus That Was
            Isolated from a Japanese Pig Born in 1990 and That Is Most Closely
            Related to Japanese Isolates of Human Hepatitis E Virus
  JOURNAL   J. Clin. Microbiol. 41 (3), 1342-1343 (2003)
  MEDLINE   22511089
   PUBMED   12624083
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-NOV-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJC1990"
                     /isolation_source="serum"
                     /specific_host="pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
                     /note="genotype III"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC65323.1"
                     /db_xref="GI:28971696"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNSRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              213           Length:        412
Score:                  131.00        Matches:       131
Percent Similarity:     95.62%        Conservative:  0
Best Local Similarity:  95.62%        Mismatches:    6
Query Match:            23.86%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB096756 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTAATGCTTTGTATCCATGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACTCCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        182 GCCCGCCATCGGCTGCGCCGCGGTGCCGACGGGACCGCTGAGCTTACTACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||    ||||||    ||||||||||||||||||    ||||||
Db        242 ACGCGTTTTATGAAGGACTTGCATTTCACTGGCACGAATGGAGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACACTGTTTAATCTTGCTGACACGCTTCTCGGTGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 391
AF228532
LOCUS       AF228532                397 bp    RNA     linear   VRL 02-FEB-2001
DEFINITION  Hepatitis E virus isolate 95-RCA structural protein gene, partial
            cds.
ACCESSION   AF228532
VERSION     AF228532.1  GI:12656042
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 397)
  AUTHORS   van Cuyck,H. and Viret,J.
  TITLE     Introduction for a modelization of Hepatitis E virus (HEV)
            evolution
  JOURNAL   Acta Biotheor. (2000) In press
REFERENCE   2  (bases 1 to 397)
  AUTHORS   Buisson,Y., Grandadam,M. and Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Transmissible Agents, CRSSA, 24 Ave des
            Maquis du Gresivaudan, BP87, La Tronche 38702, France
FEATURES             Location/Qualifiers
     source          1. .397
                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="95-RCA"
                     /db_xref="taxon:12461"
                     /country="Central African Republic"
                     /note="isolated from sporadic case in 1995"
     CDS             <1. .>397
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                     /db_xref="GI:12656043"
                     /translation="VARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTT
                     KAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLE
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Alignment Scores:
Pred. No.:              215          Length:         397
Score:                  130.00       Matches:        130
Percent Similarity:     99.24%       Conservative:   0
Best Local Similarity:  99.24%       Mismatches:     1
Query Match:            23.68%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AF228532 (1-397)

Qy        399 ValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIle 418
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Db          3 GTTGCCCGGTCACTCGACTGGACCAAGGTCACGCTCGATGGCCGCCCTCTTTCTACTATT 62

Qy        419 GlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CAGCAGTACTCTAAGACCTTCTTTGTCCTGCCGCTTCGTGGCAAGCTCTCTTTCTGGGAG 122

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeu 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GCGGGTACTACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGTGACCAATTG 182

Qy        459 LeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGly 478
              |||    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 CTCATTGAGAATGCCGCCGGACATCGGGTGGCTATTTCCACCTATACCACTAGCCTAGGT 242

Qy        479 AlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeu 498
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Db        243 GCTGGCCCTGTTTCCATCTCCGCGGTCGCTGTTTTAGCCCCCCACTCTGCTTTAGCACTG 302

Qy        499 LeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCACACTTTCGATGATTTCTGCCCGGAG 362

Qy        519 CysArgProLeuGlyLeuGlnGlyCysAlaPhe 529
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Db        363 TGCCGCCCTCTTGGCCTCCAGGGCTGTGCTTTC 395

RESULT 392
AY568357
LOCUS       AY568357                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 K capsid protein mRNA, partial
            cds.
ACCESSION   AY568357
VERSION     AY568357.1  GI:46403180
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 K"
                     /country="Algeria"
                     /note="clinical isolate"
     CDS             <1. .>409
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                     /product="capsid protein"
                     /protein_id="AAS92610.1"
                     /db_xref="GI:46403181"
                     /translation="TVARSLEWTKVTLDGRPLSTIQQYSKTFFDLPLRGKLSFWEAGT
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Alignment Scores:
Pred. No.:              215          Length:         409
Score:                  130.00       Matches:        130
Percent Similarity:     97.01%       Conservative:   0
Best Local Similarity:  97.01%       Mismatches:     4
Query Match:            23.68%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AY568357 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIle 418
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Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGTCGCCCTCTTTCTACTATT 65

Qy        419 GlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db         66 CAGCAGTACTCTAAGACTTTCTTCGACCTGCCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeu 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGly 478
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Db        186 CTTATTGAGAACGTCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeu 498
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Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCGCTG 305

Qy        499 LeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              ||||||||||||||||||||||||||||||||||||||||||
Db        366 TGCCGACCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACT 407

RESULT 393
AY568358
LOCUS       AY568358                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 J capsid protein mRNA, partial
            cds.
ACCESSION   AY568358
VERSION     AY568358.1  GI:46403182
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 J"
                     /country="Algeria"
                     /note="clinical isolate"
     CDS             <1. .>409
                     /codon_start=3
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                     /protein_id="AAS92611.1"
                     /db_xref="GI:46403183"
                     /translation="TVARSLEWTKVTLDGRPLSTIQQYSKTFFDLPLRGKLSFWEAGT
                     TKAGYPYNYNTTASDQLLIENVAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALL
                     EDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTV"

Alignment Scores:
Pred. No.:              215          Length:        409
Score:                  130.00       Matches:       130
Percent Similarity:     97.01%       Conservative:  0
Best Local Similarity:  97.01%       Mismatches:    4
Query Match:            23.68%       Indels:        0

DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AY568358 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIle 418
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Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGTCGCCCTCTTTCTACTATT 65

Qy        419 GlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db         66 CAGCAGTACTCTAAGACTTTCTTCGACCTGCCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeu 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGly 478
              |||    ||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        186 CTTATTGAGAACGTCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeu 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCACTG 305

Qy        499 LeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              ||||||||||||||||||||||||||||||||||||||||||
Db        366 TGCCGGCCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACT 407

RESULT 394
AY568361
LOCUS       AY568361                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 F capsid protein mRNA, partial
            cds.
ACCESSION   AY568361
VERSION     AY568361.1  GI:46403188
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 F"
                     /country="Algeria"
                     /note="clinical isolate"
     CDS             <1. .>409
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                     /product="capsid protein"
                     /protein_id="AAS92614.1"
                     /db_xref="GI:46403189"
                     /translation="TVARSLEWTKVTLDGRPLSTIQQYSKTFFDLPLRGKLSFWEAGT
                     TKAGYPYNYNTTASDQLLIENVAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALL
                     EDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTV"
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Alignment Scores:
Pred. No.:                215          Length:          409
Score:                    130.00       Matches:         130
Percent Similarity:       97.01%       Conservative:    0
Best Local Similarity:    97.01%       Mismatches:      4
Query Match:              23.68%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-15 (1-549) x AY568361 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIle 418
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGTCGCCCTCTTTCTACTATT 65

Qy        419 GlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db         66 CAGCAGTACTCTAAGACTTTCTTCGACCTACCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeu 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGly 478
              |||   ||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CTTATTGAGAACGTCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeu 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCACTG 305

Qy        499 LeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              |||||||||||||||||||||||||||||||||||||||||||
Db        366 TGTCGCCCCCTTGGCCTTCAGGGATGCGCTTTCCAGTCTACT 407

RESULT 395
AY568362
LOCUS       AY568362                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 E capsid protein mRNA, partial
            cds.
ACCESSION   AY568362
VERSION     AY568362.1  GI:46403190
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-2004) Lab. Biol. Med., Hospital Val-de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 E"
                     /country="Algeria"
                     /note="clinical isolate"
     CDS             <1. .>409
                     /codon_start=3
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                     /protein_id="AAS92615.1"
                     /db_xref="GI:46403191"
                     /translation="TVARSLEWTKVTLDGRPLSTIQQYSKTFFDLPLRGKLSFWEAGT
                     TKAGYPYNYNTTASDQLLIENVAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALL
                     EDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTV"

Alignment Scores:
Pred. No.:                215          Length:          409
Score:                    130.00       Matches:         130
Percent Similarity:       97.01%       Conservative:    0
Best Local Similarity:    97.01%       Mismatches:      4
Query Match:              23.68%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-15 (1-549) x AY568362 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIle 418
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGCCGGCCTCTTTCTACTATT 65

Qy        419 GlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db         66 CAGCAGTACTCTAAGACTTTCTTCGACCTACCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeu 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGly 478
              |||   ||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CTTATTGAGAACGTCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeu 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCGCTG 305

Qy        499 LeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              |||||||||||||||||||||||||||||||||||||||||||
Db        366 TGCCGACCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACT 407

RESULT 396
AY568363
LOCUS       AY568363                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 D capsid protein mRNA, partial
            cds.
ACCESSION   AY568363
VERSION     AY568363.1  GI:46403192
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
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                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
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                     /country="Algeria"
                     /note="clinical isolate"
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Alignment Scores:
Pred. No.:                215          Length:         409
Score:                    130.00       Matches:        130
Percent Similarity:       97.01%       Conservative:   0
Best Local Similarity:    97.01%       Mismatches:     4
Query Match:              23.68%       Indels:         0
DB:                       1            Gaps:           0

US-09-769-066-15 (1-549) x AY568363 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIle 418
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGTCGCCCTCTTTCTACTATT 65

Qy        419 GlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db         66 CAGCAGTACTCTAAGACTTTCTTCGACCTACCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeu 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGly 478
              |||   ||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        186 CTTATTGAGAACGTCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeu 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCACTG 305

Qy        499 LeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              |||||||||||||||||||||||||||||||||||||||||||
Db        366 TGCCGACCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACT 407

RESULT 397
AY568364
LOCUS       AY568364                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 C capsid protein mRNA, partial
            cds.
ACCESSION   AY568364
VERSION     AY568364.1  GI:46403194
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France

FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
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                     /clone="Tanef 86/87 C"
                     /country="Algeria"
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Alignment Scores:
Pred. No.:                215          Length:         409
Score:                    130.00       Matches:        130
Percent Similarity:       97.01%       Conservative:   0
Best Local Similarity:    97.01%       Mismatches:     4
Query Match:              23.68%       Indels:         0
DB:                       1            Gaps:           0

US-09-769-066-15 (1-549) x AY568364 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIle 418
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGCCGCCCTCTTTCTACTATT 65

Qy        419 GlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              ||||||   ||||||||||||||   ||||||||||||||||||||||||||||||||||
Db         66 CAGCAGCACTCTAAGACTTTCTTCGACCTGCCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeu 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGly 478
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CTTATTGAGAACGCCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeu 498
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Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCACTG 305

Qy        499 LeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              |||||||||||||||||||||||||||||||||||||||||||
Db        366 TGCCGGCCCCTTGGCCTTCAGGGTTGCGCTTTCCAGTCTACT 407

RESULT 398
AY596462
LOCUS       AY596462                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 H capsid protein mRNA, partial
            cds.
ACCESSION   AY596462
VERSION     AY596462.1  GI:46403198
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
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REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Teyssou,R. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
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                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 H"
                     /country="Algeria"
                     /note="clinical isolate"
     CDS             <1. .>409
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                     /product="capsid protein"
                     /protein_id="AAS92619.1"
                     /db_xref="GI:46403199"
                     /translation="TVARSLEWTKVTLDGRPLSTIQQHSKTFFDLPLRGKLSFWEAGT
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Alignment Scores:
Pred. No.:              215          Length:         409
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Query Match:            23.68%       Indels:         0
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US-09-769-066-15 (1-549) x AY596462 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIle 418
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Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGCCGCCCTCTTTCTACTATT 65

Qy        419 GlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
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Db         66 CAGCAGCACTCTAAGACTTTCTTCGACCTGCCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeu 458
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Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGly 478
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Qy        479 AlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeu 498
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Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCACTG 305

Qy        499 LeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGlu 518
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Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
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Db        366 TGCCGACCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACT 407

RESULT 399
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DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JF1.
ACCESSION   AB079762
VERSION     AB079762.1  GI:24636297
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Suzuki,K., Aikawa,T. and Okamoto,H.
  TITLE     Fulminant hepatitis E in Japan
  JOURNAL   N. Engl. J. Med. 347 (18), 1456 (2002)
  MEDLINE   22297680
   PUBMED   12409557
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-FEB-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi, Tochigi 329-0498, Japan
            (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Japan"
                     /note="HE-JF1 was isolated from a Japanese patient
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                     etiology-genotype IV"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              216          Length:         412
Score:                  130.00       Matches:        130
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Best Local Similarity:  94.89%       Mismatches:     7
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US-09-769-066-15 (1-549) x AB079762 (1-412)

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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAATACACCCTATACTGGTGCCCTTGGTTTGCTCGATTTTGCACTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAATTTGACACCTGGTAATACAAATACGCGCGTTTCCCGATACTCGAGCAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGATACGCTTCTTGGCGGGCTTCCGACAGAA 361
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Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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RESULT 400
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DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JF3.
ACCESSION   AB079764
VERSION     AB079764.1  GI:24636301
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Suzuki,K., Aikawa,T. and Okamoto,H.
  TITLE     Fulminant hepatitis E in Japan
  JOURNAL   N. Engl. J. Med. 347 (18), 1456 (2002)
  MEDLINE   22297680
   PUBMED   12409557
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-FEB-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi, Tochigi 329-0498, Japan
            (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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     source          1. .412
                     /organism="Hepatitis E virus"
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                     /country="Japan"
                     /note="HE-JF3 was isolated from a Japanese patient
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Alignment Scores:
Pred. No.:              216           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB079764 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTACACTAATACACCTTATACTGGTGCTCTTGGCTTGCTCGATTTCGCACTTGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTYCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 401
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LOCUS       AB082557                412 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA1.
ACCESSION   AB082557
VERSION     AB082557.1  GI:22759610
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              216           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
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DB:                    1              Gaps:          0

US-09-769-066-15 (1-549) x AB082557 (1-412)

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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTTATGCTCTGCATCCATGGATCACCTGTGAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTACACTAATACACCTTATACTGGTGCTCTTGGCTTGCTCGATTTCGCACTTGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAATACGCGCGCGTTTCCCGTTATTCGAGTAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCGCGCCACAAGCTACGTCGTGGGCCCGACGGTACTGCTGAGCTAACCACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGGTTTATGAAAGATCTTCACTTCACAGGGACCAATGGTGTTGGTGAGGTCGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 402
AB082558
LOCUS       AB082558                412 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA2.
ACCESSION   AB082558
VERSION     AB082558.1  GI:22759612
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              216             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB082558 (1-412)

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Db          2 GCGGAGGAGGAGGCCACCTCCGGCCTTGTCATGCTCTGCATCCATGGATCACCCGTGAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTACACTAATACACCCTATACTGGTGCCCTTGGCCTGCTCGATTTCGCACTCGAGCTC 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAATCTGACACCTGGCAATACGAATACGCGCGTCTCCCGCTATTCGAGTAGC 181

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Db        182 GCACGCCACAAGTTACGCCGTGGGCCCGATGGTACTGCTGAATTGACTACTACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACTCGTTTCATGAAGGATCTTCATTTTACAGGGACTAACGGAGTTGGTGAGGTTGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTGACCCTGTTTAACCTTGCTGATACGCTTCTCGGTGGGCTTCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGCGGTCAACTGTTTTATTCTCGCCCCGTCGTCTCA 412

RESULT 403
AB082559
LOCUS       AB082559                412 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA3.
ACCESSION   AB082559
VERSION     AB082559.1  GI:22759614
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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FEATURES             Location/Qualifiers
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                     /country="Japan:Hokkaido, Sapporo"
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     CDS             <1. .>412
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                     /codon_start=2
                     /protein_id="BAC10958.1"
                     /db_xref="GI:22759615"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              216             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB082559 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCATGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTCGAGCTC 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAACACACGTGTTTCCCGCTACTCGAGTAGT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||   ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTAACTACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGAAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATAGCGCTAACTCTGTTCAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTTTATTCTCGCCCCGTCGTCTCA 412

RESULT 404
AB094219
LOCUS       AB094219                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ7-1.
ACCESSION   AB094219
VERSION     AB094219.1  GI:29292693
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ7-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /note="ORF2"
                     /codon_start=2
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                     /protein_id="BAC66242.1"
                     /db_xref="GI:29292694"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              216             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB094219 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTTATGCTCTGCATTCATGGATCACCTGTGAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTACACTAATACACCTTATACTGGTGCTCTTGGCTTGCTTGATTTTGCACTTGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTCGCAATTTGACACCCGGTAATACGAATACGCGCGTCTCCCGTTATTCGAGTAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||   ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        182 GCGCGTCACAAGCTACGTCGTGGGCCCGACGGTACTGCTGAGCTAACCACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGGTTTATGAAAGACCTTCACTTCACAGGGACCAATGGTGTTGGTGAGGTCGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGCGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 405
AB094220
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LOCUS       AB094220                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
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ACCESSION   AB094220
VERSION     AB094220.1  GI:29292695
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ7-2"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /protein_id="BAC66243.1"
                     /db_xref="GI:29292696"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                216             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094220 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTTATGCTCTGCATTCATGGATCACCTGTGAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAATACACCTTATACTGGTGCTCTTGGCTTGCTTGATTTTGCACTTGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAATTTGACACCCGGTAATACGAATACGCGCGTCTCCCGTTATTCGAGTAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCGCGCCACAAGCTACGTCGTGGGCCCGACGGTACTGCTGAGCTAACCACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACACGGTTTATGAAAGACCTTCACTTCACAGGGACCAATGGTGTTGGTGAGGTCGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGCGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 406
AB094221
LOCUS       AB094221                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ7-3.
ACCESSION   AB094221
VERSION     AB094221.1  GI:29292697
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
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                     /isolate="swJ7-3"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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                     /db_xref="GI:29292698"
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Alignment Scores:
Pred. No.:                216             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB094221 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTTATGCTCTGCATTCATGGATCACCTGTGAAC 61
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTACACTAATACACCTTATACTGGTGCTCTTGGCTTGCTTGATTTTGCACTTGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAATTTGACACCCGGTAATACGAATACGCGCGTCTCCCGTTATTCGAGTAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCGCGCCACAAGCTACGTCGTGGGCCCGACGGTACTGCTGAGCTAACCACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACACGGTTTATGAAAGACCTTCACTTCACAGGGACCAATGGTGTTGGTGAGGTCGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGCGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 407
AB094222
LOCUS       AB094222                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ7-4.
ACCESSION   AB094222
VERSION     AB094222.1  GI:29292699
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:

Pred. No.:              216          Length:         412
Score:                  130.00       Matches:        130
Percent Similarity:     94.89%       Conservative:   0
Best Local Similarity:  94.89%       Mismatches:     7
Query Match:            23.68%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AB094222 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTTATGCTCTGCATTCATGGATCACCTGTGAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAATACACCTTATACTGGTGCTCTTGGCTTGCTTGATTTTGCACTTGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAATTTGACACCCGGTAATACGAATACGCGCGTCTCCCGTTATTCGAGTAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||   ||||||||||||   ||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGTCGTGGGCCCGACGGTACTGCTGAGCTAACCACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACACGGTTTATGAAAGACCTTCACTTCACAGGGACCAATGGTGTTGGTGAGGTCGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGCGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 408
AB094223
LOCUS       AB094223                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ7-5.
ACCESSION   AB094223
VERSION     AB094223.1  GI:29292701
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              216             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB094223 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTTATGCTCTGCATTCATGGATCACCTGTGAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTACACTAATACACCTTATACTGGTGCTCTTGGCTTGCTTGATTTTGCACTTGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAATTTGACACCCGGTAATACGAATACGCGCGTCTCCCGTTATTCGAGTAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCGCGCCACAAGCTACGTCGTGGGCCCGACGGTACTGCTGAGCTAACCACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGGTTTATGAAAGACCTTCACTTCACAGGGACCAATGGTGTTGGTGAGGTCGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGCGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 409
AB094224
LOCUS       AB094224                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ7-6.
ACCESSION   AB094224
VERSION     AB094224.1  GI:29292703
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES            Location/Qualifiers
     source         1. .412
                    /organism="Swine hepatitis E virus"
                    /virion
                    /mol_type="genomic RNA"
                    /isolate="swJ7-6"
                    /isolation_source="swine serum"
                    /specific_host="farm pig"
                    /db_xref="taxon:63421"
                    /country="Japan"
     CDS            <1. .>412
                    /note="ORF2"
                    /codon_start=2
                    /product="capsid protein"
                    /protein_id="BAC66247.1"
                    /db_xref="GI:29292704"
                    /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                    LTPGNTNTRVSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                    ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              216             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB094224 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTTATGCTCTGCATTCATGGATCACCTGTGAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTACACTAATACACCTTATACTGGTGCTCTTGGCTTGCTTGATTTTGCACTTGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAATTTGACACCCGGTAATACGAATACGCGCGTCTCCCGTTATTCGAGTAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||  ||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGTCGTGGGCCCGACGGTACTGCTGAGCTAACCACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGGTTTATGAAAGACCTTCACTTCACAGGGACCAATGGTGTTGGTGAGGTCGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGCGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 410
AB094225
LOCUS       AB094225                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ7-7.
ACCESSION   AB094225
VERSION     AB094225.1  GI:29292705
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
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           Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
           Hepevirus.
REFERENCE  1
  AUTHORS  Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
           Tsuda,F. and Okamoto,H.
  TITLE    Swine hepatitis E virus strains in Japan form four phylogenetic
           clusters comparable with those of Japanese isolates of human
           hepatitis E virus
  JOURNAL  J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED  12655086
REFERENCE  2  (bases 1 to 412)
  AUTHORS  Okamoto,H.
  TITLE    Direct Submission
  JOURNAL  Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
           Immunology Division and Division of Molecular Virology; 3311-1
           Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
           Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
           Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ7-7"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66248.1"
                     /db_xref="GI:29292706"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              216           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB094225 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTTATGCTCTGCATTCATGGATCACCTGTGAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAATACACCTTATACTGGTGCTCTTGGCTTGCTTGATTTTGCACTTGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAATTTGACACCCGGTAATACGAATACGCGCGTCTCCCGTTATTCGAGTAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||   ||||||||||   ||||||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGTCGTGGGCCCGACGGTACTGCTGAGCTAACCACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACACGGTTTATGAAAGACCTTCACTTCACAGGGACCAATGGTGTTGGTGAGGTCGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGCGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 411
AB094254
LOCUS       AB094254                 412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ13-1.
ACCESSION   AB094254
VERSION     AB094254.1  GI:29292763
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
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                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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                     /db_xref="GI:29292764"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              216           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB094254 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTTATGCTCTGCATCCATGGATCACCTGTGAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAATACACCTTATACTGGTGCTCTTGGCTTGCTCGATTTCGCACTTGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAATACGCGCGTTTCCCGTTATTCGAGTAGC 181
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCGCGCCACAAGCTACGTCGTGGGCCCGACGGTACTGCTGAGCTAACCACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACACGGTTTATGAAAGATCTTCACTTCACAGGGACCAATGGTGTTGGTGAGGTCGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 412
AB094255
LOCUS       AB094255                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ13-2.
ACCESSION   AB094255
VERSION     AB094255.1  GI:29292765
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              216          Length:         412
Score:                  130.00       Matches:        130
Percent Similarity:     94.89%       Conservative:   0
Best Local Similarity:  94.89%       Mismatches:     7
Query Match:            23.68%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AB094255 (1-412)
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTTATGCTCTGCATCCATGGATCACCTGTGAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAATACACCTTATACTGGTGCTCTTGGCTTGCTCGATTTCGCACTTGAACTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAATACGCGCGTTTCCCGTTATTCGAGTAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||   ||||||||||||   ||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGTCGTGGGCCCGACGGTACTGCTGAGCTAACCACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACACGGTTTATGAAGGATCTTCACTTCACAGGGACCAATGGTGTTGGTGAGGTCGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 413
AB105888
LOCUS       AB105888                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JA12.
ACCESSION   AB105888
VERSION     AB105888.1  GI:34097977
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /db_xref="taxon:12461"
                     /country="Japan:Hokkaido"
                     /note="genotype IV; sporadic acute hepatitis E"
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                     /gene="ORF2"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              216             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB105888 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCATGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACCAATACGCCYTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTYGAGCTC 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAACACACGTGTTTCCCGCTACTCGAGTAGT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||   ||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTAACTACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGAAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATAGCGCTAACTCTGTTCAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 414
AB105889
LOCUS       AB105889                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JA13.
ACCESSION   AB105889
VERSION     AB105889.1  GI:34097979
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JA13"
                     /isolation_source="human serum"
                     /db_xref="taxon:12461"
                     /country="Japan:Hokkaido"
                     /note="genotype IV; sporadic acute hepatitis E"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
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                     /db_xref="GI:34097980"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
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Alignment Scores:
Pred. No.:              216             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB105889 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCATGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTCGAGCTC 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGYAATTTGACACCCGGTAACACGAACACACGTGTTTCCCGCTACTCGAGTAGT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||   ||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTAACTACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGAAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATAGCGCTAACTCTGTTCAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 415
AB105893
LOCUS       AB105893                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JA17.
ACCESSION   AB105893
VERSION     AB105893.1  GI:34097987
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
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            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JA17"
                     /isolation_source="human serum"
                     /db_xref="taxon:12461"
                     /country="Japan:Hokkaido"
                     /note="genotype IV; sporadic acute hepatitis E"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
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                     /product="capsid protein"
                     /protein_id="BAC82170.1"
                     /db_xref="GI:34097988"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                216          Length:          412
Score:                    130.00       Matches:         130
Percent Similarity:       94.89%       Conservative:    0
Best Local Similarity:    94.89%       Mismatches:      7
Query Match:              23.68%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-15 (1-549) x AB105893 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCATGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTCGAGCTC 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAACACACGTGTTTCCCGCTACTCGAGTAGT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||  ||||||||||  ||||||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTAACTACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||  ||||||  ||||||||||||||||||  ||||||
Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGAAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTCAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCTCGCCCCGTCGTCTCA 412
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RESULT 416
AB105894
LOCUS       AB105894                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JA18.
ACCESSION   AB105894
VERSION     AB105894.1  GI:34097989
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="HE-JA18"
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                     /country="Japan:Hokkaido"
                     /note="genotype IV; sporadic acute hepatitis E"
     gene            1. .412
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     CDS             <1. .>412
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                     /db_xref="GI:34097990"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                216          Length:          412
Score:                    130.00       Matches:         130
Percent Similarity:       94.89%       Conservative:    0
Best Local Similarity:    94.89%       Mismatches:      7
Query Match:              23.68%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-15 (1-549) x AB105894 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCACGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTCGAGCTC 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAACACACGTGTTTCCCGCTACTCGAGTAGT 181
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTAACTACGACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              |||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGAAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTCAACCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTTTATTCTCGCCCCGTCGTCTCA 412
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RESULT 417
AB105895
LOCUS AB105895 412 bp RNA linear VRL 22-AUG-2003
DEFINITION Hepatitis E virus ORF2 gene for capsid protein, partial cds, isolate:HE-JA19.
ACCESSION AB105895
VERSION AB105895.1 GI:34097991
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N., Gotanda,Y. and Okamoto,H.
TITLE Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be food-borne, as suggested by the presence of hepatitis E virus in pig liver as food
JOURNAL J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
PUBMED 12917455
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School, Immunology Division and Division of Molecular Virology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
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/organism="Hepatitis E virus"
/virion
/mol_type="genomic RNA"
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/note="genotype IV; sporadic acute hepatitis E"
gene 1. .412
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CDS <1. .>412
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ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:

Pred. No.:	216	Length:	412
Score:	130.00	Matches:	130
Percent Similarity:	94.89%	Conservative:	0
Best Local Similarity:	94.89%	Mismatches:	7
Query Match:	23.68%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AB105895 (1-412)

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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTCGAGCTC 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTGACTACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGAAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCTCGCCCCGTCGTCTCA 412
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RESULT 418
AB105896
LOCUS AB105896 412 bp RNA linear VRL 22-AUG-2003
DEFINITION Hepatitis E virus ORF2 gene for capsid protein, partial cds, isolate:HE-JF4.
ACCESSION AB105896
VERSION AB105896.1 GI:34097993
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N., Gotanda,Y. and Okamoto,H.
TITLE Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be food-borne, as suggested by the presence of hepatitis E virus in pig liver as food
JOURNAL J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
PUBMED 12917455
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School, Immunology Division and Division of Molecular Virology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
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/note="genotype IV; sporadic fulminant hepatitis E"
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Alignment Scores:
Pred. No.:                216             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB105896 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCATGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTCGAGCTC 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGTTAACTCTGTTCAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 419
AB105897
LOCUS       AB105897                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JF5.
ACCESSION   AB105897
VERSION     AB105897.1  GI:34097995
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JF5"
                     /isolation_source="human serum"
                     /db_xref="taxon:12461"
                     /country="Japan:Hokkaido"
                     /note="genotype IV; sporadic fulminant hepatitis E"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC82174.1"
                     /db_xref="GI:34097996"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                216             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AB105897 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCATGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTCGAGCTC 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAACACACGTGTTTCCCGCTACTCGAGTAGT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTAACTACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGAAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATAGCGCTAACTCTGTTCAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 420
AB105902
LOCUS       AB105902                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJL145.
ACCESSION   AB105902
VERSION     AB105902.1  GI:34098005
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
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REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJL145"
                     /isolation_source="pig liver"
                     /specific_host="swine"
                     /db_xref="taxon:63421"
                     /country="Japan:Hokkaido"
                     /note="genotype IV"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC82179.1"
                     /db_xref="GI:34098006"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              216           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB105902 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCACGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTCGAGCTC 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAACACACGTGTTTCCCGCTACTCGAGTAGT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||   ||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTAACTACGACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGAAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTCAACCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTTTATTCTCGCCCCGTCGTCTCA 412

RESULT 421
AB107367
LOCUS       AB107367                412 bp    RNA     linear   VRL 07-APR-2004
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate: HE-JAS2.
ACCESSION   AB107367
VERSION     AB107367.1  GI:46250708
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yamamoto,T., Suzuki,H., Toyota,T., Takahashi,M. and Okamoto,H.
  TITLE     Three male patients with sporadic acute hepatitis E in Sendai, who
            were domestically infected with hepatitis E virus of genotype III
            or IV
  JOURNAL   J. Gastroenterol. 39, 292-298 (2004)
   PUBMED   15065009
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-APR-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JAS2"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Japan:Sendai"
                     /note="genotype IV"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD15080.1"
                     /db_xref="GI:46250709"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              216           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AB107367 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCATGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTCGAGCTC 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAACACACGTGTTTCCCGCTACTCGAGTAGT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
                |||||||||   ||||||||||   ||||||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTAACTACCACCGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
                ||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGAAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTCAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 422
AB124818
LOCUS       AB124818                412 bp    RNA     linear   VRL 25-MAR-2004
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:SB66.
ACCESSION   AB124818
VERSION     AB124818.1  GI:45736452
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wibawa,I.D., Muljono,D.H., Mulyanto, Suryadarma,I.G., Tsuda,F.,
            Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Prevalence of antibodies to hepatitis E virus among apparently
            healthy humans and pigs in Bali, Indonesia: Identification of a pig
            infected with a genotype 4 hepatitis E virus
  JOURNAL   J. Med. Virol. 73 (1), 38-44 (2004)
   PUBMED   15042646
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /isolate="SB66"
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                     /country="Indonesia:Bali"
                     /note="genotype IV"
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     CDS             <1. .>412
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                     /product="capsid protein"
                     /protein_id="BAD13317.1"
                     /db_xref="GI:45736453"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              216          Length:        412
Score:                  130.00       Matches:       130
Percent Similarity:     94.89%       Conservative:  0
Best Local Similarity:  94.89%       Mismatches:    7
Query Match:            23.68%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AB124818 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCCGGCCTTGTTATGCTTTGCATCCACGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACCGGCGCTCTTGGTCTGCTTGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAATTTGACACCTGGTAACACGAATACGCGCGTCTCCCGTTATTCGAGTAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
                |||||||||   ||||||||||   ||||||||||||||||||||||||||||||||||||
Db        182 GCGCGTCATAAGTTACGCCGAGGGCCTGATGGTACAGCGGAGTTAACCACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
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Db        242 ACACGTTTTATGAAAGACCTCCATTTCACCGGGACTAATGGTGTTGGTGAGGTTGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATAGCACTAACCCTGTTCAATCTTGCTGATACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTAATTTCGTCGGCTGGTGGCCAGCTGTTTTATTCCCGCCCCGTTGTCTCA 412

RESULT 423
AB168096
LOCUS       AB168096                412 bp    RNA     linear   VRL 07-AUG-2004
DEFINITION  Hepatitis E virus ORF2 gene for ORF2, partial cds.
ACCESSION   AB168096
VERSION     AB168096.1  GI:51036203
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Koizumi,Y., Isoda,N., Sato,Y., Iwaki,T., Ono,K., Ido,K., Sugano,K.,
            Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Infection of a Japanese patient by genotype 4 hepatitis e virus
            while traveling in Vietnam
  JOURNAL   J. Clin. Microbiol. 42 (8), 3883-3885 (2004)
   PUBMED   15297556
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-MAR-2004) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /specific_host="human"
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                     /country="Viet Nam"
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                     /db_xref="GI:51036204"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              216             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB168096 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          2 GCTGAGGAGGAGGCCACCTCCGGCCTTGTTATGCTTTGTATTCATGGGTCACCTGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACCGGCGCCCTCGGCCTGCTTGACTTTGCACTTGAGCTC 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAATCTGACACCTGGTAATACGAACACGCGTGTCTCCCGTTATTCGAGTAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||   ||||||||||   ||||||||||||||||||||||||||||||||||
Db        182 GCGCGTCATAAGTTACGCCGAGGGCCTGACGGCACTGCGGAGCTAACTACTACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||   ||||||   ||||||||||||||||||   ||||||
Db        242 ACACGTTTTATGAAAGATCTTCATTTTACTGGGACTAATGGTGTTGGTGAAGTTGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCACTGACCCTGTTTAATCTTGCTGATACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTAATTTCGTCGGCTGGTGGTCAGCTGTTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 424
AB105890
LOCUS       AB105890                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JA14.
ACCESSION   AB105890
VERSION     AB105890.1  GI:34097981
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES            Location/Qualifiers
     source         1. .412
                    /organism="Hepatitis E virus"
                    /virion
                    /mol_type="genomic RNA"
                    /isolate="HE-JA14"
                    /isolation_source="human serum"
                    /db_xref="taxon:12461"
                    /country="Japan:Hokkaido"
                    /note="genotype IV; sporadic acute hepatitis E"
     gene           1. .412
                    /gene="ORF2"
     CDS            <1. .>412
                    /gene="ORF2"
                    /codon_start=2
                    /product="capsid protein"
                    /protein_id="BAC82167.1"
                    /db_xref="GI:34097982"
                    /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                    LTPGNTNTRVSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGXVGRGI
                    ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              218             Length:         412
Score:                  129.00          Matches:        129
Percent Similarity:     94.16%          Conservative:   0
Best Local Similarity:  94.16%          Mismatches:     8
Query Match:            23.50%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AB105890 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsn 175
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCATGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTTGCACTCGAGCTC 121

Qy        196 GluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTYCGCAATTTGACACCCGGTAACACGAACACACGTGTTTCCCGCTACTCGAGTAGT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||   ||||||||||   ||||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTAACTACCACCGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArg 255
              ||||||||||||||||||||   ||||||   ||||||||||||||||   ||||||
Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGMAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTCAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 425
AY568360
LOCUS       AY568360                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 G capsid protein mRNA, partial
            cds.
ACCESSION   AY568360
VERSION     AY568360.1  GI:46403186
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
```

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           Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
           Hepevirus.
REFERENCE  1  (bases 1 to 409)
  AUTHORS  Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
           Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE    Evidence for the Hepatitis E virus quasispecies
  JOURNAL  Unpublished
REFERENCE  2  (bases 1 to 409)
  AUTHORS  Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
           Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE    Direct Submission
  JOURNAL  Submitted (08-MAR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
           bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 G"
                     /country="Algeria"
                     /note="clinical isolate"
     CDS             <1. .>409
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                     /protein_id="AAS92613.1"
                     /db_xref="GI:46403187"
                     /translation="TVARSLEWTKVTLDVRPLSTIQQYSKTFFDLPLRGKLSFWEAGT
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Alignment Scores:
Pred. No.:                221          Length:          409
Score:                    128.00       Matches:         128
Percent Similarity:       95.52%       Conservative:    0
Best Local Similarity:    95.52%       Mismatches:      6
Query Match:              23.32%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-15 (1-549) x AY568360 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrIle 418
              ||||||||||||||||  ||||||||||||||||||||  ||||||||||||||||||
Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGTCCGCCCTCTTTCTACTATT 65

Qy        419 GlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db         66 CAGCAGTACTCTAAGACTTTCTTCGACCTACCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeu 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrSerLeuGly 478
              |||   ||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        186 CTTATTGAGAACGTCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeu 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCGCAG 305

Qy        499 LeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgProLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              ||||||||||||||||||||||||||||||||||||||||||
Db        366 TGCCGTCCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACT 407

RESULT 426
HEE344182
LOCUS       HEE344182               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 1,
           isolate 152.
ACCESSION   AJ344182
VERSION     AJ344182.1  GI:15282389
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
           Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
           Hepevirus.
REFERENCE  1
  AUTHORS  Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
           Harrison,T.J.
  TITLE    Detection of sporadic cases of hepatitis E virus (HEV) infection in
           China using immunoassays based on recombinant open reading frame 2
           and 3 polypeptides from HEV genotype 4
  JOURNAL  J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE  21646397
   PUBMED  11724847
REFERENCE  2  (bases 1 to 348)
  AUTHORS  Harrison,T.J.
  TITLE    Direct Submission
  JOURNAL  Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
           University College London, Royal Free Campus, Rowland Hill Street,
           London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
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                     /mol_type="mRNA"
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     CDS             <1. .>348
                     /note="ORF2"
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                     /db_xref="UniProt/TrEMBL:Q91EB9"
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Alignment Scores:
Pred. No.:                262          Length:          348
Score:                    114.00       Matches:         114
Percent Similarity:       98.28%       Conservative:    0
Best Local Similarity:    98.28%       Mismatches:      2
Query Match:              20.77%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-15 (1-549) x HEE344182 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTTATGCTTTGCATACATGGCTCACCCGTAAATTCTTACACTAATACACCCTACACCGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGGCTGTTGGATTTTGCCCTTGAACTTGAGTTCCGCAACCTCACTCCCGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAATACTCGGGTCTCTCGTTACTCCAGCACTGCTCGCCACCGTCTTCGCCGCGGTGCA 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGGACCGCCGAGCTCACCACCACGGCTGCCACCCGCTTTATGAAGGATCTCTATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGACACTCTGCTTGGCGGCCTACCGACAGAATTAATTTCGTCGGCT 348

RESULT 427
HEE344173
LOCUS       HEE344173               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 1,
            isolate 185.
ACCESSION   AJ344173
VERSION     AJ344173.1  GI:15282371
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
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                     /note="ORF2"
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                     /db_xref="GI:15282372"
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Alignment Scores:
Pred. No.:              266             Length:         348
Score:                  113.00          Matches:        113
Percent Similarity:     97.41%          Conservative:   0
Best Local Similarity:  97.41%          Mismatches:     3
Query Match:            20.58%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x HEE344173 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGTTTTGCATACATGGCTCACCCGTAAATTCTTACACTAATACACCCTACACCGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGGCTGTTGGATTTTGCCCTTGAACTTGAGTTCCGCAACCTCACTCCCGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
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Db        121 ACCAATACTCGGGTCTCTCGTTACTCCAGCACTGCTCGCCACCGTCTTCGCCGCGGTGCA 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGGACCGCCGAGCTCACCACCACGGCTGCCACCCGCTTTATGAAGGATCTCTATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGACACTCTGCTTGGCGGCCTACCGACAGAATTGATTTCGTCGGCT 348

RESULT 428
HEE344175
LOCUS       HEE344175               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 1,
            isolate 226.
ACCESSION   AJ344175
VERSION     AJ344175.1  GI:15282375
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
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                     /virion
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Alignment Scores:
Pred. No.:              266             Length:         348
Score:                  113.00          Matches:        113
Percent Similarity:     97.41%          Conservative:   0
Best Local Similarity:  97.41%          Mismatches:     3
Query Match:            20.58%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x HEE344175 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
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Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
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Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
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Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
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Db        181 GATGGGACCGCCGAGCTCACCACCACGGCTGCCACCCGCTTTATGAAGGATCTCTATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
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Db        241 GCTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGACACTCTGCTTGGCGGCCTACCGACAGAATTGATTTCGTCGGCT 348
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RESULT 429
HEE344176
LOCUS HEE344176 348 bp mRNA linear VRL 14-DEC-2001
DEFINITION Hepatitis E virus partial mRNA for capsid protein, genotype 1, isolate 273.
ACCESSION AJ344176
VERSION AJ344176.1 GI:15282377
KEYWORDS capsid protein; ORF2.
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and Harrison,T.J.
TITLE Detection of sporadic cases of hepatitis E virus (HEV) infection in China using immunoassays based on recombinant open reading frame 2 and 3 polypeptides from HEV genotype 4
JOURNAL J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
MEDLINE 21646397
PUBMED 11724847
REFERENCE 2 (bases 1 to 348)
AUTHORS Harrison,T.J.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology, University College London, Royal Free Campus, Rowland Hill Street, London, NW3 2PF, UNITED KINGDOM
FEATURES Location/Qualifiers
source 1. .348
/organism="Hepatitis E virus"
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CDS <1. .>348
/note="ORF2"
/codon_start=1
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/protein_id="CAC51495.1"
/db_xref="GI:15282378"
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/db_xref="UniProt/TrEMBL:Q91EC5"
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TLLGGLPTELISSA"

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Alignment Scores:
Pred. No.:              266          Length:        348
Score:                  113.00       Matches:       113
Percent Similarity:     97.41%       Conservative:  0
Best Local Similarity:  97.41%       Mismatches:    3
Query Match:            20.58%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x HEE344176 (1-348)
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Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
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Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
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Db         61 GCCCTCGGGCTGTTGGATTTTGCCCTTGAACTTGAGTTCCGCAACCTCACTCCCGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
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Db        121 ACCAATACTCGGGTCTCTCGTTACTCCAGCACTGCTCGCCACCGTCTTCGCCGCGGTGCA 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
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Db        181 GATGGGACCGCCGAGCTCACCACCACGGCTGCCACCCGCTTTATGAAGGATCTCTATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGACACTCTGCTTGGCGGCCTACCGACAGAATTGATTTCGTCGGCT 348
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RESULT 430
HEE344189
LOCUS HEE344189 348 bp mRNA linear VRL 14-DEC-2001
DEFINITION Hepatitis E virus partial mRNA for capsid protein, genotype 1, isolate 153.
ACCESSION AJ344189
VERSION AJ344189.1 GI:15282403
KEYWORDS capsid protein; ORF2.
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and Harrison,T.J.
TITLE Detection of sporadic cases of hepatitis E virus (HEV) infection in China using immunoassays based on recombinant open reading frame 2 and 3 polypeptides from HEV genotype 4
JOURNAL J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
MEDLINE 21646397
PUBMED 11724847
REFERENCE 2 (bases 1 to 348)
AUTHORS Harrison,T.J.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology, University College London, Royal Free Campus, Rowland Hill Street, London, NW3 2PF, UNITED KINGDOM
FEATURES Location/Qualifiers
source 1. .348
/organism="Hepatitis E virus"
/virion
/mol_type="mRNA"
/isolate="153"
/db_xref="taxon:12461"
CDS <1. .>348
/note="ORF2"
/codon_start=1
/product="capsid protein"
/protein_id="CAC51508.1"
/db_xref="GI:15282404"
/db_xref="GOA:Q91EB2"
/db_xref="UniProt/TrEMBL:Q91EB2"
/translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
VSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFASTNGVGEIGRGIALTLFNLAD
TLLGGLPTELISSA"

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Alignment Scores:
Pred. No.:              266          Length:        348
Score:                  113.00       Matches:       113
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Percent Similarity:     97.41%          Conservative:  0
Best Local Similarity:  97.41%          Mismatches:    3
Query Match:            20.58%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-15 (1-549) x HEE344189 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGTTTTGCATACATGGCTCACCCGTAAATTCTTACACTAATACACCCTACACCGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
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Db         61 GCCCTCGGGCTGTTGGATTTTGCCCTTGAACTTGAGTTCCGCAACCTCACTCCCGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAATACTCGGGTCTCTCGTTACTCCAGCACTGCTCGCCACCGTCTTCGCCGCGGTGCA 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGGACCGCCGAGCTCACCACCACGGCTGCCACCCGCTTTATGAAGGATCTCTATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGACACTCTGCTTGGCGGCCTACCGACAGAATTGATTTCGTCGGCT 348

RESULT 431
HEE344190
LOCUS       HEE344190                348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 1,
            isolate 219.
ACCESSION   AJ344190
VERSION     AJ344190.1  GI:15282405
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
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                     /virion
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                     /isolate="219"
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     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
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                     /db_xref="GI:15282406"
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                     /db_xref="UniProt/TrEMBL:Q91EB1"
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              266             Length:        348
Score:                  113.00          Matches:       113
Percent Similarity:     97.41%          Conservative:  0
Best Local Similarity:  97.41%          Mismatches:    3
Query Match:            20.58%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-15 (1-549) x HEE344190 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||  ||||||||||||||||  ||||||||||||||||||||||||||||||||
Db          1 GTCATGTTCTGCATACATGGCTCACCCGTAAATTCTTACACTAATACACCCTACACCGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGGCTGTTGGATTTTGCCCTTGAACTTGAGTTCCGCAACCTCACTCCCGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAATACTCGGGTCTCTCGTTACTCCAGCACTGCTCGCCACCGTCTTCGCCGCGGTGCA 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGGACCGCCGAGCTCACCACCACGGCTGCCACCCGCTTTATGAAGGATCTCTATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
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Db        241 GCTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGACACTCTGCTTGGCGGCCTACCGACAGAATTAATTTCGTCGGCT 348

RESULT 432
HEE344174
LOCUS       HEE344174                348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 1,
            isolate 218.
ACCESSION   AJ344174
VERSION     AJ344174.1  GI:15282373
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
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                     /db_xref="GOA:Q91EC7"
                     /db_xref="UniProt/TrEMBL:Q91EC7"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              269           Length:         348
Score:                  112.00        Matches:        112
Percent Similarity:     96.55%        Conservative:   0
Best Local Similarity:  96.55%        Mismatches:     4
Query Match:            20.40%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x HEE344174 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGTTTTGCATACATGGCTCACCCGTAAATTCTTACACTAATACACCCTACACCGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
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Db         61 GCCCTCGGGCTGTTGGATTTTGCCCTTGAACTTGAGTTCCGCAACCTCACTCCCGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAATACTCGGGTCTCTCGTTACTCCAGCACTGCTCGCCACCGTCTTCGCCGCGGTGCA 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db        181 GATGGGACCGCCGAGCTCACCACCACGGCTGCCACCCGCTTTATGGAGGATCTCTATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGACACTCTGCTTGGCGGCCTACCGACAGAATTGATTTCGTCGGCT 348

RESULT 433
HEE344178
LOCUS       HEE344178               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 1,
            isolate 170.
ACCESSION   AJ344178
VERSION     AJ344178.1  GI:15282381
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
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                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
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                     /protein_id="CAC51497.1"
                     /db_xref="GI:15282382"
                     /db_xref="GOA:Q91EC3"
                     /db_xref="UniProt/TrEMBL:Q91EC3"
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              269           Length:         348
Score:                  112.00        Matches:        112
Percent Similarity:     96.55%        Conservative:   0
Best Local Similarity:  96.55%        Mismatches:     4
Query Match:            20.40%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x HEE344178 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGTTTTGCATACATGGCTCACCCGTAAATTCTTACACTAATACACCCTACACCGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
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Db         61 GCCCTCGGGCTGTTGGATTTTGCCCTTGAACTTGAGTTCCGCAACCTCACTCCCGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAATACTCGGGTCTCTCGTTACTCCAGCACTGCTCGCCACCGTCTTCGCCGCGGTGCA 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGGACCGCCGAGCCCACCACCACGGCTGCCACCCGCTTTATGAAGGATCTCTATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGACACTCTGCTTGGCGGCCTACCGACAGAATTAATTTCGTCGGCT 348

RESULT 434
HEE344187
LOCUS       HEE344187               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 1,
            isolate 290.
ACCESSION   AJ344187
VERSION     AJ344187.1  GI:15282399
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
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REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:12461"
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Alignment Scores:
Pred. No.:                269             Length:         348
Score:                    112.00          Matches:        112
Percent Similarity:       96.55%          Conservative:   0
Best Local Similarity:    96.55%          Mismatches:     4
Query Match:              20.40%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x HEE344187 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGTTTTGCATACATGGCTCACCCGTAAATTCTTACACTAATACACCCTACACCGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGGCTGTTGGATTTTGCCCTTGAACTTGAGTTCCGCAACCTCACTCCCGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAATACTCGGGTCTCTCGTTACTCCAGCACTGCTCGCCACCGTCTTCGCCGCGGTGCA 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGGACCGCCGAGCTCACCACCACGGCTGCCACCCGCTTTATGAAGGATCTCTATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        241 GCTAGTACTAATGGTGTCGATGAGATCGGCCGCGGGATAGCCCTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGACACTCTGCTTGGCGGCCTACCGACAGAATTAATTTCGTCGGCT 348

RESULT 435
AY621097
LOCUS       AY621097                348 bp    RNA     linear   VRL 27-JUN-2004
DEFINITION  Swine hepatitis E virus isolate swCH116 capsid protein gene,
            partial cds.
ACCESSION   AY621097
VERSION     AY621097.1  GI:49036116
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="swCH116"
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                     /db_xref="taxon:63421"
     CDS             <1. .>348
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:                276             Length:         348
Score:                    110.00          Matches:        110
Percent Similarity:       94.83%          Conservative:   0
Best Local Similarity:    94.83%          Mismatches:     6
Query Match:              20.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AY621097 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGCTTTGCATACATGGCTCACCTGTGAATTCTTACACTAATACACCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCCTACTTGATTTCGCACTTGAGCTTGAGTTCCGTAACTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||||||
Db        121 ACTAATACGCGTGTTTCTCGTTACTCGAGTAGCGCGCGACACAAATTGCGCCGAGGGGCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGTACTGCTGAGCTTACTACCACTGCTGCCACACGTTTTATGAAAGACCTTCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        241 ACGGGAACTAATGGTGTTGGCGAGGTCGGTCGTGGTATAGCGTTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGACACGCTTCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348

RESULT 436
AY621100
LOCUS       AY621100                348 bp    RNA     linear   VRL 27-JUN-2004
DEFINITION  Swine hepatitis E virus isolate swCH110 capsid protein gene,
            partial cds.
ACCESSION   AY621100
VERSION     AY621100.1  GI:49036122
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
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```
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="swCH110"
                     /isolation_source="pig feces"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT48734.1"
                     /db_xref="GI:49036123"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:                276             Length:         348
Score:                    110.00          Matches:        110
Percent Similarity:       94.83%          Conservative:   0
Best Local Similarity:    94.83%          Mismatches:     6
Query Match:              20.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AY621100 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db          1 GTTATGCTTTGCATACATGGCTCACCTGTGAATTCTTACACTAATACACCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCCTACTTGATTTCGCACTTGAGCTTGAGTTCCGTAATTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||  |||||||||  ||||||||||||||||
Db        121 ACTAATACGCGTGTTTCTCGTTACTCGAGTAGCGCGCGACACAAATTGCGCCGAGGGGCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGTACTGCTGAGCTTACTACCACTGCTGCCACACGTTTTATGAAAGACCTTCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        241 ACGGGAACTAATGGTGTTGGCGAGGTCGGTCGTGGTATAGCGTTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCCGACACGCTTCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 437
HEE344171
LOCUS       HEE344171               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 87.
ACCESSION   AJ344171
VERSION     AJ344171.1  GI:15282367
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="mRNA"
                     /isolate="87"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51490.1"
                     /db_xref="GI:15282368"
                     /db_xref="GOA:Q91ED0"
                     /db_xref="UniProt/TrEMBL:Q91ED0"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:                276             Length:         348
Score:                    110.00          Matches:        110
Percent Similarity:       94.83%          Conservative:   0
Best Local Similarity:    94.83%          Mismatches:     6
Query Match:              20.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x HEE344171 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db          1 GTCATGCTTTGCATACATGGCTCACCTGTGAACTCCTATACCAATACACCTTATACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTTGGCCTGCTCGATTTTGCGCTTGAGCTTGAGTTTCGTAATTTGACACCCGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||  |||||||||  ||||||||||||||||
Db        121 ACAAACACGCGCGTTTCTCGTTATTCGAGCAGTGCGCGCCACAAACTGCGCCGGGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GACGGCACTGCTGAGCTAACTACTACTGCTGCCACACGGTTTATGAAGGATCTTCATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        241 ACAGGGACTAATGGTGTTGGTGAGGTCGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGACACACTTCTCGGCGGGCTTCCGACAGAATTGATTTCGTCGGCT 348

RESULT 438
AF172999
LOCUS       AF172999                359 bp    RNA     linear   VRL 14-APR-2000
DEFINITION  Hepatitis E virus isolate Nig1 capsid protein gene, partial cds.
ACCESSION   AF172999
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VERSION     AF172999.1  GI:5764617
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Identification of a novel hepatitis E virus in Nigeria
  JOURNAL   J. Gen. Virol. 81 (Pt 4), 903-909 (2000)
  MEDLINE   20191950
   PUBMED   10725415
REFERENCE   2  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUL-1999) Biology, Hopital Val-de-Grace, 74,
            boulevard de Port Royal, Paris 75005, France
FEATURES             Location/Qualifiers
     source          1. .359
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="Nig1"
                     /db_xref="taxon:12461"
                     /country="Nigeria: Port-Harcourt"
                     /note="strain isolated from a patient with acute
                     hepatitis"
     CDS             <1. .>359
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAD51341.1"
                     /db_xref="GI:5764618"
                     /translation="VTLDGRPLPTIEQYSKSFFVLPLRGKLSFWEAGTTKAGYPYNYN
                     TTASDQILIENAAGHRVAISTYTTSLGAGPVAISAAAVLAPRSALALLEDTLDYPARA
                     HTFDDFCPECRALGLQG"

Alignment Scores:
Pred. No.:              277           Length:         359
Score:                  110.00        Matches:        110
Percent Similarity:     92.44%        Conservative:   0
Best Local Similarity:  92.44%        Mismatches:     9
Query Match:            20.04%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF172999 (1-359)

Qy        408 ValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheVal 427
              ||||||||||||||||||||||||    ||||||   ||||||||||   |||||||||
Db          1 GTTACTCTTGACGGGCGGCCCCTCCCTACTATTGAGCAGTACTCCAAGTCATTCTTTGTG 60

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGCCCCTTCGCGGTAAGCTCTCTTTTTGGGAGGCTGGTACAACGAAAGCGGGCTACCCT 120

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||   |||   ||||||||||||||||||||
Db        121 TATAATTACAACACCACAGCTAGCGACCAGATTTTGATTGAGAATGCAGCCGGCCACCGA 180

Qy        468 ValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaVal 487
              |||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        181 GTTGCTATTTCGACCTATACCACCAGCCTTGGGGCTGGCCCGGTCGCAATCTCTGCGGCC 240

Qy        488 AlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAla 507
              ||||||||||||||   |||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGTCTTAGCCCCCCGTTCGGCCTTGGCCCTTCTTGAGGATACCCTTGATTACCCGGCG 300

Qy        508 ArgAlaHisThrPheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGly 526
              ||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        301 CGGGCCCATACGTTTGATGATTTTTGCCCTGAGTGCCGTGCCCTGGGTCTCCAGGGT 357
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RESULT 439
AF173000
LOCUS       AF173000                359 bp    RNA     linear   VRL 14-APR-2000
DEFINITION  Hepatitis E virus isolate Nig4 capsid protein gene, partial cds.
ACCESSION   AF173000
VERSION     AF173000.1  GI:5764619
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Identification of a novel hepatitis E virus in Nigeria
  JOURNAL   J. Gen. Virol. 81 (Pt 4), 903-909 (2000)
  MEDLINE   20191950
   PUBMED   10725415
REFERENCE   2  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUL-1999) Biology, Hopital Val-de-Grace, 74,
            boulevard de Port Royal, Paris 75005, France
FEATURES             Location/Qualifiers
     source          1. .359
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="Nig4"
                     /db_xref="taxon:12461"
                     /country="Nigeria: Port-Harcourt"
                     /note="strain isolated from a patient with acute
                     hepatitis"
     CDS             <1. .>359
                     /codon_start=1
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                     /protein_id="AAD51342.1"
                     /db_xref="GI:5764620"
                     /translation="VTLDGRPLPTIEQYSKSFFVLPLRGKLSFWEAGTTKAGYPYNYN
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                     HTFDDFCPECRALGLQG"

Alignment Scores:
Pred. No.:              277           Length:         359
Score:                  110.00        Matches:        110
Percent Similarity:     92.44%        Conservative:   0
Best Local Similarity:  92.44%        Mismatches:     9
Query Match:            20.04%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF173000 (1-359)

Qy        408 ValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheVal 427
              ||||||||||||||||||||||||    ||||||   ||||||||||   |||||||||
Db          1 GTTACTCTTGACGGGCGGCCCCTCCCTACTATTGAGCAGTACTCCAAGTCATTCTTTGTG 60

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGCCCCTTCGCGGTAAGCTCTCTTTTTGGGAGGCTGGTACAACGAAAGCGGGCTACCCT 120

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||   |||   ||||||||||||||||||||
Db        121 TATAATTACAACACCACAGCTAGCGACCAGATTTTGATTGAGAATGCAGCCGGCCACCGA 180

Qy        468 ValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaVal 487
              |||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        181 GTTGCTATTTCGACCTATACCACCAGCCTTGGGGCTGGCCCGGTCGCAATCTCTGCGGCC 240

Qy        488 AlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAla 507
              ||||||||||||||   |||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGTCTTAGCCCCCCGTTCGGCCTTGGCCCTTCTTGAGGATACCCTTGATTACCCGGCG 300
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Qy        508 ArgAlaHisThrPheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGly 526
              ||||||||||||||||||||||||||||||||||||||    ||||||||||||||||
Db        301 CGGGCCCATACGTTTGATGATTTTTGCCCTGAGTGCCGTGCCCTGGGTCTCCAGGGT 357

RESULT 440
AF173001
LOCUS       AF173001                 359 bp    RNA     linear   VRL 14-APR-2000
DEFINITION  Hepatitis E virus isolate Nig5 capsid protein gene, partial cds.
ACCESSION   AF173001
VERSION     AF173001.1  GI:5764621
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Identification of a novel hepatitis E virus in Nigeria
  JOURNAL   J. Gen. Virol. 81 (Pt 4), 903-909 (2000)
  MEDLINE   20191950
   PUBMED   10725415
REFERENCE   2  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUL-1999) Biology, Hopital Val-de-Grace, 74,
            boulevard de Port Royal, Paris 75005, France
FEATURES             Location/Qualifiers
     source          1. .359
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="Nig5"
                     /db_xref="taxon:12461"
                     /country="Nigeria: Port-Harcourt"
                     /note="strain isolated from a patient with acute
                     hepatitis"
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Alignment Scores:
Pred. No.:                277             Length:          359
Score:                    110.00          Matches:         110
Percent Similarity:       92.44%          Conservative:    0
Best Local Similarity:    92.44%          Mismatches:      9
Query Match:              20.04%          Indels:          0
DB:                       1               Gaps:            0

US-09-769-066-15 (1-549) x AF173001 (1-359)

Qy        408 ValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheVal 427
              |||||||||||||||||||||||    ||||||   ||||||||||||   |||||||||
Db          1 GTTACTCTTGACGGGCGGCCCCTCCCTACTATTGAGCAGTACTCCAAGTCATTCTTTGTG 60

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGCCCCTTCGCGGTAAGCTCTCTTTTTGGGAGGCTGGTACAACGAAAGCGGGCTACCCT 120

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||||||   |||   ||||||||||||||||||||
Db        121 TATAATTACAACACCACAGCTAGCGACCAGATTTTGATTGAGAATGCAGCCGGCCACCGA 180

Qy        468 ValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaVal 487
              |||||||||||||||||||||||||||||||||||||||||||||||   |||||||||

Db        181 GTTGCTATTTCGACCTATACCACCAGCCTTGGGGCTGGCCCGGTCGCAATCTCTGCGGCC 240

Qy        488 AlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAla 507
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGTCTTAGCCCCCCGTTCGGCCTTGGCCCTTCTTGAGGATACCCTTGATTACCCGGCG 300

Qy        508 ArgAlaHisThrPheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGly 526
              ||||||||||||||||||||||||||||||||||||||    ||||||||||||||||
Db        301 CGGGCCCATACGTTTGATGATTTTTGCCCTGAGTGCCGTGCCCTGGGTCTCCAGGGT 357

RESULT 441
AF173230
LOCUS       AF173230                 359 bp    RNA     linear   VRL 14-APR-2000
DEFINITION  Hepatitis E virus strain Nig6 capsid protein gene, partial cds.
ACCESSION   AF173230
VERSION     AF173230.1  GI:5764637
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Identification of a novel hepatitis E virus in Nigeria
  JOURNAL   J. Gen. Virol. 81 (Pt 4), 903-909 (2000)
  MEDLINE   20191950
   PUBMED   10725415
REFERENCE   2  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUL-1999) Biology, Hopital Val-de-Grace, 74,
            Boulevard de Port Royal, Paris 75005, France
FEATURES             Location/Qualifiers
     source          1. .359
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="Nig6"
                     /db_xref="taxon:12461"
                     /country="Nigeria: Port-Harcourt"
                     /note="isolated from a patient with acute hepatitis"
     CDS             <1. .>359
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAD51353.1"
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                     HTFDDFCPECRALGLQG"

Alignment Scores:
Pred. No.:                277             Length:          359
Score:                    110.00          Matches:         110
Percent Similarity:       92.44%          Conservative:    0
Best Local Similarity:    92.44%          Mismatches:      9
Query Match:              20.04%          Indels:          0
DB:                       1               Gaps:            0

US-09-769-066-15 (1-549) x AF173230 (1-359)

Qy        408 ValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheVal 427
              |||||||||||||||||||||||    ||||||   ||||||||||||   |||||||||
Db          1 GTTACTCTTGACGGGCGGCCCCTCCCTACTATTGAGCAGTACTCCAAGTCATTCTTTGTG 60

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGCCCCTTCGCGGTAAGCTCTCTTTTTGGGAGGCTGGTACAACGAAAGCGGGCTACCCT 120

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArg 467
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                ||||||||||||||||||||||||||||||   |||   ||||||||||||||||||||
Db        121 TATAATTACAACACCACAGCTAGCGACCAGATTTTGATTGAGAATGCAGCCGGCCACCGA 180

Qy        468 ValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaVal 487
                ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        181 GTTGCTATTTCGACCTATACCACCAGCCTTGGGGCTGGCCCGGTCGCAATCTCTGCGGCC 240

Qy        488 AlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAla 507
                |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGTCTTAGCCCCCCGTTCGGCCTTGGCCCTTCTTGAGGATACCCTTGATTACCCGGCG 300

Qy        508 ArgAlaHisThrPheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGly 526
                ||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        301 CGGGCCCATACGTTTGATGATTTTTGCCCTGAGTGCCGTGCCCTGGGTCTCCAGGGT 357

RESULT 442
AF173231
LOCUS       AF173231                359 bp    RNA     linear   VRL 14-APR-2000
DEFINITION  Hepatitis E virus strain Nig7 capsid protein gene, partial cds.
ACCESSION   AF173231
VERSION     AF173231.1  GI:5764639
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Identification of a novel hepatitis E virus in Nigeria
  JOURNAL   J. Gen. Virol. 81 (Pt 4), 903-909 (2000)
  MEDLINE   20191950
   PUBMED   10725415
REFERENCE   2  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUL-1999) Biology, Hopital Val-de-Grace, 74,
            Boulevard de Port Royal, Paris 75005, France
FEATURES             Location/Qualifiers
     source          1. .359
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="Nig7"
                     /db_xref="taxon:12461"
                     /country="Nigeria: Port-Harcourt"
                     /note="isolated from a patient with acute hepatitis"
     CDS             <1. .>359
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAD51354.1"
                     /db_xref="GI:5764640"
                     /translation="VTLDGRPLPTIEQYSKSFFVLPLRGKLSFWEAGTTKAGYPYNYN
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Alignment Scores:
Pred. No.:              277             Length:         359
Score:                  110.00          Matches:        110
Percent Similarity:     92.44%          Conservative:   0
Best Local Similarity:  92.44%          Mismatches:     9
Query Match:            20.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF173231 (1-359)

Qy        408 ValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheVal 427
                ||||||||||||||||||||||   ||||||   ||||||||||||   |||||||||
Db          1 GTTACTCTTGACGGGCGGCCCCTCCCTACTATTGAGCAGTACTCCAAGTCATTCTTTGTG 60

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGCCCCTTCGCGGTAAGCTCTCTTTTTGGGAGGCTGGTACAACGAAAGCGGGCTACCCT 120

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArg 467
                ||||||||||||||||||||||||||||||   |||   ||||||||||||||||||||
Db        121 TATAATTACAACACCACAGCTAGCGACCAGATTTTGATTGAGAATGCAGCCGGCCACCGA 180

Qy        468 ValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaVal 487
                ||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        181 GTTGCTATTTCGACCTATACCACCAGCCTTGGGGCTGGCCCGGTCGCAATCTCTGCGGCC 240

Qy        488 AlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAla 507
                |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGTCTTAGCCCCCCGTTCGGCCTTGGCCCTTCTTGAGGATACCCTTGATTACCCGGCG 300

Qy        508 ArgAlaHisThrPheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGly 526
                ||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        301 CGGGCCCATACGTTTGATGATTTTTGCCCTGAGTGCCGTGCCCTGGGTCTCCAGGGT 357

RESULT 443
AF173232
LOCUS       AF173232                359 bp    RNA     linear   VRL 14-APR-2000
DEFINITION  Hepatitis E virus strain Nig9 capsid protein gene, partial cds.
ACCESSION   AF173232
VERSION     AF173232.1  GI:5764641
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Identification of a novel hepatitis E virus in Nigeria
  JOURNAL   J. Gen. Virol. 81 (Pt 4), 903-909 (2000)
  MEDLINE   20191950
   PUBMED   10725415
REFERENCE   2  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUL-1999) Biology, Hopital Val-de-Grace, 74,
            Boulevard de Port Royal, Paris 75005, France
FEATURES             Location/Qualifiers
     source          1. .359
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="Nig9"
                     /db_xref="taxon:12461"
                     /country="Nigeria: Port-Harcourt"
                     /note="isolated from a patient with acute hepatitis"
     CDS             <1. .>359
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAD51355.1"
                     /db_xref="GI:5764642"
                     /translation="VTLDGRPLPTIEQYSKSFFVLPLRGKLSFWEAGTTKAGYPYNYN
                     TTASDQILIENAAGHRVAISTYTTSLGAGPVAISAAAVLAPRSALALLEDTLDYPARA
                     HTFDDFCPECRALGLQG"

Alignment Scores:
Pred. No.:              277             Length:         359
Score:                  110.00          Matches:        110
Percent Similarity:     92.44%          Conservative:   0
Best Local Similarity:  92.44%          Mismatches:     9
Query Match:            20.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF173232 (1-359)
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Qy        408 ValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheVal 427
              ||||||||||||||||||||||   ||||||  ||||||||||||  |||||||||
Db          1 GTTACTCTTGACGGGCGGCCCCTCCCTACTATTGAGCAGTATTCCAAGTCATTCTTTGTG 60

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGCCCCTTCGCGGTAAGCTCTCTTTTTGGGAGGCTGGTACAACGAAAGCGGGCTACCCT 120

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||||||   |||   ||||||||||||||||||||
Db        121 TATAATTACAACACCACAGCTAGCGATCAGATTTTGATCGAGAATGCAGCCGGCCACCGA 180

Qy        468 ValAlaIleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaVal 487
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTTGCTATTTCGACCTATACCACCAGTCTTGGGGCTGGCCCGGTCGCAATCTCTGCGGCC 240

Qy        488 AlaValLeuAlaProHisSerAlaLeuAlaLeuLeuGluAspThrLeuAspTyrProAla 507
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        241 GCGGTCTTAGCCCCCCGTTCGGCCTTGGCCCTTCTTGAGGATACGCTTGATTACCCGGCG 300

Qy        508 ArgAlaHisThrPheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGly 526
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        301 CGGGCCCATACATTTGATGATTTTTGCCCTGAGTGCCGTGCCCTGGGTCTCCAGGGT 357

RESULT 444
AF117275
LOCUS       AF117275                 346 bp    mRNA    linear   VRL 12-SEP-2000
DEFINITION  Hepatitis E virus strain TW8E-2 nucleocapsid protein mRNA, partial
            cds.
ACCESSION   AF117275
VERSION     AF117275.1  GI:10086226
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 346)
  AUTHORS   Wu,J.C., Chen,C.M., Chiang,T.Y., Sheen,I.J., Chen,J.Y., Tsai,W.H.,
            Huang,Y.H. and Lee,S.D.
  TITLE     Clinical and epidemiological implications of swine hepatitis E
            virus infection
  JOURNAL   J. Med. Virol. 60 (2), 166-171 (2000)
  MEDLINE   20062925
   PUBMED   10596016
REFERENCE   2  (bases 1 to 346)
  AUTHORS   Wu,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-DEC-1998) Division of Gastroenterology, Department of
            Medicine, Graduate Institute of Clinical Medicine, Veterans General
            Hospital-Taipei, National Yang-Ming University School of Medicine,
            Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .346
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="TW8E-2"
                     /db_xref="taxon:12461"
                     /country="Taiwan"
                     /note="isolated from a patient with acute hepatitis"
     CDS             <1. .>346
                     /note="ORF2"
                     /codon_start=1
                     /product="nucleocapsid protein"
                     /protein_id="AAG12448.1"
                     /db_xref="GI:10086227"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISS"

Alignment Scores:
Pred. No.:              280          Length:        346
Score:                  109.00       Matches:       109
Percent Similarity:     94.78%       Conservative:  0
Best Local Similarity:  94.78%       Mismatches:    6
Query Match:            19.85%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AF117275 (1-346)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db          1 GTTATGCTTTGCATACATGGCTCACCTGTGAACTCCTATACCAATACACCTTATACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTCTCGGCCTGCTCGACTTCGCGCTTGAGCTTGAGTTTCGTAATTTGACACCTGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||   |||||||||   ||||||||||||||
Db        121 ACAAACACGCGCGTTTCTCGTTATTCGAGCAGTGCACGCCACAAATTGCGCCGAGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GACGGCACCGCTGAGCTAACTACTACTGCTGCTACACGGTTTATGAAGGATCTTCATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        241 ACAGGGACTAATGGTGTTGGTGAGGTTGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSer 279
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACACTTCTCGGCGGGCTCCCGACAGAATTGATTTCGTCG 345

RESULT 445
AF117278
LOCUS       AF117278                 346 bp    mRNA    linear   VRL 12-SEP-2000
DEFINITION  Hepatitis E virus strain TW6196E nucleocapsid protein mRNA, partial
            cds.
ACCESSION   AF117278
VERSION     AF117278.1  GI:10086232
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 346)
  AUTHORS   Wu,J.C., Chen,C.M., Chiang,T.Y., Sheen,I.J., Chen,J.Y., Tsai,W.H.,
            Huang,Y.H. and Lee,S.D.
  TITLE     Clinical and epidemiological implications of swine hepatitis E
            virus infection
  JOURNAL   J. Med. Virol. 60 (2), 166-171 (2000)
  MEDLINE   20062925
   PUBMED   10596016
REFERENCE   2  (bases 1 to 346)
  AUTHORS   Wu,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-DEC-1998) Division of Gastroenterology, Department of
            Medicine, Graduate Institute of Clinical Medicine, Veterans General
            Hospital-Taipei, National Yang-Ming University School of Medicine,
            Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .346
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="TW6196E"
                     /db_xref="taxon:12461"
                     /country="Taiwan"
                     /note="isolated from a patient with acute hepatitis"
     CDS             <1. .>346
                     /codon_start=1
                     /product="nucleocapsid protein"
                     /protein_id="AAG12451.1"
                     /db_xref="GI:10086233"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                    TLLGGLPTELISS"

Alignment Scores:
Pred. No.:              280           Length:         346
Score:                  109.00        Matches:        109
Percent Similarity:     94.78%        Conservative:   0
Best Local Similarity:  94.78%        Mismatches:     6
Query Match:            19.85%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF117278 (1-346)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db          1 GTTATGCTTTGCATACATGGCTCACCTGTGAACTCCTATACCAATACACCTTATACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTCTCGGCCTGCTCGACTTCGCGCTTGAGCTTGAGTTTCGTAATTTGACACCTGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||||
Db        121 ACAAACACGCGCGTTTCTCGTTATTCGAGCAGTGCACGCCACAAATTGCGCCGAGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GACGGCACCGCTGAGCTAACTACTACTGCTGCTACACGGTTTATGAAGGATCTTCATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        241 ACAGGGACTAATGGTGTTGGTGAGGTTGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSer 279
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACACTTCTCGGCGGGCTCCCGACAGAATTGATTTCGTCG 345

RESULT 446
AF117279
LOCUS       AF117279                346 bp    mRNA    linear   VRL 12-SEP-2000
DEFINITION  Hepatitis E virus strain TW6310E nucleocapsid protein mRNA, partial
            cds.
ACCESSION   AF117279
VERSION     AF117279.1  GI:10086234
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 346)
  AUTHORS   Wu,J.C., Chen,C.M., Chiang,T.Y., Sheen,I.J., Chen,J.Y., Tsai,W.H.,
            Huang,Y.H. and Lee,S.D.
  TITLE     Clinical and epidemiological implications of swine hepatitis E
            virus infection
  JOURNAL   J. Med. Virol. 60 (2), 166-171 (2000)
  MEDLINE   20062925
   PUBMED   10596016
REFERENCE   2  (bases 1 to 346)
  AUTHORS   Wu,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-DEC-1998) Division of Gastroenterology, Department of
            Medicine, Graduate Institute of Clinical Medicine, Veterans General
            Hospital-Taipei, National Yang-Ming University School of Medicine,
            Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .346
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="TW6310E"
                     /db_xref="taxon:12461"
                     /country="Taiwan"
                     /note="isolated from a patient with acute hepatitis"
     CDS             <1. .>346
                     /note="ORF2"
                     /codon_start=1
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                     /protein_id="AAG12452.1"
                     /db_xref="GI:10086235"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                     TLLGGLPTELISS"

Alignment Scores:
Pred. No.:              280           Length:         346
Score:                  109.00        Matches:        109
Percent Similarity:     94.78%        Conservative:   0
Best Local Similarity:  94.78%        Mismatches:     6
Query Match:            19.85%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF117279 (1-346)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTTATGCTTTGCATACATGGCTCACCTGTGAACTCCTACACTAATACACCTTACACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTCTTGGCCTGCTCGATTTTGCGCTTGAGCTTGAGTTTCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||||
Db        121 ACAAACACGCGCGTCTCTCGTTATTCGAGCAGTGCGCGCCATAAACTGCGCCGAGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GACGGTACTGCTGAATTGACTACTACTGCTGCTACACGATTTATGAAGGATCTTCATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        241 ACAGGGACTAATGGCGTAGGTGAGGTTGGTCGCGGGATAGCGCTTACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSer 279
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACACTTCTCGGCGGTCTCCCGACAGAATTGATTTCGTCG 345

RESULT 447
AY596309
LOCUS       AY596309                348 bp    RNA     linear   VRL 09-MAY-2004
DEFINITION  Swine hepatitis E virus strain swCH70 capsid protein gene, partial
            cds.
ACCESSION   AY596309
VERSION     AY596309.1  GI:46981703
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-APR-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="swCH70"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
                     /note="ORF2"
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                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT07938.1"
                     /db_xref="GI:46981704"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:                280             Length:         348
Score:                    109.00          Matches:        109
Percent Similarity:       93.97%          Conservative:   0
Best Local Similarity:    93.97%          Mismatches:     7
Query Match:              19.85%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AY596309 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 GTTATGCTCTGCATACATGGCTCGCCTGTGAACTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGCAGCGCACGTCATAAATTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGTACTGCAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGTTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348

RESULT 448
AY596315
LOCUS       AY596315                348 bp    RNA     linear   VRL 09-MAY-2004
DEFINITION  Swine hepatitis E virus strain swCH24 capsid protein gene, partial
            cds.
ACCESSION   AY596315
VERSION     AY596315.1  GI:46981715
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-APR-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="swCH24"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT07944.1"
                     /db_xref="GI:46981716"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:                280             Length:         348
Score:                    109.00          Matches:        109
Percent Similarity:       93.97%          Conservative:   0
Best Local Similarity:    93.97%          Mismatches:     7
Query Match:              19.85%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AY596315 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 GTCATGCTCTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACTAATACGCGCGTTTCTCGCTATTCGAGTAGCGCACGTCATAAACTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGTACTGCAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGCTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348

RESULT 449
AY621098
LOCUS       AY621098                348 bp    RNA     linear   VRL 27-JUN-2004
DEFINITION  Swine hepatitis E virus isolate swCH112 capsid protein gene,
            partial cds.
ACCESSION   AY621098
VERSION     AY621098.1  GI:49036118
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="swCH112"
                     /isolation_source="pig feces"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
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                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT48732.1"
                     /db_xref="GI:49036119"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              280           Length:         348
Score:                  109.00        Matches:        109
Percent Similarity:     93.97%        Conservative:   0
Best Local Similarity:  93.97%        Mismatches:     7
Query Match:            19.85%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AY621098 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 GTCATGTTTTGCATACATGGCTCACCTGTGAATTCTTACACTAATACACCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCCTACTTGATTTCGCACTTGAGCTTGAGTTCCGTAATTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||||
Db        121 ACTAATACGCGTGTTTCTCGTTACTCGAGTAGCGCGCGACACAAATTGCGCCGAGGGGCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGTACTGCTGAGCTTACTACCACTGCTGCCACACGTTTTATGAAAGACCTTCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        241 ACGGGAACTAATGGTGTTGGCGAGGTCGGTCGTGGTATAGCGTTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCCGACACGCTTCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 450
AY621099
LOCUS       AY621099                348 bp    RNA     linear   VRL 27-JUN-2004
DEFINITION  Swine hepatitis E virus isolate swCH111 capsid protein gene,
            partial cds.
ACCESSION   AY621099
VERSION     AY621099.1  GI:49036120
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="swCH111"
                     /isolation_source="pig feces"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT48733.1"
                     /db_xref="GI:49036121"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              280           Length:         348
Score:                  109.00        Matches:        109
Percent Similarity:     93.97%        Conservative:   0
Best Local Similarity:  93.97%        Mismatches:     7
Query Match:            19.85%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AY621099 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 GTCATGTTTTGCATACATGGCTCACCTGTGAATTCTTACACTAATACACCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCCTACTTGATTTCGCACTTGAGCTTGAGTTCCGTAATTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||||
Db        121 ACTAATACGCGTGTTTCTCGTTACTCGAGTAGCGCGCGACACAAATTGCGCCGAGGGGCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGTACTGCTGAGCTTACTACCACTGCTGCCACACGTTTTATGAAAGACCTTCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        241 ACGGGAACTAATGGTGTTGGCGAGGTCGGTCGTGGTATAGCGTTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCCGACACGCTTCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 451
HEE344172
LOCUS       HEE344172               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 292.
ACCESSION   AJ344172
VERSION     AJ344172.1  GI:15282369
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
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                     /organism="Hepatitis E virus"
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                     /mol_type="mRNA"
                     /isolate="292"
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     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51491.1"
                     /db_xref="GI:15282370"
                     /db_xref="GOA:Q91EC9"
                     /db_xref="UniProt/TrEMBL:Q91EC9"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAN
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:                280             Length:         348
Score:                    109.00          Matches:        109
Percent Similarity:       93.97%          Conservative:   0
Best Local Similarity:    93.97%          Mismatches:     7
Query Match:              19.85%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x HEE344172 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db          1 GTTATGCTTTGCATACATGGCTCACCTGTGAACTCCTATACCAATACACCTTATACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTTGGCCTGCTCGATTTTGCGCTTGAGCTTGAGTTTCGTAATTTGACACCCGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||  |||||||||  ||||||||||||||||
Db        121 ACAAACACGCGCGTTTCTCGTTATTCGAGCAGTGCGCGCCACAAACTGCGCCGGGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GACGGCACTGCTGAGCTAACTACTACTGCTGCCACACGGTTTATGAAGGATCTTCATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||  ||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        241 ACAGGGACTAATGGTGTTGGTGAGGTCGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||  ||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTAACACACTTCTCGGCGGGCTTCCGACAGAATTGATTTCGTCGGCT 348

RESULT 452
HEE344179
LOCUS       HEE344179               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 241.
ACCESSION   AJ344179
VERSION     AJ344179.1  GI:15282383
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
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                     /virion
                     /mol_type="mRNA"
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                     /db_xref="taxon:12461"
     CDS             <1. .>345
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51498.1"
                     /db_xref="GI:15282384"
                     /db_xref="GOA:Q91EC2"
                     /db_xref="UniProt/TrEMBL:Q91EC2"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                     TLLGGLPTELISS"

Alignment Scores:
Pred. No.:                280             Length:         348
Score:                    109.00          Matches:        109
Percent Similarity:       93.97%          Conservative:   0
Best Local Similarity:    93.97%          Mismatches:     7
Query Match:              19.85%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x HEE344179 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||  ||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db          1 GTCATGTTTTGCATACATGGCTCACCTGTAAACTCCTACACTAATACACCTTACACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTCTTGGCCTGCTCGACTTTGCGCTTGAGCTTGAGTTTCGTAATTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||  |||||||||  ||||||||||||||||
Db        121 ACAAACACGCGCGTCTCTCGCTATTCGAGCAGTGCGCGCCATAAACTGCGCCGAGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GACGGCACTGCTGAGCTAACCACTACTGCTGCCACACGGTTTATGAAAGATCTTCATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||  ||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        241 ACAGGGACCAACGGTGTTGGTGAGGTCGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACACTTCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 453
HEE344180
LOCUS       HEE344180               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 255.
ACCESSION   AJ344180
VERSION     AJ344180.1  GI:15282385
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
```

```
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="mRNA"
                     /isolate="255"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51499.1"
                     /db_xref="GI:15282386"
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                     /db_xref="UniProt/TrEMBL:Q91EC1"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              280             Length:         348
Score:                  109.00          Matches:        109
Percent Similarity:     93.97%          Conservative:   0
Best Local Similarity:  93.97%          Mismatches:     7
Query Match:            19.85%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x HEE344180 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 GTTATGTTTTGCATACATGGCTCACCTGTAAACTCCTACACTAATACACCTTACACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTCTTGGCCTGCTCGACTTTGCGCTTGAGCTTGAGTTTCGTAATTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||||||
Db        121 ACAAACACGCGCGTCTCTCGCTATTCGAGCAGTGCGCGCCATAAACTGCGCCGAGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GACGGCACTGCTGAGCTAACCACTACTGCTGCCACACGGTTTATGAAAGATCTTCATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        241 ACAGGGACCAACGGTGTTGGTGAGGTTGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACACTTCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 454
HEE344183
LOCUS       HEE344183               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 277.
ACCESSION   AJ344183
VERSION     AJ344183.1  GI:15282391
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="mRNA"
                     /isolate="277"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51502.1"
                     /db_xref="GI:15282392"
                     /db_xref="GOA:Q91EB8"
                     /db_xref="UniProt/TrEMBL:Q91EB8"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              280             Length:         348
Score:                  109.00          Matches:        109
Percent Similarity:     93.97%          Conservative:   0
Best Local Similarity:  93.97%          Mismatches:     7
Query Match:            19.85%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x HEE344183 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 GTTATGTTTTGCATACATGGCTCACCTGTGAACTCCTATACCAATACACCTTATACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTTGGCCTGCTCGATTTTGCGCTTGAGCTTGAGTTTCGTAATTTGACACCCGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||||||
Db        121 ACAAACACGCGCGTTTCTCGTTATTCGAGCAGTGCGCGCCACAAACTGCGCCGGGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GACGGCACTGCTGAGCTAACTACTACTGCTGCCACACGGTTTATGAAGGATCTTCATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        241 ACAGGGACTAATGGTGTTGGTGAGGTCGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGACACACTTCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348

RESULT 455
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HEE344184
LOCUS       HEE344184                348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 202.
ACCESSION   AJ344184
VERSION     AJ344184.1  GI:15282393
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="mRNA"
                     /isolate="202"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51503.1"
                     /db_xref="GI:15282394"
                     /db_xref="GOA:Q91EB7"
                     /db_xref="UniProt/TrEMBL:Q91EB7"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              280             Length:         348
Score:                  109.00          Matches:        109
Percent Similarity:     93.97%          Conservative:   0
Best Local Similarity:  93.97%          Mismatches:     7
Query Match:            19.85%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x HEE344184 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db          1 GTTATGCTTTGCATACATGGCTCACCTGTGAATTCCTACACTAATACACCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCTTACTTGATTTTGCACTCGAGCTCGAGTTCCGCAACTTAACACCTGGCAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACTAACACGCGCGTTTCCCGCTATTCGAGTAGCGCGCGTCACAAATTGCGCCGAGGGCCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGCACTGCTGAGTTGACTACTACTGCTGCCACACGCTTTATGAAAGACCTCCATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        241 ACGGGGACCAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACTCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGACACGCTTCTCGGTGGGCTTCCGACAGAATTGATTTCGTCGGCT 348

RESULT 456
HEE344192
LOCUS       HEE344192                348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 210.
ACCESSION   AJ344192
VERSION     AJ344192.1  GI:15282409
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="mRNA"
                     /isolate="210"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51511.1"
                     /db_xref="GI:15282410"
                     /db_xref="GOA:Q91EA9"
                     /db_xref="UniProt/TrEMBL:Q91EA9"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              280             Length:         348
Score:                  109.00          Matches:        109
Percent Similarity:     93.97%          Conservative:   0
Best Local Similarity:  93.97%          Mismatches:     7
Query Match:            19.85%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x HEE344192 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db          1 GTTATGCTTTGCATACATGGCTCACCTGTAAATTCCTATACTAATACACCTTACACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGTTTGCTTGACTTTGCACTCGAACTCGAGTTTCGCAATTTGACACCTGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACGAACACGCGTGTCTCCCGTTATTCGAGTAGCGCGCGTCACAAGTTGCGCCGAGGACCT 180
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Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GACGGTACAGCGGAGCTAACTACTACTGCTGCTACACGTTTTATGAAAGACCTTCATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        241 ACTGGGACTAATGGTGTTGGTGAGGTTGGTCGTGGTATAGCACTGACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGCTTCTTGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 457
HEE344193
LOCUS       HEE344193                348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 266.
ACCESSION   AJ344193
VERSION     AJ344193.1  GI:15282411
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="mRNA"
                     /isolate="266"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51512.1"
                     /db_xref="GI:15282412"
                     /db_xref="GOA:Q91EA8"
                     /db_xref="UniProt/TrEMBL:Q91EA8"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              280           Length:         348
Score:                  109.00        Matches:        109
Percent Similarity:     93.97%        Conservative:   0
Best Local Similarity:  93.97%        Mismatches:     7
Query Match:            19.85%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x HEE344193 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||   ||||||||||||||||||||||||||||||||||
Db          1 GTCATGTTTTGCATACATGGCTCACCTGTAAACTCCTACACTAATACACCTTACACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTCTTGGCCTGCTCGACTTTGCGCTTGAGCTTGAGTTTCGTAATTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||   ||||||||   ||||||||||||||||||
Db        121 ACAAACACGCGCGTCTCTCGCTATTCGAGCAGTGCGCGCCATAAACTGCGCCGAGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GACGGCACTGCTGAGCTAACCACTACTGCTGCCACACGGTTTATGAAAGATCTTCATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        241 ACAGGGACCAACGGTGTTGGTGAGGTCGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACACTTCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 458
HEE344194
LOCUS       HEE344194                348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 287.
ACCESSION   AJ344194
VERSION     AJ344194.1  GI:15282413
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="mRNA"
                     /isolate="287"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51513.1"
                     /db_xref="GI:15282414"
                     /db_xref="GOA:Q91EA7"
                     /db_xref="UniProt/TrEMBL:Q91EA7"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              280           Length:         348
Score:                  109.00        Matches:        109
Percent Similarity:     93.97%        Conservative:   0
Best Local Similarity:  93.97%        Mismatches:     7
Query Match:            19.85%        Indels:         0
DB:                     1             Gaps:           0
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US-09-769-066-15 (1-549) x HEE344194 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGTTTTGCATACATGGCTCACCTGTAAACTCCTACACTAATACACCTTACACTGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTCTTGGCCTGCTCGACTTTGCGCTTGAGCTTGAGTTTCGTAATTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||  |||||||||  ||||||||||||||||
Db        121 ACAAACACGCGCGTCTCTCGCTATTCGAGCAGTGCGCGCCATAAACTGCGCCGAGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        181 GACGGCACTGCTGAGCTAACCACTACTGCTGCCACACGGTTTATGAAAGATCTTCATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||  ||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        241 ACAGGGACCAACGGTGTTGGTGAGGTTGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACACTTCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 459
AF117276
LOCUS       AF117276                346 bp    mRNA    linear   VRL 12-SEP-2000
DEFINITION  Hepatitis E virus strain TW 2494E nucleocapsid protein mRNA,
            partial cds.
ACCESSION   AF117276
VERSION     AF117276.1  GI:10086228
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 346)
  AUTHORS   Wu,J.C., Chen,C.M., Chiang,T.Y., Sheen,I.J., Chen,J.Y., Tsai,W.H.,
            Huang,Y.H. and Lee,S.D.
  TITLE     Clinical and epidemiological implications of swine hepatitis E
            virus infection
  JOURNAL   J. Med. Virol. 60 (2), 166-171 (2000)
  MEDLINE   20062925
   PUBMED   10596016
REFERENCE   2  (bases 1 to 346)
  AUTHORS   Wu,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-DEC-1998) Division of Gastroenterology, Department of
            Medicine, Graduate Institute of Clinical Medicine, Veterans General
            Hospital-Taipei, National Yang-Ming University School of Medicine,
            Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .346
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="TW2494E"
                     /db_xref="taxon:12461"
                     /country="Taiwan"
                     /note="isolated from a patient with acute hepatitis"
     CDS             <1. .>346
                     /note="ORF2"
                     /codon_start=1
                     /product="nucleocapsid protein"
                     /protein_id="AAG12449.1"
                     /db_xref="GI:10086229"
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Alignment Scores:

Pred. No.:                283          Length:          346
Score:                    108.00       Matches:         108
Percent Similarity:       93.91%       Conservative:    0
Best Local Similarity:    93.91%       Mismatches:      7
Query Match:              19.67%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-15 (1-549) x AF117276 (1-346)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db          1 GTTATGCTTTGCATACATGGCTCACCTGTGAACTCCTATACCAATACACCTTATACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTCTCGGCCTGCTCGACTTCGCGCTTGAGCTTGAGTTTCGTAATTTGACACCTGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||  |||||||||  ||||||||||||||||
Db        121 ACAAACACGCGCGTTTCTCGTTATTCGAGCAGTGCACGCCACAAATTGCGCCGAGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGGCACCGCTGAGCTAACTACTACTGCTGCTACACGGTTTATGAAGGATCTTCATTCT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||  ||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        241 ACAGGGACTAATGGTGTTGGTGAGGTTGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSer 279
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACACTTCTCGGCGGGCTCCCGACAGAATTGATTTCGTCG 345

RESULT 460
AF117277
LOCUS       AF117277                346 bp    mRNA    linear   VRL 12-SEP-2000
DEFINITION  Hepatitis E virus strain TW5483E nucleocapsid protein mRNA, partial
            cds.
ACCESSION   AF117277
VERSION     AF117277.1  GI:10086230
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 346)
  AUTHORS   Wu,J.C., Chen,C.M., Chiang,T.Y., Sheen,I.J., Chen,J.Y., Tsai,W.H.,
            Huang,Y.H. and Lee,S.D.
  TITLE     Clinical and epidemiological implications of swine hepatitis E
            virus infection
  JOURNAL   J. Med. Virol. 60 (2), 166-171 (2000)
  MEDLINE   20062925
   PUBMED   10596016
REFERENCE   2  (bases 1 to 346)
  AUTHORS   Wu,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-DEC-1998) Division of Gastroenterology, Department of
            Medicine, Graduate Institute of Clinical Medicine, Veterans General
            Hospital-Taipei, National Yang-Ming University School of Medicine,
            Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .346
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="TW5483E"
                     /db_xref="taxon:12461"
                     /country="Taiwan"
                     /note="isolated from a patient with acute hepatitis"
     CDS             <1. .>346
                     /note="ORF2"
                     /codon_start=1
                     /product="nucleocapsid protein"
                     /protein_id="AAG12450.1"
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/db_xref="GI:10086231"
/translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
TLLGGLPTELISS"

Alignment Scores:

Pred. No.:	283	Length:	346
Score:	108.00	Matches:	108
Percent Similarity:	93.91%	Conservative:	0
Best Local Similarity:	93.91%	Mismatches:	7
Query Match:	19.67%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AF117277 (1-346)

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Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||   |||||||||||||||||||||||||||||||||||
Db          1 GTTATGCTTTGCATACATGGCTCACCTGTAAATTCCTATACTAACACACCCTACACTGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGTCTGCTCGATTTCGCACTCGAGCTCGAGTTTCGTAATTTAACACCTGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACGAACACGCGTGTCTCCCGTTATTCGAGTAGTGCGCGTCATAAGCTACGCCGAGGGCCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGCACAGCAGAACTAACCACCACTGCTGCGACACGTTTTATGAAAGATTTACATTTC 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||   |||||||||||||||||||||||||||||||||
Db        241 ACCGGGACTAATGGTGTTGGTGAGGTTGGTCGTGGTATAGCACTAACCCTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSer 279
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGCTTCTCGGCGGGCTTCCGACAGAATTGATTTCGTCG 345
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RESULT 461
AY596308
LOCUS AY596308 348 bp RNA linear VRL 09-MAY-2004
DEFINITION Swine hepatitis E virus strain swCH72 capsid protein gene, partial cds.
ACCESSION AY596308
VERSION AY596308.1 GI:46981701
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Detection and analysis of partial sequences of swine hepatitis E virus in Xinjiang
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Direct Submission
JOURNAL Submitted (09-APR-2004) College of Animal Medicine, Nanjing Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu 210095, P. R. China
FEATURES Location/Qualifiers
source 1. .348
/organism="Swine hepatitis E virus"
/mol_type="genomic RNA"
/strain="swCH72"
/db_xref="taxon:63421"
CDS <1. .>348
/note="ORF2"
/codon_start=1
/product="capsid protein"
/protein_id="AAT07937.1"

/db_xref="GI:46981702"
/translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
TLLGGLPTELISSA"

Alignment Scores:

Pred. No.:	283	Length:	348
Score:	108.00	Matches:	108
Percent Similarity:	93.10%	Conservative:	0
Best Local Similarity:	93.10%	Mismatches:	8
Query Match:	19.67%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AY596308 (1-348)

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Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||   |||||||||||||||||||||||||||||||||||
Db          1 GTCATGTTCTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGTAGCGCACGTCATAAATTGCGCCGTGGGCCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGTACTGCAGAACTGACTACTACTGCCGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||   |||||||||||||||||||||||||||||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGTTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348
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RESULT 462
AY596311
LOCUS AY596311 348 bp RNA linear VRL 09-MAY-2004
DEFINITION Swine hepatitis E virus strain swCH62 capsid protein gene, partial cds.
ACCESSION AY596311
VERSION AY596311.1 GI:46981707
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Detection and analysis of partial sequences of swine hepatitis E virus in Xinjiang
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Direct Submission
JOURNAL Submitted (09-APR-2004) College of Animal Medicine, Nanjing Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu 210095, P. R. China
FEATURES Location/Qualifiers
source 1. .348
/organism="Swine hepatitis E virus"
/mol_type="genomic RNA"
/strain="swCH62"
/db_xref="taxon:63421"
CDS <1. .>348
/note="ORF2"
/codon_start=1
/product="capsid protein"
/protein_id="AAT07940.1"

/db_xref="GI:46981708"
/translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
TLLGGLPTELISSA"

Alignment Scores:

Pred. No.:	283	Length:	348
Score:	108.00	Matches:	108
Percent Similarity:	93.10%	Conservative:	0
Best Local Similarity:	93.10%	Mismatches:	8
Query Match:	19.67%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AY596311 (1-348)

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Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 GTTATGTTTTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGCAGCGCACGTCATAAATTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGTACTGCAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGATACGTTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348
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RESULT 463
AY596312
LOCUS AY596312 348 bp RNA linear VRL 09-MAY-2004
DEFINITION Swine hepatitis E virus strain swCH57 capsid protein gene, partial cds.
ACCESSION AY596312
VERSION AY596312.1 GI:46981709
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Detection and analysis of partial sequences of swine hepatitis E virus in Xinjiang
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Direct Submission
JOURNAL Submitted (09-APR-2004) College of Animal Medicine, Nanjing Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu 210095, P. R. China
FEATURES Location/Qualifiers
source 1. .348
/organism="Swine hepatitis E virus"
/mol_type="genomic RNA"
/strain="swCH57"
/db_xref="taxon:63421"
CDS <1. .>348
/note="ORF2"
/codon_start=1
/product="capsid protein"
/protein_id="AAT07941.1"

/db_xref="GI:46981710"
/translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
TLLGGLPTELISSA"

Alignment Scores:

Pred. No.:	283	Length:	348
Score:	108.00	Matches:	108
Percent Similarity:	93.10%	Conservative:	0
Best Local Similarity:	93.10%	Mismatches:	8
Query Match:	19.67%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AY596312 (1-348)

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Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 GTCATGTTTTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACTAATACGCGCGTTTCCCGCTATTCGAGTAGCGCACGTCATAAGCTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGTACTGCAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGCTGCTCGGCGGGCTTCCGACAGAATTGATTTCGTCGGCT 348
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RESULT 464
AY596313
LOCUS AY596313 348 bp RNA linear VRL 09-MAY-2004
DEFINITION Swine hepatitis E virus strain swCH28 capsid protein gene, partial cds.
ACCESSION AY596313
VERSION AY596313.1 GI:46981711
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Detection and analysis of partial sequences of swine hepatitis E virus in Xinjiang
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Direct Submission
JOURNAL Submitted (09-APR-2004) College of Animal Medicine, Nanjing Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu 210095, P. R. China
FEATURES Location/Qualifiers
source 1. .348
/organism="Swine hepatitis E virus"
/mol_type="genomic RNA"
/strain="swCH28"
/db_xref="taxon:63421"
CDS <1. .>348
/note="ORF2"
/codon_start=1
/product="capsid protein"
/protein_id="AAT07942.1"

/db_xref="GI:46981712"
/translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
TLLGGLPTELISSA"

Alignment Scores:

Pred. No.:	283	Length:	348
Score:	108.00	Matches:	108
Percent Similarity:	93.10%	Conservative:	0
Best Local Similarity:	93.10%	Mismatches:	8
Query Match:	19.67%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AY596313 (1-348)

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Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 GTCATGTTTTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGCAGCGCACGTCATAAATTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGTACTGCAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGTTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348
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RESULT 465
AY596317
LOCUS AY596317 348 bp RNA linear VRL 09-MAY-2004
DEFINITION Swine hepatitis E virus strain swCH22 capsid protein gene, partial cds.
ACCESSION AY596317
VERSION AY596317.1 GI:46981719
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Detection and analysis of partial sequences of swine hepatitis E virus in Xinjiang
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Direct Submission
JOURNAL Submitted (09-APR-2004) College of Animal Medicine, Nanjing Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu 210095, P. R. China
FEATURES Location/Qualifiers
source 1. .348
/organism="Swine hepatitis E virus"
/mol_type="genomic RNA"
/strain="swCH22"
/db_xref="taxon:63421"
CDS <1. .>348
/note="ORF2"
/codon_start=1
/product="capsid protein"
/protein_id="AAT07946.1"

/db_xref="GI:46981720"
/translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
TLLGGLPTELISSA"

Alignment Scores:

Pred. No.:	283	Length:	348
Score:	108.00	Matches:	108
Percent Similarity:	93.10%	Conservative:	0
Best Local Similarity:	93.10%	Mismatches:	8
Query Match:	19.67%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AY596317 (1-348)

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Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 GTTATGTTTTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGCAGCGCACGTCATAAATTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGTACTGCAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGATACGTTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348
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RESULT 466
AY596318
LOCUS AY596318 348 bp RNA linear VRL 09-MAY-2004
DEFINITION Swine hepatitis E virus strain swCH15 capsid protein gene, partial cds.
ACCESSION AY596318
VERSION AY596318.1 GI:46981721
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Detection and analysis of partial sequences of swine hepatitis E virus in Xinjiang
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Direct Submission
JOURNAL Submitted (09-APR-2004) College of Animal Medicine, Nanjing Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu 210095, P. R. China
FEATURES Location/Qualifiers
source 1. .348
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/protein_id="AAT07947.1"

/db_xref="GI:46981722"
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TLLGGLPTELISSA"

Alignment Scores:

Pred. No.:	283	Length:	348
Score:	108.00	Matches:	108
Percent Similarity:	93.10%	Conservative:	0
Best Local Similarity:	93.10%	Mismatches:	8
Query Match:	19.67%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AY596318 (1-348)

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Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTTATGTTTTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
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Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
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Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGCAGCGCACGTCATAAATTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
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Db        181 GATGGTACTGCAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
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Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGATACGTTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCA 348
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RESULT 467
AY596319
LOCUS AY596319 348 bp RNA linear VRL 09-MAY-2004
DEFINITION Swine hepatitis E virus strain swCH12 capsid protein gene, partial cds.
ACCESSION AY596319
VERSION AY596319.1 GI:46981723
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Detection and analysis of partial sequences of swine hepatitis E virus in Xinjiang
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Direct Submission
JOURNAL Submitted (09-APR-2004) College of Animal Medicine, Nanjing Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu 210095, P. R. China
FEATURES Location/Qualifiers
source 1. .348
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/mol_type="genomic RNA"
/strain="swCH12"
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TLLGGLPTELISSA"

Alignment Scores:

Pred. No.:	283	Length:	348
Score:	108.00	Matches:	108
Percent Similarity:	93.10%	Conservative:	0
Best Local Similarity:	93.10%	Mismatches:	8
Query Match:	19.67%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AY596319 (1-348)

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Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTTATGCTTTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
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Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
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Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGCAGCACACGTCATAAATTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
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Db        181 GATGGTACTGCGGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
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Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGATACGTTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348
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RESULT 468
AY596320
LOCUS AY596320 348 bp RNA linear VRL 09-MAY-2004
DEFINITION Swine hepatitis E virus strain swCH11 capsid protein gene, partial cds.
ACCESSION AY596320
VERSION AY596320.1 GI:46981725
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Detection and analysis of partial sequences of swine hepatitis E virus in Xinjiang
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Direct Submission
JOURNAL Submitted (09-APR-2004) College of Animal Medicine, Nanjing Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu 210095, P. R. China
FEATURES Location/Qualifiers
source 1. .348
/organism="Swine hepatitis E virus"
/mol_type="genomic RNA"
/strain="swCH11"
/db_xref="taxon:63421"
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/codon_start=1
/product="capsid protein"
/protein_id="AAT07949.1"

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                     /db_xref="GI:46981726"
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Alignment Scores:
Pred. No.:              283           Length:        348
Score:                  108.00        Matches:       108
Percent Similarity:     93.10%        Conservative:  0
Best Local Similarity:  93.10%        Mismatches:    8
Query Match:            19.67%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AY596320 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTTATGTTTTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
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Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGCAGCGCACGTCATAAACTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
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Db        181 GATGGTACTGCAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
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Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGATACGCTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348

RESULT 469
AY621096
LOCUS       AY621096                348 bp    RNA     linear   VRL 27-JUN-2004
DEFINITION  Swine hepatitis E virus isolate swCH119 capsid protein gene,
            partial cds.
ACCESSION   AY621096
VERSION     AY621096.1  GI:49036114
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              283           Length:        348
Score:                  108.00        Matches:       108
Percent Similarity:     93.10%        Conservative:  0
Best Local Similarity:  93.10%        Mismatches:    8
Query Match:            19.67%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AY621096 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTTATGTTTTGCATACATGGCTCACCTGTGAATTCTTACACTAATACATCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
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Db         61 GCCCTCGGCCTACTTGATTTCGCACTTGAGCTTGAGTTCCGTAACTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
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Db        121 ACTAATACGCGTGTTTCTCGTTACTCGAGTAGCGCGCGACACAAATTGCGCCGAGGGGCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGTACTGCTGAGCTTACTACCACTGCTGCCACACGTTTTATGAAAGACCTTCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
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Db        241 ACGGGAACTAATGGTGTTGGCGAGGTCGGTCGTGGTATAGCGTTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCCGACACGCTTCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 470
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LOCUS       HEE344185               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 253.
ACCESSION   AJ344185
VERSION     AJ344185.1  GI:15282395
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
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                /db_xref="UniProt/TrEMBL:Q91EB6"
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                VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:                283             Length:         348
Score:                    108.00          Matches:        108
Percent Similarity:       93.10%          Conservative:   0
Best Local Similarity:    93.10%          Mismatches:     8
Query Match:              19.67%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x HEE344185 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGTTTTGCATACATGGCTCACCTGTGAATTCCTACACTAATACACCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
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Db         61 GCCCTCGGCTTACTTGATTTTGCACTCGAGCTCGAGTTCCGCAACTTAACACCTGGCAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
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Db        121 ACTAACACGCGCGTTTCCCGCTATTCGAGTAGCGCGCGTCACAAATTGCGCCGAGGGCCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
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Db        181 GATGGTACTGCTGAGTTGACTACTACTGCTGCCACACGCTTTATGAAAGACCTCCATTTT 240

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Db        241 ACGGGGACCAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACTCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGACACGCTTCTCGGTGGGCTTCCGACAGAATTAATTTCGTCGGCT 348

RESULT 471
HEE344191
LOCUS       HEE344191               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 194.
ACCESSION   AJ344191
VERSION     AJ344191.1  GI:15282407
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
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                     /db_xref="GI:15282408"
                     /db_xref="GOA:Q91EB0"
                     /db_xref="UniProt/TrEMBL:Q91EB0"
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:                283             Length:         348
Score:                    108.00          Matches:        108
Percent Similarity:       93.10%          Conservative:   0
Best Local Similarity:    93.10%          Mismatches:     8
Query Match:              19.67%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x HEE344191 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGTTTTGCATACATGGCTCACCTGTGAATTCCTACACTAATACACCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACTAACACGCGCGTTTCCCGCTATTCGAGTAGCGCGCGTCACAAATTGCGCCGAGGGCCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGTACTGCTGAGTTGACTACTACTGCTGCCACACGCTTTATGAAAGACCTCCATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        241 ACGGGGACCAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACTCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGACACGCTTCTCGGTGGGCTTCCGACAGAATTAATTTCGTCGGCT 348

RESULT 472
AF117280
LOCUS       AF117280                346 bp    mRNA    linear   VRL 12-SEP-2000
DEFINITION  Swine hepatitis E virus strain TW32SW nucleocapsid protein mRNA,
            partial cds.
ACCESSION   AF117280
VERSION     AF117280.1  GI:10086236
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 346)
  AUTHORS   Wu,J.C., Chen,C.M., Chiang,T.Y., Sheen,I.J., Chen,J.Y., Tsai,W.H.,
            Huang,Y.H. and Lee,S.D.
  TITLE     Clinical and epidemiological implications of swine hepatitis E
            virus infection
  JOURNAL   J. Med. Virol. 60 (2), 166-171 (2000)
  MEDLINE   20062925
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   PUBMED   10596016
REFERENCE   2  (bases 1 to 346)
  AUTHORS   Wu,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-DEC-1998) Division of Gastroenterology, Department of
            Medicine, Graduate Institute of Clinical Medicine, Veterans General
            Hospital-Taipei, National Yang-Ming University School of Medicine,
            Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .346
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                     /strain="TW32SW"
                     /db_xref="taxon:63421"
                     /country="Taiwan"
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                     /codon_start=1
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                     /protein_id="AAG12453.1"
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                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                     TLLGGLPTELISS"

Alignment Scores:
Pred. No.:              287           Length:        346
Score:                  107.00        Matches:       107
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Best Local Similarity:  93.04%        Mismatches:    8
Query Match:            19.49%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AF117280 (1-346)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 GTAATGCTTTGCATTCACGGATCACCTGTAAATTCTTATACTAATACACCCTACACCGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGTCTGCTCGATTTTGCACTCGAGCTCGAGTTTCGTAACTTAACACCTGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACAAACACGCGTGTCTCTCGTTATTCGAGTAGTGCGCGTCATAAGTTACGCCGAGGGCCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGCACAGCAGAACTAACTACTACTGCTGCAACACGCTTTATGAAAGATTTACATTCC 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        241 ACCGGGACTAATGGTGTTGGTGAGGTTGGTCGTGGTATAGCACTAACCCTGTTCAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSer 279
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGCTTCTCGGCGGGCTTCCGACAGAATTGATTTCGTCG 345

RESULT 473
AF117281
LOCUS       AF117281                346 bp    mRNA    linear   VRL 12-SEP-2000
DEFINITION  Swine hepatitis E virus strain TW74SW nucleocapsid protein mRNA,
            partial cds.
ACCESSION   AF117281
VERSION     AF117281.1  GI:10086238
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 346)
  AUTHORS   Wu,J.C., Chen,C.M., Chiang,T.Y., Sheen,I.J., Chen,J.Y., Tsai,W.H.,
            Huang,Y.H. and Lee,S.D.
  TITLE     Clinical and epidemiological implications of swine hepatitis E
            virus infection
  JOURNAL   J. Med. Virol. 60 (2), 166-171 (2000)
  MEDLINE   20062925
   PUBMED   10596016
REFERENCE   2  (bases 1 to 346)
  AUTHORS   Wu,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-DEC-1998) Division of Gastroenterology, Department of
            Medicine, Graduate Institute of Clinical Medicine, Veterans General
            Hospital-Taipei, National Yang-Ming University School of Medicine,
            Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .346
                     /organism="Swine hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="TW74SW"
                     /db_xref="taxon:63421"
                     /country="Taiwan"
     CDS             <1. .>346
                     /note="ORF2"
                     /codon_start=1
                     /product="nucleocapsid protein"
                     /protein_id="AAG12454.1"
                     /db_xref="GI:10086239"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TPLGGLPTELISS"

Alignment Scores:
Pred. No.:              287           Length:        346
Score:                  107.00        Matches:       107
Percent Similarity:     93.04%        Conservative:  0
Best Local Similarity:  93.04%        Mismatches:    8
Query Match:            19.49%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AF117281 (1-346)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 GTAATGCTTTGCATTCACGGGTCACCTGTGAATTCTTACACTAACACACCCTACACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCTTGCTCGATTTTGCACTCGAACTCGAGTTTCGTAATTTAACACCTGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACGAACACGCGTGTCTCCCGTTATTCGAGCAGCGCGCGTCATAAGCTACGCCGAGGGCCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GACGGTACAGCAGAGCTAACCACCACTGCTGCAACACGTTTTATGAAAGATCTTCATTTC 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        241 ACTGGGACTAATGGTGTTGGTGAGGTTGGTCGTGGTATAGCACTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSer 279
              |||||||||   ||||||||||||||||||||||||||||||||
Db        301 GCTGATACGCCTCTCGGTGGGCTCCCGACAGAATTGATTTCGTCG 345

RESULT 474
AY596310
LOCUS       AY596310                348 bp    RNA     linear   VRL 09-MAY-2004
DEFINITION  Swine hepatitis E virus strain swCH65 capsid protein gene, partial
            cds.
ACCESSION   AY596310
VERSION     AY596310.1  GI:46981705
KEYWORDS    .
SOURCE      Swine hepatitis E virus
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  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-APR-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="swCH65"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT07939.1"
                     /db_xref="GI:46981706"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGCGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:                287             Length:         348
Score:                    107.00          Matches:        107
Percent Similarity:       92.24%          Conservative:   0
Best Local Similarity:    92.24%          Mismatches:     9
Query Match:              19.49%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AY596310 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 GTTATGTTTTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGTAGCGCACGTCATAAATTGCGCCGTGGGCCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGTACTGCAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||||   |||   ||||||||||||||||||||||||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTTGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGTTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348

RESULT 475
AY596314
LOCUS       AY596314                348 bp    RNA     linear   VRL 09-MAY-2004
DEFINITION  Swine hepatitis E virus strain swCH25 capsid protein gene, partial
            cds.
ACCESSION   AY596314
VERSION     AY596314.1  GI:46981713
KEYWORDS    .
SOURCE      Swine hepatitis E virus
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  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-APR-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="swCH25"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT07943.1"
                     /db_xref="GI:46981714"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGPDGTVELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:                287             Length:         348
Score:                    107.00          Matches:        107
Percent Similarity:       92.24%          Conservative:   0
Best Local Similarity:    92.24%          Mismatches:     9
Query Match:              19.49%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AY596314 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 GTCATGTTTTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACGCCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGTAGCGCACGTCATAAATTGCGCCGTGGGCCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              |||||||||   ||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGTACTGTAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGTTGCTCGGCGGGCTTCCGACAGAATTGATTTCGTCGGCT 348

RESULT 476
AY596316
LOCUS       AY596316                348 bp    RNA     linear   VRL 09-MAY-2004
DEFINITION  Swine hepatitis E virus strain swCH23 capsid protein gene, partial
            cds.
ACCESSION   AY596316
VERSION     AY596316.1  GI:46981717
KEYWORDS    .
SOURCE      Swine hepatitis E virus
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  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-APR-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="swCH23"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT07945.1"
                     /db_xref="GI:46981718"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                     TLLGGLPTELISPA"

Alignment Scores:
Pred. No.:                287             Length:         348
Score:                    107.00          Matches:        107
Percent Similarity:       92.24%          Conservative:   0
Best Local Similarity:    92.24%          Mismatches:     9
Query Match:              19.49%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AY596316 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTTATGTTCTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTCGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGCAGCGCACGTCATAAATTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGTACTGCAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        301 GCTGATACGTTGCTCGGCGGGCTTCCGACAGAATTAATTTCGCCGGCT 348

RESULT 477
HEE344177
LOCUS       HEE344177               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 297.
ACCESSION   AJ344177
VERSION     AJ344177.1  GI:15282379
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="297"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51496.1"
                     /db_xref="GI:15282380"
                     /db_xref="GOA:Q91EC4"
                     /db_xref="UniProt/TrEMBL:Q91EC4"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGSLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:                287             Length:         348
Score:                    107.00          Matches:        107
Percent Similarity:       92.24%          Conservative:   0
Best Local Similarity:    92.24%          Mismatches:     9
Query Match:              19.49%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x HEE344177 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGTTTTGCATACATGGCTCACCTGTAAATTCCTATACTAATACACCTTACACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGTTCGCTTGACTTTGCACTCGAACTCGAGTTTCGCAATTTGACACCTGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACGAACACGCGTGTCTCCCGTTATTCGAGTAGCGCGCGTCACAAGTTGCGCCGAGGACCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GACGGTACAGCGGAGCTAACTACTACTGCTGCTACACGTTTTATGAAAGACCTTCATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        241 ACTGGGACTAATGGTGTTGGTGAGGTTGGTCGTGGTATAGCACTGACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGCTTCTTGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 478
HEE344181
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LOCUS       HEE344181               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 108.
ACCESSION   AJ344181
VERSION     AJ344181.1  GI:15282387
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="mRNA"
                     /isolate="108"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51500.1"
                     /db_xref="GI:15282388"
                     /db_xref="GOA:Q91EC0"
                     /db_xref="UniProt/TrEMBL:Q91EC0"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGHGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:                287           Length:         348
Score:                    107.00        Matches:        107
Percent Similarity:       92.24%        Conservative:   0
Best Local Similarity:    92.24%        Mismatches:     9
Query Match:              19.49%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x HEE344181 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              |||||||   ||||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 GTCATGTTTTGCATACATGGCTCACCTGTGAATTCTTACACTAATACACCCTATACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCTTACTTGATTTTGCGCTCGAGCTCGAGTTCCGCAATTTAACACCTGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACTAACACGCGCGTTTCTCGCTACTCGAGTAGCGCGCGTCACAAATTGCGCCGAGGGCCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGCACTGCTGAGTTGACTACTACTGCCGCCACACGCTTTATGAAAGACCTTCATTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||||   |||   ||||||||||||||||||||||||||||
Db        241 ACAGGGACTAATGGTGTTGGTGAAGTCGGTCATGGTATAGCGTTAACTTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGACACGCTTCTCGGTGGGCTTCCGACAGAATTGATTTCGTCGGCT 348

RESULT 479
HEE344186
LOCUS       HEE344186               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 254.
ACCESSION   AJ344186
VERSION     AJ344186.1  GI:15282397
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="mRNA"
                     /isolate="254"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51505.1"
                     /db_xref="GI:15282398"
                     /db_xref="GOA:Q91EB5"
                     /db_xref="UniProt/TrEMBL:Q91EB5"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIVLTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:                287           Length:         348
Score:                    107.00        Matches:        107
Percent Similarity:       92.24%        Conservative:   0
Best Local Similarity:    92.24%        Mismatches:     9
Query Match:              19.49%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x HEE344186 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 GTTATGTTTTGCATACATGGCTCACCTGTAAATTCCTATACTAATACACCTTACACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGTTTGCTTGACTTTGCACTCGAACTCGAGTTTCGCAATTTGACACCTGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACGAACACGCGTGTCTCCCGTTATTCGAGTAGCGCGCGTCACAAGTTGCGCCGAGGACCT 180
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Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
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Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GAGCTTGAGTTTCGTAACCTTACCCCCGGTAACACTAATACGCGGGTTTCCCGTTATTCC 123

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AGCACTGCCCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACG 183

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCTGCTACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 243

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCG 303

Qy        274 ThrGluLeuIleSer 278
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Db        304 ACAGAATTGATTTCG 318
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RESULT 482
AF446095
LOCUS       AF446095                317 bp    RNA     linear   VRL 02-JAN-2003
DEFINITION  Hepatitis E virus isolate NANDED99 structural protein 2 gene,
            partial cds.
ACCESSION   AF446095
VERSION     AF446095.1  GI:27462558
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 317)
  AUTHORS   Chobe,L.P., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Hepatitis E Outbreaks in Maharashtra (1999-2000), India:
            Phylogenetic Analysis of Currently Prevalent HEV Isolates
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 317)
  AUTHORS   Chobe,L.P., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-NOV-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .317
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NANDED99"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>317
                     /note="ORF2"
                     /codon_start=1
                     /product="structural protein 2"
                     /protein_id="AAO15475.1"
                     /db_xref="GI:27462559"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPT
                     ELIS"
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Alignment Scores:
Pred. No.:              296           Length:         317
Score:                  104.00        Matches:        104
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            18.94%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF446095 (1-317)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTT 63
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Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GAGCTTGAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTTTCCCGTTATTCC 123

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AGCACTGCCCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACG 183

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCTGCTACCCGCTTCATGAAGGACCTCTATTTTACTAGTACCAATGGTGTTGGTGAGATC 243

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 GGCCGCGGGATAGCCCTTACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCG 303

Qy        274 ThrGluLeuIle 277
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Db        304 ACAGAATTGATT 315
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RESULT 483
AF446093
LOCUS       AF446093                312 bp    RNA     linear   VRL 02-JAN-2003
DEFINITION  Hepatitis E virus isolate AMRAV99 structural protein 2 gene,
            partial cds.
ACCESSION   AF446093
VERSION     AF446093.1  GI:27462554
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 312)
  AUTHORS   Chobe,L.P., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Hepatitis E Outbreaks in Maharashtra (1999-2000), India:
            Phylogenetic Analysis of Currently Prevalent HEV Isolates
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 312)
  AUTHORS   Chobe,L.P., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-NOV-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .312
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="AMRAV99"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>312
                     /note="ORF2"
                     /codon_start=2
                     /product="structural protein 2"
                     /protein_id="AAO15473.1"
                     /db_xref="GI:27462555"
                     /translation="NSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARH
                     RLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTEL
                     IS"
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Alignment Scores:
Pred. No.:              300           Length:         312
Score:                  103.00        Matches:        103
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            18.76%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF446093 (1-312)

Qy        175 AsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGlu 194
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Db          2 AATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTCGAG 61

Qy        195 LeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSer 214
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTTTCCCGTTATTCCAGC 121

Qy        215 ThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAla 234
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACTGCCCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCT 181

Qy        235 AlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGly 254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGC 241

Qy        255 ArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThr 274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 CGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACA 301

Qy        275 GluLeuIle 277
              |||||||||
Db        302 GAATTGATT 310

RESULT 484
AF093896
LOCUS       AF093896                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate K75 polyprotein gene, partial cds.
ACCESSION   AF093896
VERSION     AF093896.1  GI:4336439
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="K75"
                     /db_xref="taxon:12461"
                     /country="India: Karnal"
                     /note="isolated in 1987"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17807.1"
                     /db_xref="GI:4336455"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              315             Length:         304
Score:                  99.00           Matches:        99
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            18.03%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF093896 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTATTCC 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACCGCCGAGCTTACCACCACG 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GCCGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 485
AF093897
LOCUS       AF093897                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate K45 polyprotein gene, partial cds.
ACCESSION   AF093897
VERSION     AF093897.1  GI:4336440
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="K45"
                     /db_xref="taxon:12461"
                     /country="India: Karnal"
                     /note="isolated in 1987"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17808.1"
                     /db_xref="GI:4336456"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              315             Length:         304
Score:                  99.00           Matches:        99
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            18.03%          Indels:         0
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DB:                    1              Gaps:          0

US-09-769-066-15 (1-549) x AF093897 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTCTCCCGTTATTCC 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACCGCCGAGCTTACCACCACG 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GCCGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 486
AF093898
LOCUS       AF093898                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate Y2 polyprotein gene, partial cds.
ACCESSION   AF093898
VERSION     AF093898.1  GI:4336441
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="Y2"
                     /db_xref="taxon:12461"
                     /country="India: Yamunanagar"
                     /note="isolated in 1989"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17809.1"
                     /db_xref="GI:4336457"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              315          Length:        304
Score:                  99.00        Matches:       99
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0

Query Match:            18.03%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AF093898 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTCTCCCGTTATTCC 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACCGCCGAGCTTACCACCACG 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GCCGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 487
AF093900
LOCUS       AF093900                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate M67 polyprotein gene, partial cds.
ACCESSION   AF093900
VERSION     AF093900.1  GI:4336443
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="M67"
                     /db_xref="taxon:12461"
                     /country="India: Meerut"
                     /note="isolated in 1996"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17811.1"
                     /db_xref="GI:4336459"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              315          Length:        304
Score:                  99.00        Matches:       99
Percent Similarity:     100.00%      Conservative:  0
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Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            18.03%         Indels:        0
DB:                     1              Gaps:          0

US-09-769-066-15 (1-549) x AF093900 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
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Db          6 GTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTCGCAACCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCC 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACG 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GCTGCTACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATC 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 488
AF093901
LOCUS       AF093901                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate M82 polyprotein gene, partial cds.
ACCESSION   AF093901
VERSION     AF093901.1  GI:4336444
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="M82"
                     /db_xref="taxon:12461"
                     /country="India: Meerut"
                     /note="isolated in 1996"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17812.1"
                     /db_xref="GI:4336460"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              315            Length:        304
Score:                  99.00          Matches:       99
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Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            18.03%         Indels:        0
DB:                     1              Gaps:          0

US-09-769-066-15 (1-549) x AF093901 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTATTCC 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACG 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GCTGCTACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATC 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 489
AF093902
LOCUS       AF093902                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate M70 polyprotein gene, partial cds.
ACCESSION   AF093902
VERSION     AF093902.1  GI:4336445
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="M70"
                     /db_xref="taxon:12461"
                     /country="India: Meerut"
                     /note="isolated in 1996"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17813.1"
                     /db_xref="GI:4336461"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              315            Length:        304
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Score:                  99.00          Matches:        99
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            18.03%         Indels:         0
DB:                     1              Gaps:           0

US-09-769-066-15 (1-549) x AF093902 (1-304)

Qy      174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6 GTAAACTCTTATACTAATACACCTTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTT 65

Qy      194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       66 GAGCTTGAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCC 125

Qy      214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      126 AGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACG 185

Qy      234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      186 GCTGCTACCCGCTTTATGAAGGACCTTTATTTTACTAGTACTAATGGTGTCGGTGAGATC 245

Qy      254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      246 GGCCGCGGGATAGCCCTCACCCTTTTTAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 490
AF093903
LOCUS       AF093903                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate 331 polyprotein gene, partial cds.
ACCESSION   AF093903
VERSION     AF093903.1  GI:4336446
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="331"
                     /db_xref="taxon:12461"
                     /country="India: Lucknow"
                     /note="sporadic hepatitis E; isolated in 1996"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17814.1"
                     /db_xref="GI:4336462"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:

Pred. No.:              315            Length:         304
Score:                  99.00          Matches:        99
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            18.03%         Indels:         0
DB:                     1              Gaps:           0

US-09-769-066-15 (1-549) x AF093903 (1-304)

Qy      174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
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Db        6 GTAAATTCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTC 65

Qy      194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       66 GAACTTGAGTTCCGCAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCC 125

Qy      214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      126 AGCACTGCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACG 185

Qy      234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      186 GCTGCCACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 245

Qy      254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      246 GGCCGCGGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTA 302

RESULT 491
AF093904
LOCUS       AF093904                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate K46 polyprotein gene, partial cds.
ACCESSION   AF093904
VERSION     AF093904.1  GI:4336447
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="K46"
                     /db_xref="taxon:12461"
                     /country="India: Karnal"
                     /note="isolated in 1987"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17815.1"
                     /db_xref="GI:4336463"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"
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Alignment Scores:
Pred. No.:              315             Length:         304
Score:                  99.00           Matches:        99
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            18.03%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF093904 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
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Db          6 GTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
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Db         66 GAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTATTCC 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
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Db        126 AGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACCGCCGAGCTTACCACCACG 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
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Db        186 GCCGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 492
AF093905
LOCUS       AF093905                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate K70 polyprotein gene, partial cds.
ACCESSION   AF093905
VERSION     AF093905.1  GI:4336448
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="K70"
                     /db_xref="taxon:12461"
                     /country="India: Karnal"
                     /note="isolated in 1987"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17816.1"
                     /db_xref="GI:4336464"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              315             Length:         304
Score:                  99.00           Matches:        99
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            18.03%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF093905 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
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Db          6 GTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
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Db         66 GAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTATTCC 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACCGCCGAGCTTACCACCACG 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GCCGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 493
AF093906
LOCUS       AF093906                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate K74 polyprotein gene, partial cds.
ACCESSION   AF093906
VERSION     AF093906.1  GI:4336449
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:12461"
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                     /note="isolated in 1987"
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Alignment Scores:
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US-09-769-066-15 (1-549) x AF093906 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
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Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
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Db         66 GAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTATTCC 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
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Db        126 AGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACCGCCGAGCTTACCACCACG 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
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Db        186 GCCGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
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Db        246 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 494
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LOCUS       AF093907                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate Y3 polyprotein gene, partial cds.
ACCESSION   AF093907
VERSION     AF093907.1  GI:4336450
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
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                     /note="isolated in 1989"
     CDS             <1. .>304
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Alignment Scores:
Pred. No.:              315             Length:         304
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DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF093907 (1-304)

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Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
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Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
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Db        246 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 495
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DEFINITION  Hepatitis E virus isolate Y11 polyprotein gene, partial cds.
ACCESSION   AF093908
VERSION     AF093908.1  GI:4336451
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              315           Length:        304
Score:                  99.00         Matches:       99
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DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AF093908 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
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Db          6 GTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
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Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
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Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
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Db        246 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 496
AF093909
LOCUS       AF093909                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate Y66 polyprotein gene, partial cds.
ACCESSION   AF093909
VERSION     AF093909.1  GI:4336452
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              315           Length:        304
Score:                  99.00         Matches:       99
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US-09-769-066-15 (1-549) x AF093909 (1-304)

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Db         66 GAGCTTGAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTCTCCCGTTATTCC 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
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Db        126 AGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACCGCCGAGCTTACCACCACG 185

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Db        186 GCCGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
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RESULT 497
AF093910
LOCUS       AF093910                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate Y67 polyprotein gene, partial cds.
ACCESSION   AF093910
VERSION     AF093910.1  GI:4336453
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:                315             Length:         304
Score:                    99.00           Matches:        99
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DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AF093910 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
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Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
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Db        186 GCCGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
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Db        246 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 498
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LOCUS       AF093899                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate M73 polyprotein gene, partial cds.
ACCESSION   AF093899
VERSION     AF093899.1  GI:4336442
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
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                     /note="isolated in 1996"
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Alignment Scores:
Pred. No.:                318             Length:         304
Score:                    98.00           Matches:        98
Percent Similarity:       98.99%          Conservative:   0
Best Local Similarity:    98.99%          Mismatches:     1
Query Match:              17.85%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AF093899 (1-304)

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Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
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Db         66 GAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTATTCC 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
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Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
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Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
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Db        246 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 499
AF093911
LOCUS       AF093911                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate M75 polyprotein gene, partial cds.
ACCESSION   AF093911
VERSION     AF093911.1  GI:4336454
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
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REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
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                     /db_xref="GI:4336470"
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                     RHRLRRGADGTAELTTTAATRFMKDLYFASTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              318           Length:        304
Score:                  98.00         Matches:       98
Percent Similarity:     98.99%        Conservative:  0
Best Local Similarity:  98.99%        Mismatches:    1
Query Match:            17.85%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AF093911 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTATTCC 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACG 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        186 GCTGCTACCCGCTTCATGAAGGACCTCTATTTTGCTAGTACTAACGGTGTTGGTGAGATC 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 500
AF302069
LOCUS       AF302069                 304 bp    mRNA    linear   VRL 02-DEC-2001
DEFINITION  Hepatitis E virus strain Nepal 7138 capsid protein mRNA, partial
            cds.
ACCESSION   AF302069
VERSION     AF302069.1  GI:17224603
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.C.
  TITLE     Hepatitis E virus cross-species infection in human and swine
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-AUG-2000) Division of Gastroenterology, Taipei
            Veterans General Hospital & Institute of Clinical Medicine,
            National Yang-Ming University, 201 Shih-Pai Road, Sec. 2, Taipei
            112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Nepal 7138"
                     /db_xref="taxon:12461"
                     /country="Nepal"
                     /note="isolated from patient's serum"
     CDS             <1. .>304
                     /note="ORF2"
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAL37039.1"
                     /db_xref="GI:17224604"
                     /translation="PVNFYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              318           Length:        304
Score:                  98.00         Matches:       98
Percent Similarity:     98.99%        Conservative:  0
Best Local Similarity:  98.99%        Mismatches:    1
Query Match:            17.85%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AF302069 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTAAATTTTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTC 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAACTTGAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCC 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCACTGCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACG 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GCTGCCACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGCGGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTA 302

RESULT 501
AF446092
LOCUS       AF446092                 295 bp    RNA     linear   VRL 02-JAN-2003
DEFINITION  Hepatitis E virus isolate AKOLA99 structural protein 2 gene,
            partial cds.
ACCESSION   AF446092
VERSION     AF446092.1  GI:27462552
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 295)
  AUTHORS   Chobe,L.P., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Hepatitis E Outbreaks in Maharashtra (1999-2000), India:
            Phylogenetic Analysis of Currently Prevalent HEV Isolates
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 295)
  AUTHORS   Chobe,L.P., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-NOV-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .295
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="AKOLA99"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>295
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein 2"
                     /protein_id="AAO15472.1"
                     /db_xref="GI:27462553"
                     /translation="PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGA
                     DGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELIS"
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Alignment Scores:
Pred. No.:                322             Length:         295
Score:                    97.00           Matches:        97
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              17.67%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AF446092 (1-295)

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTCGAGCTTGAGTTTCGCAACCTT 62

Qy        201 ThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 ACCCCCGGTAACACTAATACGCGGGTTTCCCGTTATTCCAGCACTGCCCGCCACCGCCTT 122

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTCATGAAG 182

Qy        241 AspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGCGGGATAGCCCTCACC 242

Qy        261 LeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATT 293

RESULT 502
AF105021
LOCUS       AF105021                 296 bp    RNA     linear   VRL 01-DEC-2000
DEFINITION  Hepatitis E virus structural protein 2 gene, partial cds.
ACCESSION   AF105021
VERSION     AF105021.1  GI:6650540
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 296)
  AUTHORS   He,J., Binn,L.N., Tsarev,S.A., Hayes,C.G., Frean,J.A., Isaacson,M.
            and Innis,B.L.
  TITLE     Molecular characterization of a hepatitis E virus isolate from
            Namibia
  JOURNAL   J. Biomed. Sci. 7 (4), 334-338 (2000)
  MEDLINE   20355243
   PUBMED   10895057
REFERENCE   2  (bases 1 to 296)
  AUTHORS   He,J., Binn,L., Tsarev,S., Frean,J. and Innis,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-NOV-1998) Department of Virus Diseases, WRAIR,
            Washington, DC 20307
FEATURES             Location/Qualifiers
     source          1. .296
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="83-Namibia"
                     /db_xref="taxon:12461"
                     /country="Namibia"
     CDS             <1. .>296
                     /note="ORF-2"
                     /codon_start=3
                     /product="structural protein 2"
                     /protein_id="AAF21896.1"
                     /db_xref="GI:6650541"
                     /translation="STIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLL
                     IENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLEDTLDYPARAHTFD"

Alignment Scores:
Pred. No.:                322             Length:         296
Score:                    97.00           Matches:        97
Percent Similarity:       98.98%          Conservative:   0
Best Local Similarity:    98.98%          Mismatches:     1
Query Match:              17.67%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AF105021 (1-296)

Qy        416 SerThrIleGlnGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSer 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 TCTACGATTCAGCAGTATTCGAAGACTTTCTTCGTCCTGCCGCTTCGTGGCAAGCTCTCC 62

Qy        436 PheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSer 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 TTCTGGGAGGCGGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACTACTGCTAGC 122

Qy        456 AspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThr 475
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GACCAATTGCTTATCGAGAACGCCGCTGGGCATCGGGTGGCCATTTCTACTTATACCACT 182

Qy        476 SerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAla 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AGCTTGGGTGCAGGCCCTGTTTCCATCTCCGCGGTCGCTGTTCTAGCCCCCCACTCTGCT 242

Qy        496 LeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAsp 513
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 TTAGCATTGCTCGAGGATACCTTGGATTACCCTGCCCGTGCTCATACTTTTGAT 296

RESULT 503
HEE428851
LOCUS       HEE428851                300 bp    RNA     linear   VRL 12-JUL-2002
DEFINITION  Hepatitis E virus type 1 partial polyprotein gene for capsid
            protein, human isolate F8.
ACCESSION   AJ428851
VERSION     AJ428851.1  GI:18447769
KEYWORDS    capsid protein; polyprotein gene.
SOURCE      Hepatitis E virus type 1
  ORGANISM  Hepatitis E virus type 1
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Xia,N., Peng,G., Lan,H., Zhuang,H., Zhu,Y.,
            Li,S., Tian,K., Gu,W., Lin,J., Wu,X., Li,H. and Harrison,T.J.
  TITLE     Prevalence, isolation, and partial sequence analysis of hepatitis E
            virus from domestic animals in China
  JOURNAL   J. Med. Virol. 67 (4), 516-521 (2002)
  MEDLINE   22110701
   PUBMED   12115997
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2002) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Hepatitis E virus type 1"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="F8"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:185579"
                     /country="China:Xinjiang"
     CDS             <1. .>300
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="CAD21787.1"
                     /db_xref="GI:18447770"
                     /db_xref="GOA:Q8UZ77"
                     /db_xref="UniProt/TrEMBL:Q8UZ77"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGTDGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGG"
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Alignment Scores:
Pred. No.:              322           Length:        300
Score:                  97.00         Matches:       97
Percent Similarity:     98.98%        Conservative:  0
Best Local Similarity:  98.98%        Mismatches:    1
Query Match:            17.67%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x HEE428851 (1-300)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTAAATTCTTATACTAACACACCTTATACCGGTGCCCTTGGGCTGTTGGATTTTGCCCTC 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAACTTGAGTTCCGCAACCTCACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCC 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        126 AGCACTGCCCGTCACCGCCTTCGTCGCGGTACAGATGGGACTGCCGAGCTCACCACCACG 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GCTGCTACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGly 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGCGGGATAGCGCTTACCCTGTTTAACCTTGCTGACACCCTGCTTGGCGGT 299

RESULT 504
AF466660
LOCUS       AF466660                300 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-19248-3 capsid protein gene,
            partial cds.
ACCESSION   AF466660
VERSION     AF466660.1  GI:19919472
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-19248-3"
                     /db_xref="taxon:63421"
     CDS             <1. .>300
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM08292.1"
                     /db_xref="GI:19919473"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              330           Length:        300
Score:                  95.00         Matches:       95
Percent Similarity:     95.96%        Conservative:  0
Best Local Similarity:  95.96%        Mismatches:    4
Query Match:            17.30%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AF466660 (1-300)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GTTAATTCCTATACTAATACACCTTACACTGGTGCATTGGGGCTTCTTGATTTTGCATTA 63

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GAGCTTGAATTTAGAAATCTGACACCTGGGAACACTAACACCCGTGTTTCCAGGTATACT 123

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AGCACAGCCCGCCATCGGCTGCGCCGCGGTGCTGACGGGACCGCTGAGCTCACTACCACA 183

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||    ||||||   ||||||||||||||||||
Db        184 GCAGCCACACGTTTTATGAAGGATTTACATTTTACTGGCACGAACGGTGTCGGTGAGGTT 243

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 GGTCGTGGTATCGCTCTGACATTGTTTAACCTTGCTGACACGCTTCTCGGTGGTTTA 300

RESULT 505
AF466661
LOCUS       AF466661                300 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-18934D1 capsid protein gene,
            partial cds.
ACCESSION   AF466661
VERSION     AF466661.1  GI:19919474
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-18934D1"
                     /db_xref="taxon:63421"
     CDS             <1. .>300
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM08293.1"
                     /db_xref="GI:19919475"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              330           Length:        300
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Score:                  95.00          Matches:        95
Percent Similarity:     95.96%         Conservative:   0
Best Local Similarity:  95.96%         Mismatches:     4
Query Match:            17.30%         Indels:         0
DB:                     1              Gaps:           0

US-09-769-066-15 (1-549) x AF466661 (1-300)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GTTAATTCCTATACCAATACACCTTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTA 63

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GAGCTTGAATTTAGAAATTTGACACCTGGGAACACTAACACCCGTGTTTCTAGATATACC 123

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACA 183

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        184 GCAGCCACACGTTTCATGAAGGATTTGCATTTTACTGGCACGAACGGTGTTGGTGAGGTG 243

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 GGCCGTGGTATTGCTCTGACATTGTTTAATCTTGCTGACACGCTTCTTGGTGGTTTA 300

RESULT 506
AF466662
LOCUS       AF466662                 300 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-18934C1 capsid protein gene,
            partial cds.
ACCESSION   AF466662
VERSION     AF466662.1  GI:19919476
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-18934C1"
                     /db_xref="taxon:63421"
     CDS             <1. .>300
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM08294.1"
                     /db_xref="GI:19919477"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              330            Length:         300
Score:                  95.00          Matches:        95
Percent Similarity:     95.96%         Conservative:   0
Best Local Similarity:  95.96%         Mismatches:     4
Query Match:            17.30%         Indels:         0
DB:                     1              Gaps:           0

US-09-769-066-15 (1-549) x AF466662 (1-300)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GTTAATTCCTATACTAATACACCCTACACCGGTGCACTAGGGCTTCTTGATTTCGCATTA 63

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GAGCTTGAATTTAGAAACCTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACC 123

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AGCACAGCTCGCCACCGGCTGCGCCGTGGTGCTGATGGGACCGCTGAGCTTACAACCACA 183

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        184 GCAGCTACACGTTTCATGAAAGATCTGCATTTTACTGGCACGAATGGTGTTGGTGAGGTG 243

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 GGCCGTGGTATCGCTTTAACATTGTTTAATCTTGCTGATACGCTTCTCGGCGGTTTA 300

RESULT 507
AF466663
LOCUS       AF466663                 300 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-18356-1 capsid protein gene,
            partial cds.
ACCESSION   AF466663
VERSION     AF466663.1  GI:19919478
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-18356-1"
                     /db_xref="taxon:63421"
     CDS             <1. .>300
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM08295.1"
                     /db_xref="GI:19919479"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              330            Length:         300
Score:                  95.00          Matches:        95
Percent Similarity:     95.96%         Conservative:   0
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Best Local Similarity:  95.96%          Mismatches:     4
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF466663 (1-300)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GTTAATTCCTACACTAATACACCTTATACTGGTGCATTGGGGCTTCTTGATTTTGCATTA 63

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GAACTTGAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTACACC 123

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AGTACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACA 183

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||   ||||||   ||||||||||||||||||||||
Db        184 GCAGCCACACGCTTCATGAAGGATTTGCATTTTACTGGCACGAACGGCGTTGGTGAGGTG 243

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 GGTCGCGGCATTGCCCTGACACTGTTTAATCTTGCTGATACGCTTCTTGGCGGTTTA 300

RESULT 508
AF466666
LOCUS       AF466666                300 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain UMC9A capsid protein gene, partial
            cds.
ACCESSION   AF466666
VERSION     AF466666.1  GI:19919484
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="UMC9A"
                     /db_xref="taxon:63421"
     CDS             <1. .>300
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM08298.1"
                     /db_xref="GI:19919485"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              330             Length:         300
Score:                  95.00           Matches:        95
Percent Similarity:     95.96%          Conservative:   0
Best Local Similarity:  95.96%          Mismatches:     4
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF466666 (1-300)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTTCTTGACTTTGCATTA 63

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GAACTTGAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACC 123

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AGTACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGCACCGCTGAGCTTACTACTACG 183

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||   ||||||   ||||||||||||||||||||||
Db        184 GCAGCCACACGCTTCATGAAGGACTTGCATTTTACTGGTACGAACGGTGTTGGTGAGGTG 243

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 GGCCGTGGTATCGCTCTGACACTGTTTAATCTCGCTGACACGCTTCTCGGTGGTTTA 300

RESULT 509
AF466667
LOCUS       AF466667                300 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain UMC7A capsid protein gene, partial
            cds.
ACCESSION   AF466667
VERSION     AF466667.1  GI:19919486
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="UMC7A"
                     /db_xref="taxon:63421"
     CDS             <1. .>300
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM08299.1"
                     /db_xref="GI:19919487"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              330             Length:         300
Score:                  95.00           Matches:        95
Percent Similarity:     95.96%          Conservative:   0
Best Local Similarity:  95.96%          Mismatches:     4
Query Match:            17.30%          Indels:         0
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DB:                    1              Gaps:          0

US-09-769-066-15 (1-549) x AF466667 (1-300)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GTCAATTCTTATACTAATACACCTTACACGGGTGCACTGGGGCTTCTTGATTTTGCATTA 63

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GAACTTGAATTTAGAAATTTAACACCTGGGAACACTAACACCCGTGTTTCCCGGTATACC 123

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AGTACAGCCCGCCACCGGCTGCGTCGCGGTGCTGATGGCACCGCTGAGCTTACTACCACG 183

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||||
Db        184 GCAGCCACACGTTTCATGAAGGACCTGCATTTTACTGGTACGAACGGCGTCGGTGAGGTG 243

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 GGCCGTGGTATCGCTCTGACACTGTTTAATCTCGCTGACACGCTTCTCGGTGGTTTA 300

RESULT 510
AF466665
LOCUS       AF466665                 301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain UMC12B capsid protein gene, partial
            cds.
ACCESSION   AF466665
VERSION     AF466665.1  GI:19919482
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="UMC12B"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08297.1"
                     /db_xref="GI:19919483"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              330          Length:          301
Score:                  95.00        Matches:         95
Percent Similarity:     95.96%       Conservative:    0
Best Local Similarity:  95.96%       Mismatches:      4
Query Match:            17.30%       Indels:          0
DB:                     1            Gaps:            0
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US-09-769-066-15 (1-549) x AF466665 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTTCTTGACTTTGCATTA 64

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAACTTGAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACC 124

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AGTACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGCACCGCTGAGCTTACTACTACG 184

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||||
Db        185 GCAGCCACACGTTTTATGAAGGACTTGCATTTTACTGGTACGAACGGTGTTGGTGAGGTG 244

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GGCCGTGGTATCGCTCTGACACTGTTTAATCTTGCTGACACGCTTCTTGGTGGTTTA 301

RESULT 511
AF466668
LOCUS       AF466668                 301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-161371-1 capsid protein gene,
            partial cds.
ACCESSION   AF466668
VERSION     AF466668.1  GI:19919488
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-161371-1"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08300.1"
                     /db_xref="GI:19919489"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              330          Length:          301
Score:                  95.00        Matches:         95
Percent Similarity:     95.96%       Conservative:    0
Best Local Similarity:  95.96%       Mismatches:      4
Query Match:            17.30%       Indels:          0
DB:                     1            Gaps:            0
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US-09-769-066-15 (1-549) x AF466668 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTTCTTGATTTCGCATTA 64

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAGCTTGAATTTAGAAACTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACC 124

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AGCACAGCCCGTCACCGGCTGCGCCGTGGTGCTGATGGGACCGCTGAGCTCACCACCACA 184

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        185 GCAGCCACACGTTTCATGAAGGACTTGCATTTTACTGGCACGAACGGCGTCGGTGAGGTG 244

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GGTCGTGGTATCGCTCTAACACTGTTCAATCTCGCTGATACGCTTCTCGGTGGTTTA 301

RESULT 512
AF466669
LOCUS       AF466669                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-16138-2 capsid protein gene,
            partial cds.
ACCESSION   AF466669
VERSION     AF466669.1  GI:19919490
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-16138-2"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
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                     /product="capsid protein"
                     /protein_id="AAM08301.1"
                     /db_xref="GI:19919491"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              330             Length:         301
Score:                  95.00           Matches:        95
Percent Similarity:     95.96%          Conservative:   0
Best Local Similarity:  95.96%          Mismatches:     4
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF466669 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTTCTTGATTTCGCATTA 64

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAGCTTGAATTTAGAAACTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACC 124

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AGCACAGCCCGTCACCGGCTGCGCCGTGGTGCTGATGGGACCGCTGAGCTCACCACCACA 184

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        185 GCAGCCACACGTTTCATGAAGGACTTGCATTTTACTGGCACGAACGGCGTCGGTGAGGTG 244

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GGTCGTGGTATCGCTCTAACACTGTTCAATCTCGCTGATACGCTTCTCGGTGGTTTA 301

RESULT 513
AF466670
LOCUS       AF466670                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-16138-3 capsid protein gene,
            partial cds.
ACCESSION   AF466670
VERSION     AF466670.1  GI:19919492
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-16138-3"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08302.1"
                     /db_xref="GI:19919493"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              330             Length:         301
Score:                  95.00           Matches:        95
Percent Similarity:     95.96%          Conservative:   0
Best Local Similarity:  95.96%          Mismatches:     4
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF466670 (1-301)
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Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTTCTTGATTTCGCATTA 64

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAGCTTGAATTTAGAAACTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACC 124

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AGCACAGCCCGTCACCGGCTGCGCCGTGGTGCTGATGGGACCGCTGAGCTCACCACCACA 184

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||  ||||||  ||||||||||||||||||||||||||
Db        185 GCAGCCACACGTTTCATGAAGGACTTGCATTTTACTGGCACGAACGGCGTCGGTGAGGTG 244

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GGTCGTGGTATCGCTCTAACACTGTTCAATCTCGCTGATACGCTTCTCGGTGGTTTA 301
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RESULT 514
AF466671
LOCUS AF466671 301 bp RNA linear VRL 04-APR-2002
DEFINITION Swine hepatitis E virus strain 01-16139-2 capsid protein gene, partial cds.
ACCESSION AF466671
VERSION AF466671.1 GI:19919494
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 301)
AUTHORS Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G., Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
TITLE Detection by reverse transcription-PCR and genetic characterization of field isolates of swine hepatitis E virus from pigs in different geographic regions of the United States
JOURNAL J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
MEDLINE 21920873
PUBMED 11923352
REFERENCE 2 (bases 1 to 301)
AUTHORS Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S., Pierson,F., Toth,T. and Meng,X.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia Polytechnic Institute and State University, 1410 Prices Fork Road, Blacksburg, VA 24060, USA
FEATURES Location/Qualifiers
source 1. .301
/organism="Swine hepatitis E virus"
/mol_type="genomic RNA"
/strain="01-16139-2"
/db_xref="taxon:63421"
CDS <1. .>301
/codon_start=2
/product="capsid protein"
/protein_id="AAM08303.1"
/db_xref="GI:19919495"
/translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:

Pred. No.:	330	Length:	301
Score:	95.00	Matches:	95
Percent Similarity:	95.96%	Conservative:	0
Best Local Similarity:	95.96%	Mismatches:	4
Query Match:	17.30%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AF466671 (1-301)

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Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTTCTTGATTTCGCATTA 64

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAGCTTGAATTTAGAAACTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACC 124

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AGCACAGCCCGTCACCGGCTGCGCCGTGGTGCTGATGGGACCGCTGAGCTCACCACCACA 184

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||  ||||||  ||||||||||||||||||||||||||
Db        185 GCAGCCACACGTTTCATGAAGGACTTGCATTTTACTGGCACGAACGGCGTCGGTGAGGTG 244

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GGTCGTGGTATCGCTCTAACACTGTTCAATCTCGCTGATACGCTTCTCGGTGGTTTA 301
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RESULT 515
AF466672
LOCUS AF466672 301 bp RNA linear VRL 04-APR-2002
DEFINITION Swine hepatitis E virus strain 01-16140-3 capsid protein gene, partial cds.
ACCESSION AF466672
VERSION AF466672.1 GI:19919496
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 301)
AUTHORS Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G., Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
TITLE Detection by reverse transcription-PCR and genetic characterization of field isolates of swine hepatitis E virus from pigs in different geographic regions of the United States
JOURNAL J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
MEDLINE 21920873
PUBMED 11923352
REFERENCE 2 (bases 1 to 301)
AUTHORS Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S., Pierson,F., Toth,T. and Meng,X.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia Polytechnic Institute and State University, 1410 Prices Fork Road, Blacksburg, VA 24060, USA
FEATURES Location/Qualifiers
source 1. .301
/organism="Swine hepatitis E virus"
/mol_type="genomic RNA"
/strain="01-16140-3"
/db_xref="taxon:63421"
CDS <1. .>301
/codon_start=2
/product="capsid protein"
/protein_id="AAM08304.1"
/db_xref="GI:19919497"
/translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:

Pred. No.:	330	Length:	301
Score:	95.00	Matches:	95
Percent Similarity:	95.96%	Conservative:	0
Best Local Similarity:	95.96%	Mismatches:	4
Query Match:	17.30%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AF466672 (1-301)

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Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db          5 GTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTTCTTGATTTCGCATTA 64

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAGCTTGAATTTAGAAACTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACC 124

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
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Db        125 AGCACAGCCCGTCACCGGCTGCGCCGTGGTGCTGATGGGACCGCTGAGCTCACCACCACA 184

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||    ||||||    ||||||||||||||||||
Db        185 GCAGCCACACGTTTCATGAAGGACTTGCATTTTACTGGCACCAACGGCGTCGGTGAGGTG 244

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
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Db        245 GGTCGCGGTATCGCTCTAACACTGTTCAATCTCGCTGATACGCTTCTCGGCGGTTTA 301
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RESULT 516
AF466673
LOCUS AF466673 301 bp RNA linear VRL 04-APR-2002
DEFINITION Swine hepatitis E virus strain 01-22171B1 capsid protein gene, partial cds.
ACCESSION AF466673
VERSION AF466673.1 GI:19919498
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 301)
AUTHORS Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G., Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
TITLE Detection by reverse transcription-PCR and genetic characterization of field isolates of swine hepatitis E virus from pigs in different geographic regions of the United States
JOURNAL J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
MEDLINE 21920873
PUBMED 11923352
REFERENCE 2 (bases 1 to 301)
AUTHORS Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S., Pierson,F., Toth,T. and Meng,X.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia Polytechnic Institute and State University, 1410 Prices Fork Road, Blacksburg, VA 24060, USA
FEATURES Location/Qualifiers
source 1. .301
/organism="Swine hepatitis E virus"
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/db_xref="taxon:63421"
CDS <1. .>301
/codon_start=2
/product="capsid protein"
/protein_id="AAM08305.1"
/db_xref="GI:19919499"
/translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
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Alignment Scores:
Pred. No.:              330           Length:         301
Score:                  95.00         Matches:        95
Percent Similarity:     95.96%        Conservative:   0
Best Local Similarity:  95.96%        Mismatches:     4
Query Match:            17.30%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF466673 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTCCTTGATTTCGCATTA 64

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAGCTTGAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACC 124

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
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Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
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Db        185 GCAGCCACACGTTTCATGAAGGACTTGCATTTTACTGGCACGAACGGCGTCGGTGAGGTG 244

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
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Db        245 GGTCGTGGTATCGCTCTAACACTGTTCAATCTCGCTGATACGCTTCTCGGTGGTTTA 301
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RESULT 517
AF466674
LOCUS AF466674 301 bp RNA linear VRL 04-APR-2002
DEFINITION Swine hepatitis E virus strain 01-19248-1 capsid protein gene, partial cds.
ACCESSION AF466674
VERSION AF466674.1 GI:19919500
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 301)
AUTHORS Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G., Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
TITLE Detection by reverse transcription-PCR and genetic characterization of field isolates of swine hepatitis E virus from pigs in different geographic regions of the United States
JOURNAL J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
MEDLINE 21920873
PUBMED 11923352
REFERENCE 2 (bases 1 to 301)
AUTHORS Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S., Pierson,F., Toth,T. and Meng,X.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia Polytechnic Institute and State University, 1410 Prices Fork Road, Blacksburg, VA 24060, USA
FEATURES Location/Qualifiers
source 1. .301
/organism="Swine hepatitis E virus"
/mol_type="genomic RNA"
/strain="01-19248-1"
/db_xref="taxon:63421"
CDS <1. .>301
/codon_start=2
/product="capsid protein"
/protein_id="AAM08306.1"
/db_xref="GI:19919501"
/translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

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Alignment Scores:
Pred. No.:              330           Length:         301
Score:                  95.00         Matches:        95
Percent Similarity:     95.96%        Conservative:   0
Best Local Similarity:  95.96%        Mismatches:     4
Query Match:            17.30%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF466674 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTTCTTGATTTCGCATTA 64
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Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
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Db         65 GAGCTTGAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACC 124

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AGCACAGCCCGTCACCGGCTGCGCCGTGGTGCTGATGGGACCGCTGAGCTCACCACCACA 184

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||
Db        185 GCAGCCACACGTTTCATGAAGGACTTGCATTTTACTGGCACGAACGGCGTCGGTGAGGTG 244

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
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Db        245 GGTCGTGGTATCGCTCTAACACTGTTCAATCTCGCTGATACGCTTCTCGGTGGTTTA 301

RESULT 518
AF466675
LOCUS       AF466675                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-16139-1 capsid protein gene,
            partial cds.
ACCESSION   AF466675
VERSION     AF466675.1  GI:19919502
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
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Alignment Scores:
Pred. No.:              330             Length:         301
Score:                  95.00           Matches:        95
Percent Similarity:     95.96%          Conservative:   0
Best Local Similarity:  95.96%          Mismatches:     4
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF466675 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTTCTTGATTTTGCATTA 64

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAGCTTGAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACC 124

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AGCACAGCCCGTCACCGGCTGCGCCGTGGTGCTGATGGGACCGCTGAGCTCACCACCACA 184

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||
Db        185 GCAGCCACACGTTTCATGAAGGACTTGCATTTTACTGGCACGAACGGCGTCGGTGAGGTG 244

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GGTCGTGGTATCGCTCTAACACTGTTCAATCTCGCTGATACGCTTCTCGGTGGTTTA 301

RESULT 519
AF466677
LOCUS       AF466677                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-12116-2 capsid protein gene,
            partial cds.
ACCESSION   AF466677
VERSION     AF466677.1  GI:19919506
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-12116-2"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08309.1"
                     /db_xref="GI:19919507"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              330             Length:         301
Score:                  95.00           Matches:        95
Percent Similarity:     95.96%          Conservative:   0
Best Local Similarity:  95.96%          Mismatches:     4
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF466677 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GTTAATTCCTATACTAACACACCTTATACTGGTGCATTGGGGCTCCTTGATTTTGCATTA 64

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         65 GAGCTTGAATTCAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTACACC 124

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACA 184

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||||    ||||||   ||||||||||||||||||
Db        185 GCAGCCACACGTTTCATGAAGGACTTGCATTTCACCGGCACGAACGGCGTTGGTGAGGTG 244

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GGTCGCGGTATAGCTCTAACACTGTTTAACCTTGCTGATACGCTTCTCGGTGGTTTA 301

RESULT 520
AF466678
LOCUS       AF466678                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain UMC13A capsid protein gene, partial
            cds.
ACCESSION   AF466678
VERSION     AF466678.1  GI:19919508
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="UMC13A"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08310.1"
                     /db_xref="GI:19919509"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              330             Length:         301
Score:                  95.00           Matches:        95
Percent Similarity:     95.96%          Conservative:   0
Best Local Similarity:  95.96%          Mismatches:     4
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF466678 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GTTAATTCCTATACTAATACACCCTATACTGGTGCGCTGGGGCTTCTTGACTTTGCACTA 64

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAGCTTGAATTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACC 124

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACTGCTGAACTTACCACCACA 184

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||||    ||||||   ||||||||||||||||||
Db        185 GCAGCCACACGTTTCATGAAGGATCTGCACTTCACTGGCACGAACGGCGTTGGTGAGGTG 244

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GGTCGTGGTATCGCCCTGACACTGTTCAATCTCGCTGATACGCTTCTCGGCGGTTTA 301

RESULT 521
AF466679
LOCUS       AF466679                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-22807-1 capsid protein gene,
            partial cds.
ACCESSION   AF466679
VERSION     AF466679.1  GI:19919510
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-22807-1"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08311.1"
                     /db_xref="GI:19919511"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              330             Length:         301
Score:                  95.00           Matches:        95
Percent Similarity:     95.96%          Conservative:   0
Best Local Similarity:  95.96%          Mismatches:     4
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF466679 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GTCAATTCTTATACTAATACACCTTACACCGGTGCACTGGGGCTTCTTGATTTTGCACTA 64

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAGCTTGAGTTCAGGAATCTGACACCCGGGAACACCAACACCCGTGTCTCCCGGTATACC 124
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Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACA 184

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||
Db        185 GCAGCCACACGTTTCATGAAGGACCTGCACTTCACTGGCACGAACGGAGTTGGTGAGGTG 244

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GGTCGTGGTATCGCCCTGACACTGTTCAATCTCGCTGACACGCTTCTCGGCGGTTTA 301

RESULT 522
AF466680
LOCUS       AF466680                 301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-22807-2 capsid protein gene,
            partial cds.
ACCESSION   AF466680
VERSION     AF466680.1  GI:19919512
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-22807-2"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08312.1"
                     /db_xref="GI:19919513"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:                330          Length:          301
Score:                    95.00        Matches:         95
Percent Similarity:       95.96%       Conservative:    0
Best Local Similarity:    95.96%       Mismatches:      4
Query Match:              17.30%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-15 (1-549) x AF466680 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GTCAATTCTTATACTAATACACCTTACACCGGTGCACTGGGGCTTCTTGATTTTGCACTA 64

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAGCTTGAGTTCAGGAATCTGACACCCGGGAACACCAACACCCGTGTCTCCCGGTATACC 124

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACA 184

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||
Db        185 GCAGCCACACGTTTCATGAAGGACCTGCACTTCACTGGCACGAACGGAGTTGGTGAGGTG 244

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GGTCGTGGTATCGCCCTGACACTGTTCAATCTCGCTGACACGCTTCTCGGCGGTTTA 301

RESULT 523
AF466681
LOCUS       AF466681                 301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-18934D2 capsid protein gene,
            partial cds.
ACCESSION   AF466681
VERSION     AF466681.1  GI:19919514
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-18934D2"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08313.1"
                     /db_xref="GI:19919515"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:                330          Length:          301
Score:                    95.00        Matches:         95
Percent Similarity:       95.96%       Conservative:    0
Best Local Similarity:    95.96%       Mismatches:      4
Query Match:              17.30%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-15 (1-549) x AF466681 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GTTAATTCCTATACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGATTTTGCACTA 64

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAGCTTGAATTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACC 124

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        125 AGCACAGCCCGCCATCGGCTGCGCCGCGGTGCTGATGGGACTGCTGAGCTTACTACCACA 184

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        185 GCAGCCACACGTTTCATGAAGGACCTGCATTTTACTGGCACGAACGGCGTTGGCGAGGTA 244

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GGTCGTGGTATCGCTCTCACACTGTTCAATCTTGCTGATACGCTTCTTGGCGGTTTA 301

RESULT 524
AF466682
LOCUS       AF466682                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-31692C1 capsid protein gene,
            partial cds.
ACCESSION   AF466682
VERSION     AF466682.1  GI:19919516
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-31692C1"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08314.1"
                     /db_xref="GI:19919517"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              330           Length:         301
Score:                  95.00         Matches:        95
Percent Similarity:     95.96%        Conservative:   0
Best Local Similarity:  95.96%        Mismatches:     4
Query Match:            17.30%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF466682 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GTCAATTCTTACACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGATTTCGCACTA 64

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAGCTTGAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCCGGTACACC 124

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACA 184

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        185 GCAGCCACACGTTTCATGAAGGATTTACACTTCACTGGCACGAACGGCGTTGGTGAGGTG 244

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GGTCGTGGTATCGCTCTGACACTGTTCAATCTTGCTGATACGCTTCTCGGTGGCTTA 301

RESULT 525
AF466683
LOCUS       AF466683                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-15555A capsid protein gene,
            partial cds.
ACCESSION   AF466683
VERSION     AF466683.1  GI:19919518
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-15555A"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08315.1"
                     /db_xref="GI:19919519"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              330           Length:         301
Score:                  95.00         Matches:        95
Percent Similarity:     95.96%        Conservative:   0
Best Local Similarity:  95.96%        Mismatches:     4
Query Match:            17.30%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF466683 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
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Db          5 GTTAATTCTTATACTAATACACCTTACACTGGTGCACTGGGGCTCCTTGACTTCGCACTA 64

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAGCTTGAATTTAGAAATTTGACACCCGGGAACACTAACACCCGCGTTTCCCGGTATACC 124

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTCACCACCACA 184
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Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
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Db        185 GCAGCCACACGTTTCATGAAGGATTTGCATTTCACTGGCACGAACGGTGTTGGTGAGGTG 244

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
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Db        245 GGCCGTGGTATCGCCCTGACACTATTTAATCTCGCTGATACGCTTCTCGGTGGCTTA 301

RESULT 526
AF466684
LOCUS       AF466684                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-15025-3 capsid protein gene,
            partial cds.
ACCESSION   AF466684
VERSION     AF466684.1  GI:19919520
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-15025-3"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08316.1"
                     /db_xref="GI:19919521"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              330             Length:         301
Score:                  95.00           Matches:        95
Percent Similarity:     95.96%          Conservative:   0
Best Local Similarity:  95.96%          Mismatches:     4
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF466684 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
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Db          5 GTTAATTCGTATACCAATACACCTTACACTGGTGCATTGGGGCTCCTTGATTTTGCATTA 64

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAGCTTGAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACC 124

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
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Db        125 AGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACA 184

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||  ||||||  ||||||||||||||||||
Db        185 GCAGCCACACGCTTTATGAAGGATTTGCATTTCACCGGCACGAATGGTGTTGGCGAGGTG 244

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GGTCGCGGTATCGCCCTGACACTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTA 301

RESULT 527
AF466685
LOCUS       AF466685                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-14185-1 capsid protein gene,
            partial cds.
ACCESSION   AF466685
VERSION     AF466685.1  GI:19919522
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-14185-1"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08317.1"
                     /db_xref="GI:19919523"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
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Alignment Scores:
Pred. No.:              330             Length:         301
Score:                  95.00           Matches:        95
Percent Similarity:     95.96%          Conservative:   0
Best Local Similarity:  95.96%          Mismatches:     4
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF466685 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GTTAATTCGTATACCAATACACCTTACACTGGTGCACTCGGGCTCCTTGATTTTGCACTA 64

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAGCTTGAGTTTAGAAATCTAACACCCGGGAACACCAACACCCGTGTTTCCCGGTACACC 124

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
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Db        125 AGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACA 184

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
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Db        185 GCAGCCACACGCTTTATGAAGGATTTACATTTCACCGGCACGAATGGTGTTGGCGAGGTG 244

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GGTCGCGGTATCGCCCTGACACTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTA 301

RESULT 528
AF195061
LOCUS       AF195061                 304 bp    RNA     linear   VRL 07-NOV-2000
DEFINITION  Hepatitis E virus strain VH1 putative capsid protein gene, partial
            cds.
ACCESSION   AF195061
VERSION     AF195061.1  GI:10802597
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Pina,S., Buti,M., Cotrina,M., Piella,J. and Girones,R.
  TITLE     HEV identified in serum from humans with acute hepatitis and in
            sewage of animal origin in Spain
  JOURNAL   J. Hepatol. 33 (5), 826-833 (2000)
  MEDLINE   20547280
   PUBMED   11097493
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Pina,S., Buti,M., Cotrina,M., Piella,J. and Girones,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-OCT-1999) Microbiology, Fac. Biologia, Diagonal Ave.
            645, Barcelona 08020, Spain
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="VH1"
                     /db_xref="taxon:12461"
                     /note="isolated from serum of an acute hepatitis patient"
     CDS             <1. .>304
                     /note="ORF2"
                     /codon_start=3
                     /product="putative capsid protein"
                     /protein_id="AAG23523.1"
                     /db_xref="GI:10802598"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              331           Length:         304
Score:                  95.00         Matches:        95
Percent Similarity:     95.96%        Conservative:   0
Best Local Similarity:  95.96%        Mismatches:     4
Query Match:            17.30%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF195061 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
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Db          6 GTTAATTCCTATACCAACACGCCCTATACCGGGGCGCTGGGGCTCCTCGACTTTGCACTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
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Db         66 GAGCTTGAATTTAGAAATTTGACCCCCGGGAACACTAACACCCGAGTGTCCCGTTACACT 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
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Db        126 AGCACAGCCCGACACCGTTTGCGCCGTGGTGCCGATGGTACTGCCGAGCTTACAACCACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
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Db        186 GCAGCCACACGTTTTATGAAGGACTTGCATTTCACCGGGACAAATGGTGTTGGCGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
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Db        246 GGCCGTGGTATAGCTTTAACGCTATTTAATCTTGCTGATACACTTCTCGGCGGGCTG 302

RESULT 529
AF195062
LOCUS       AF195062                 304 bp    RNA     linear   VRL 07-NOV-2000
DEFINITION  Hepatitis E virus strain VH2 putative capsid protein gene, partial
            cds.
ACCESSION   AF195062
VERSION     AF195062.1  GI:10802599
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Pina,S., Buti,M., Cotrina,M., Piella,J. and Girones,R.
  TITLE     HEV identified in serum from humans with acute hepatitis and in
            sewage of animal origin in Spain
  JOURNAL   J. Hepatol. 33 (5), 826-833 (2000)
  MEDLINE   20547280
   PUBMED   11097493
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Pina,S., Buti,M., Cotrina,M., Piella,J. and Girones,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-OCT-1999) Microbiology, Fac. Biologia, Diagonal Ave.
            645, Barcelona 08020, Spain
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="VH2"
                     /db_xref="taxon:12461"
                     /note="isolated from serum of an acute hepatitis patient"
     CDS             <1. .>304
                     /note="ORF2"
                     /codon_start=3
                     /product="putative capsid protein"
                     /protein_id="AAG23524.1"
                     /db_xref="GI:10802600"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              331           Length:         304
Score:                  95.00         Matches:        95
Percent Similarity:     95.96%        Conservative:   0
Best Local Similarity:  95.96%        Mismatches:     4
Query Match:            17.30%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF195062 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
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Db          6 GTTAATTCCTACACCAACACGCCCTATACTGGGGCATTAGGGCTCCTCGACTTTGCACTC 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
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Db         66 GAGCTTGAATTTAGAAATTTAACCCCTGGGAACACTAACACCCGTGTGTCCCGATACACT 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
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Db        126 AGTACAGCCCGGCACCGTTTGCGCCGTGGTGCCGATGGGACAGCCGAGCTTACAACTACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
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Db        186 GCAGCCACACGTTTTATGAAGGACTTGCACTTCACTGGGACAAATGGTGTTGGTGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
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Db        246 GGCCGTGGTATAGCCCTAACGCTATTTAATCTTGCTGATACACTTCTCGGCGGGCTG 302
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RESULT 530
AF296165
LOCUS       AF296165                 304 bp    RNA     linear   VRL 12-SEP-2001
DEFINITION  Hepatitis E virus strain TW12SW nucleocapsid protein gene, partial
            cds.
ACCESSION   AF296165
VERSION     AF296165.1  GI:15558953
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2000) Department of Medicine, Division of
            Gastroenterology, Taipei Veterans General Hospital, Institute of
            Clinical Medicine, National Yang-Ming University School of
            Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW12SW"
                     /db_xref="taxon:12461"
                     /note="from swine stool"
     CDS             <1. .>304
                     /codon_start=3
                     /product="nucleocapsid protein"
                     /protein_id="AAL02059.1"
                     /db_xref="GI:15558954"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              331             Length:         304
Score:                  95.00           Matches:        95
Percent Similarity:     95.96%          Conservative:   0
Best Local Similarity:  95.96%          Mismatches:     4
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF296165 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
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Db          6 GTTAATTCCTATACTAACACACCTTATACTGGCGCACTTGGACTTCTTGATTTTGCGCTG 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
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Db         66 GAGCTTGAATTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTTTCCCGATATACT 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGTACAGCCCGCCACCGGCTGCGCCGTGGTGCGGACGGGACTGCTGAGCTTACAACTACA 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        186 GCAGCCACGCGCTTCATGAAAGACCTGCATTTTACAGGCACGAATGGGGTCGGCGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
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Db        246 GGCCGCGGTATTGCTCTTACATTGTTCAATCTTGCTGACACTCTCCTTGGTGGGTTG 302

RESULT 531
AF296166
LOCUS       AF296166                 304 bp    RNA     linear   VRL 12-SEP-2001
DEFINITION  Hepatitis E virus strain TW13SW nucleocapsid protein gene, partial
            cds.
ACCESSION   AF296166
VERSION     AF296166.1  GI:15558955
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2000) Department of Medicine, Division of
            Gastroenterology, Taipei Veterans General Hospital, Institute of
            Clinical Medicine, National Yang-Ming University School of
            Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW13SW"
                     /db_xref="taxon:12461"
                     /note="from swine stool"
     CDS             <1. .>304
                     /codon_start=3
                     /product="nucleocapsid protein"
                     /protein_id="AAL02060.1"
                     /db_xref="GI:15558956"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
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Alignment Scores:
Pred. No.:              331             Length:         304
Score:                  95.00           Matches:        95
Percent Similarity:     95.96%          Conservative:   0
Best Local Similarity:  95.96%          Mismatches:     4
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF296166 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTTAATTCCTATACTAACACACCTTATACTGGCGCACTTGGACTTCTTGATTTTGCGCTG 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAATTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTCTCCCGATATACT 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGTACAGCCCGCCACCGACTGCGCCGTGGTGCAGACGGGACTGCTGAGCTTACAACCACA 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        186 GCAGCCACGCGCTTCATGAAAGACCTGCATTTTACAGGCACGAATGGGGTCGGCGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGCGGTATTGCTCTTACATTGTTCAATCTTGCTGACACTCTCCTTGGTGGGTTG 302

RESULT 532
AY032756
LOCUS       AY032756                 304 bp ss-RNA     linear   VRL 01-FEB-2002
DEFINITION  Swine hepatitis E virus isolate NLSW68 structural protein gene,
            partial cds.
ACCESSION   AY032756
VERSION     AY032756.1  GI:18476127
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
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           Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
           Hepevirus.
REFERENCE  1  (bases 1 to 304)
  AUTHORS  van der Poel,W.H.M., Verschoor,F. and van de Heide,R.
  TITLE    Hepatitis E virus sequences in swine in the Netherlands are closely
           related to human hepatitis E virus sequences
  JOURNAL  Unpublished
REFERENCE  2  (bases 1 to 304)
  AUTHORS  van der Poel,W.H.M., Verschoor,F., van de Heide,R. and de Roda
           Husman,A.M.
  TITLE    Direct Submission
  JOURNAL  Submitted (17-APR-2001) MGB, RIVM, Antonie v. Leeuwenhoeklaan 9,
           Bilthoven, Utrecht 3720 BA, Nederland
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW68"
                     /db_xref="taxon:63421"
     CDS             <1. .>304
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAK53068.1"
                     /db_xref="GI:18476128"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              331           Length:         304
Score:                  95.00         Matches:        95
Percent Similarity:     95.96%        Conservative:   0
Best Local Similarity:  95.96%        Mismatches:     4
Query Match:            17.30%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AY032756 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTTAATTCTTACACCAATACTCCCTATACTGGGGCGCTCGGGCTTCTTGATTTTGCTTTA 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTAGGAACCTTACACCCGGGAACACCAATACTCGTGTTTCCCGGTATACA 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGTACAGCCCGCCATCGGCTGCGTCGTGGTGCTGATGGCACCGCCGAGCTTACCACCACA 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||
Db        186 GCGGCCACGCGCTTCATGAAGGACCTGCACTTCACCGGTACGAATGGGGTCGGTGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGCATCGCCCTCACTCTCTTTAATCTTGCTGACACGCTTCTCGGTGGTTTG 302

RESULT 533
AY032757
LOCUS       AY032757                304 bp ss-RNA     linear   VRL 01-FEB-2002
DEFINITION  Swine hepatitis E virus isolate NLSW76 structural protein gene,
            partial cds.
ACCESSION   AY032757
VERSION     AY032757.1  GI:18476129
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   van der Poel,W.H.M., Verschoor,F. and van de Heide,R.
  TITLE     Hepatitis E virus sequences in swine in the Netherlands are closely
            related to human hepatitis E virus sequences
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van de Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-APR-2001) MGB, RIVM, Antonie v. Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Nederland
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW76"
                     /db_xref="taxon:63421"
     CDS             <1. .>304
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAK53069.1"
                     /db_xref="GI:18476130"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              331           Length:         304
Score:                  95.00         Matches:        95
Percent Similarity:     95.96%        Conservative:   0
Best Local Similarity:  95.96%        Mismatches:     4
Query Match:            17.30%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AY032757 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTTAATTCTTATACCAATACACCCTATACTGGGGCATTGGGGCTTCTTGACTTTGCTCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTAGAAATCTGACCCCTGGGAATACTAACACCCGTGTGTCCCGTTATACT 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGTACAGCCCGACACCGTTTGCGCCGTGGTGCCGACGGGACAGCCGAGCTTACAACCACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||
Db        186 GCAGCTACACGTTTTATGAAGGACTTGCATTTTACCGGGACAAATGGTGTTGGCGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGTATAGCCCTAACGCTATTTAATCTTGCTGATACACTTCTCGGCGGGCTG 302

RESULT 534
AY032758
LOCUS       AY032758                304 bp ss-RNA     linear   VRL 01-FEB-2002
DEFINITION  Swine hepatitis E virus isolate NLSW50 structural protein gene,
            partial cds.
ACCESSION   AY032758
VERSION     AY032758.1  GI:18476131
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   van der Poel,W.H.M., Verschoor,F. and van de Heide,R.
  TITLE     Hepatitis E virus sequences in swine in the Netherlands are closely
            related to human hepatitis E virus sequences
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van de Heide,R. and de Roda
            Husman,A.M.
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  TITLE     Direct Submission
  JOURNAL   Submitted (17-APR-2001) MGB, RIVM, Antonie v. Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Nederland
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW50"
                     /db_xref="taxon:63421"
     CDS             <1. .>304
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAK53070.1"
                     /db_xref="GI:18476132"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:                331             Length:         304
Score:                    95.00           Matches:        95
Percent Similarity:       95.96%          Conservative:   0
Best Local Similarity:    95.96%          Mismatches:     4
Query Match:              17.30%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AY032758 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTTAATTCTTATACCAATACACCCTATACTGGGGCATTGGGGCTTCTTGACTTTGCCCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTAGAAATCTGACCCCTGGCAATACTAACACCCGTGTGTCCCGTTATACT 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCACAGCCCGACACCGTTTGCGCCGTGGTGCCGATGGGACAGCCGAGCTTACAACCACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||    ||||||    ||||||||||||||||||||
Db        186 GCAGCCACACGTTTTATGAAGGACTTGCATTTTACCGGGACAAATGGTGTTGGCGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGTATAGCCCTAACGCTATTTAATCTTGCTGATACACTTCTCGGCGGGCTG 302

RESULT 535
AY032759
LOCUS       AY032759                304 bp ss-RNA     linear   VRL 01-FEB-2002
DEFINITION  Swine hepatitis E virus isolate NLSW91 structural protein gene,
            partial cds.
ACCESSION   AY032759
VERSION     AY032759.1  GI:18476133
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   van der Poel,W.H.M., Verschoor,F. and van de Heide,R.
  TITLE     Hepatitis E virus sequences in swine in the Netherlands are closely
            related to human hepatitis E virus sequences
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van de Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-APR-2001) MGB, RIVM, Antonie v. Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Nederland
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW91"
                     /db_xref="taxon:63421"
     CDS             <1. .>304
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAK53071.1"
                     /db_xref="GI:18476134"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:                331             Length:         304
Score:                    95.00           Matches:        95
Percent Similarity:       95.96%          Conservative:   0
Best Local Similarity:    95.96%          Mismatches:     4
Query Match:              17.30%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AY032759 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTTAACTCCTATACCAATACGCCCTATACCGGGGCGCTGGGGCTTCTTGACTTCGCACTC 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAATTTAGAAACTTGACCCCTGGGAACACCAACACCCGTGTGTCTCGCTACACT 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCACAGCCCGACACCGTTTGCGTCGTGGCGCCGATGGGACAGCCGAGCTCACAACCACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||    ||||||    ||||||||||||||||||||
Db        186 GCAGCCACACGTTTTATGAAGGATCTGCATTTCACTGGGACAAATGGTGTTGGCGAGGTA 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGTATAGCCTTAACGCTATTTAATCTTGCTGATACACTTCTCGGCGGGCTG 302

RESULT 536
AY362357
LOCUS       AY362357                304 bp    RNA     linear   VRL 05-AUG-2004
DEFINITION  Hepatitis E virus isolate UK 8734 capsid protein gene, partial cds.
ACCESSION   AY362357
VERSION     AY362357.1  GI:38224519
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Banks,M., Bendall,R.P., Grierson,S.S., Heath,G.S., Mitchell,J. and
            Dalton,H.
  TITLE     United Kingdom acquired hepatitis E is due to porcine strain of
            hepatitis E virus
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Banks,M., Bendall,R.P., Grierson,S.S., Heath,G.S., Mitchell,J. and
            Dalton,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-AUG-2003) Department of Virology, Veterinary
            Laboratories Agency, Woodham Lane, New Haw, Addlestone, Surrey KT15
            3NB, United Kingdom
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="UK 8734"
                     /isolation_source="human serum"
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                     /db_xref="taxon:12461"
                     /country="United Kingdom"
     CDS             <1. .>304
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAR14144.1"
                     /db_xref="GI:38224520"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              331           Length:         304
Score:                  95.00         Matches:        95
Percent Similarity:     95.96%        Conservative:   0
Best Local Similarity:  95.96%        Mismatches:     4
Query Match:            17.30%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AY362357 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTAAACTCTTATACTAATACGCCCTACACTGGAGCATTGGGCCTTCTTGACTTTGCACTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAATTTAGAAATTTGACCCCTGGGAACACTAACACCCGTGTCTCCCGGTACACT 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCACGGCTCGTCACCGCTTACGCCGTGGCGCTGATGGAACTGCTGAGCTTACGACCACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||
Db        186 GCGGCCACGCGTTTCATGAAGGACCTGCACTTCACTGGGACGAATGGCGTCGGTGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGCATAGCCCTAACTTTATTTAACCTTGCTGACACACTTCTCGGCGGCTTG 302

RESULT 537
AF324501
LOCUS       AF324501                299 bp    RNA     linear   VRL 26-AUG-2002
DEFINITION  Swine hepatitis E virus isolate IND-SW1 nucleocapsid protein gene,
            partial cds.
ACCESSION   AF324501
VERSION     AF324501.1  GI:22476826
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 299)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 299)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B.R. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-NOV-2000) Hepatitis Department, National Institute of
            Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune,
            Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .299
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW1"
                     /specific_host="swine"
                     /db_xref="taxon:63421"
                     /country="India"
     CDS             <1. .>299
                     /codon_start=1
                     /product="nucleocapsid protein"
                     /protein_id="AAM97324.1"
                     /db_xref="GI:22476827"
                     /translation="NTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRR
                     GADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPTELIS"

Alignment Scores:
Pred. No.:              334           Length:         299
Score:                  94.00         Matches:        94
Percent Similarity:     94.95%        Conservative:   0
Best Local Similarity:  94.95%        Mismatches:     5
Query Match:            17.12%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF324501 (1-299)

Qy        179 AsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArg 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATACACCCTACACCGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGT 60

Qy        199 AsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHis 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db         61 AACTTAACACCTGGCAATACGAACACTCGTGTGTCCCGTTACTCGAGCAGCGCGCGTCAT 120

Qy        219 ArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPhe 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGTTGCGCCGGGGGGCTGATGGTACTGCTGAGTTAACCACTACTGCTGCTACACGTTTT 180

Qy        239 MetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAla 258
              ||||||||||||  ||||||  ||||||||||||||||||  ||||||||||||||||
Db        181 ATGAAGGACCTCCACTTTACTGGGACCAATGGTGTTGGTGAAGTCGGTCGTGGTATAGCG 240

Qy        259 LeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGACCTTATTTAATCTTGCTGATACACTGCTCGGCGGCCTGCCGACAGAATTGATT 297

RESULT 538
AF324502
LOCUS       AF324502                299 bp    RNA     linear   VRL 26-AUG-2002
DEFINITION  Swine hepatitis E virus isolate IND-SW2 nucleocapsid protein gene,
            partial cds.
ACCESSION   AF324502
VERSION     AF324502.1  GI:22476828
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 299)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 299)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B.R. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-NOV-2000) Hepatitis Department, National Institute of
            Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune,
            Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .299
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW2"
                     /specific_host="swine"
                     /db_xref="taxon:63421"
                     /country="India"
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     CDS             <1. .>299
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                     /product="nucleocapsid protein"
                     /protein_id="AAM97325.1"
                     /db_xref="GI:22476829"
                     /translation="NTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRR
                     GADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPTELIS"

Alignment Scores:
Pred. No.:              334             Length:         299
Score:                  94.00           Matches:        94
Percent Similarity:     94.95%          Conservative:   0
Best Local Similarity:  94.95%          Mismatches:     5
Query Match:            17.12%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF324502 (1-299)

Qy        179 AsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArg 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATACACCTTACACCGGCGCCCTCGGTCTGCTCGATTTTGCGCTCGAACTCGAGTTTCGT 60

Qy        199 AsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHis 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db         61 AACTTAACACCTGGTAATACGAATACCCGTGTGTCCCGTTATTCGAGCAGTGCGCGTCAT 120

Qy        219 ArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPhe 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGCTGCGCCGAGGGGCTGATGGTACTGCTGAGTTAACCACTACTGCCGCTACACGCTTT 180

Qy        239 MetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAla 258
              ||||||||||||  ||||||  ||||||||||||||||||  ||||||||||||||||||
Db        181 ATGAAGGACCTTCACTTTACTGGGACCAACGGTGTTGGTGAAGTTGGCCGTGGTATAGCG 240

Qy        259 LeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGACCCTATTTAATCTTGCTGATACACTTCTCGGCGGGCTCCCGACAGAATTGATT 297

RESULT 539
AF324503
LOCUS       AF324503                299 bp    RNA     linear   VRL 26-AUG-2002
DEFINITION  Swine hepatitis E virus isolate IND-SW3 nucleocapsid protein gene,
            partial cds.
ACCESSION   AF324503
VERSION     AF324503.1  GI:22476830
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 299)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 299)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B.R. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-NOV-2000) Hepatitis Department, National Institute of
            Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune,
            Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .299
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW3"
                     /specific_host="swine"
                     /db_xref="taxon:63421"
                     /country="India"
     CDS             <1. .>299
                     /codon_start=1
                     /product="nucleocapsid protein"
                     /protein_id="AAM97326.1"
                     /db_xref="GI:22476831"
                     /translation="NTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRR
                     GADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPTELIS"

Alignment Scores:
Pred. No.:              334             Length:         299
Score:                  94.00           Matches:        94
Percent Similarity:     94.95%          Conservative:   0
Best Local Similarity:  94.95%          Mismatches:     5
Query Match:            17.12%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF324503 (1-299)

Qy        179 AsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArg 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATACACCTTACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGT 60

Qy        199 AsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHis 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db         61 AACTTAACACCTGGCAATACGAACACCCGTGTGTCCCGTTACTCGAGCAGCGCGCGTCAT 120

Qy        219 ArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPhe 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGTTGCGCCGGGGGGCTGATGGCACTGCTGAGTTAACCACTACTGCTGCTACACGTTTT 180

Qy        239 MetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAla 258
              ||||||||||||  ||||||  ||||||||||||||||||  ||||||||||||||||||
Db        181 ATGAAGGACCTCCATTTTACTGGGACCAACGGTGTTGGTGAAGTTGGTCGTGGTATAGCG 240

Qy        259 LeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGACCTTATTTAATCTTGCTGATACACTTCTCGGCGGGCTTCCGACAGAATTGATT 297

RESULT 540
AF466659
LOCUS       AF466659                300 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-21160-1 capsid protein gene,
            partial cds.
ACCESSION   AF466659
VERSION     AF466659.1  GI:19919470
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-21160-1"
                     /db_xref="taxon:63421"
     CDS             <1. .>300
                     /codon_start=1
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                     /product="capsid protein"
                     /protein_id="AAM08291.1"
                     /db_xref="GI:19919471"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNIRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:                334             Length:         300
Score:                    94.00           Matches:        94
Percent Similarity:       94.95%          Conservative:   0
Best Local Similarity:    94.95%          Mismatches:     5
Query Match:              17.12%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AF466659 (1-300)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GTTAATTCCTACACCAATACACCTTACACTGGTGCTCTGGGGCTTCTTGATTTTGCATTA 63

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db         64 GAGCTTGAATTCAGAAATTTGACACCTGGGAACACCAACATCCGTGTTTCCAGGTATACC 123

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACA 183

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        184 GCAGCCACACGTTTTATGAAGGATTTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTG 243

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 GGTCGTGGTATCGCTCTGACACTGTTTAACCTTGCTGATACGCTTCTCGGTGGTTTA 300

RESULT 541
AF466664
LOCUS       AF466664                300 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain UMC7B capsid protein gene, partial
            cds.
ACCESSION   AF466664
VERSION     AF466664.1  GI:19919480
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="UMC7B"
                     /db_xref="taxon:63421"
     CDS             <1. .>300
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM08296.1"
                     /db_xref="GI:19919481"
                     /translation="PVNSYTNTPYTAALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:                334             Length:         300
Score:                    94.00           Matches:        94
Percent Similarity:       94.95%          Conservative:   0
Best Local Similarity:    94.95%          Mismatches:     5
Query Match:              17.12%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AF466664 (1-300)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db          4 GTTAATTCCTATACTAATACACCTTACACTGCTGCACTGGGGCTCCTTGATTTTGCATTA 63

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GAGCTTGAGTTTAGAAATTTGACACCCGGGAACACTAATACCCGTGTTTCCCGGTATACC 123

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
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Db        124 AGCACAGCCCGCCACCGGCTGCGTCGCGGTGCTGATGGGACCGCTGAACTTACAACCACA 183

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              |||||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        184 GCAGCCACACGTTTCATGAAGGATCTGCATTTTACTGGTACGAACGGCGTTGGTGAGGTG 243

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 GGTCGTGGTATCGCTCTGACACTGTTTAATCTTGCTGATACGCTTCTTGGTGGTTTA 300

RESULT 542
AF466676
LOCUS       AF466676                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-9913 capsid protein gene, partial
            cds.
ACCESSION   AF466676
VERSION     AF466676.1  GI:19919504
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-9913"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08308.1"
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                     /db_xref="GI:19919505"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTWFNLADTLLGGL"

Alignment Scores:
Pred. No.:                334             Length:         301
Score:                    94.00           Matches:        94
Percent Similarity:       94.95%          Conservative:   0
Best Local Similarity:    94.95%          Mismatches:     5
Query Match:              17.12%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AF466676 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
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Db          5 GTTAACTCCTATACTAACACACCTTACACTGGTGCATTGGGGCTTCTTGATTTTGCATTA 64

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAGCTTGAATTTAGAAATTTGACACCCGGGAACACTAACACCCGCGTTTCCCGGTACACC 124

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACA 184

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||
Db        185 GCAGCCACACGTTTCATGAAGGACTTGCATTTCACTGGCACGAATGGCGTTGGTGAGGTG 244

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        245 GGTCGCGGTATAGCTCTAACATGGTTTAACCTTGCTGATACGCTTCTCGGTGGTTTA 301

RESULT 543
AF195063
LOCUS       AF195063                304 bp    RNA     linear   VRL 07-NOV-2000
DEFINITION  Hepatitis E virus strain E11 putative capsid protein gene, partial
            cds.
ACCESSION   AF195063
VERSION     AF195063.1  GI:10802601
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Pina,S., Buti,M., Cotrina,M., Piella,J. and Girones,R.
  TITLE     HEV identified in serum from humans with acute hepatitis and in
            sewage of animal origin in Spain
  JOURNAL   J. Hepatol. 33 (5), 826-833 (2000)
  MEDLINE   20547280
   PUBMED   11097493
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Pina,S., Buti,M., Cotrina,M., Piella,J. and Girones,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-OCT-1999) Microbiology, Fac. Biologia, Diagonal Ave.
            645, Barcelona 08020, Spain
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="E11"
                     /db_xref="taxon:12461"
                     /note="isolated from porcine slaughterhouse sewage"
     CDS             <1. .>304
                     /note="ORF2"
                     /codon_start=3
                     /product="putative capsid protein"
                     /protein_id="AAG23525.1"
                     /db_xref="GI:10802602"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGITLTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:                335             Length:         304
Score:                    94.00           Matches:        94
Percent Similarity:       94.95%          Conservative:   0
Best Local Similarity:    94.95%          Mismatches:     5
Query Match:              17.12%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AF195063 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTTAACTCTTATACCAACACGCCCTATACTGGGGCATTGGGGCTCCTCGACTTTGCACTC 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTCGAATTTAGAAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGTTACACT 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGTACAGCCCGGCACCGCCTGCGTCGTGGTGCCGATGGGACAGCTGAGCTTACAACCACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||
Db        186 GCAGCCACACGTTTTATGAAGGACTTGCATTTCACCGGGACAAATGGTGTTGGTGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGTCGTGGTATAACCCTAACGCTATTTAATCTTGCTGATACACTTCTCGGTGGGTTG 302

RESULT 544
AF296159
LOCUS       AF296159                304 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus strain TW1108E nucleocapsid protein gene, partial
            cds.
ACCESSION   AF296159
VERSION     AF296159.1  GI:22384853
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2000) Department of Medicine, Division of
            Gastroenterology, Taipei Veterans General Hospital, Institute of
            Clinical Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW1108E"
                     /db_xref="taxon:12461"
                     /note="from patient serum"
     CDS             <1. .>304
                     /codon_start=3
                     /product="nucleocapsid protein"
                     /protein_id="AAM96006.1"
                     /db_xref="GI:22384854"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:                335             Length:         304
Score:                    94.00           Matches:        94
Percent Similarity:       94.95%          Conservative:   0
Best Local Similarity:    94.95%          Mismatches:     5
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Query Match:            17.12%      Indels:        0
DB:                     1           Gaps:          0

US-09-769-066-15 (1-549) x AF296159 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
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Db          6 GTGAACTCCTATACCAATACACCTTATACTGGTGCCCTCGGCCTGCTCGACTTCGCGCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTCGTAATTTGACACCTGGTAATACAAACACGCGCGTTTCTCGTTATTCG 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||   |||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCAGTGCACGCCACAAATTGCGCCGAGGGGCCGACGGCACCGCTGAGCTAACTACTACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        186 GCTGCTACACGGTTTATGAAGGATCTTCATTTTACAGGGACTAATGGTGTTGGTGAGGTT 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGGATAGCGCTTACCTTGTTTAACCTTGCTGATACACTTCTCGGCGGGCTC 302

RESULT 545
AF296160
LOCUS       AF296160                304 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus strain TW261E nucleocapsid protein gene, partial
            cds.
ACCESSION   AF296160
VERSION     AF296160.1  GI:22384856
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2000) Department of Medicine, Division of
            Gastroenterology, Taipei Veterans General Hospital, Institute of
            Clinical Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW261E"
                     /db_xref="taxon:12461"
                     /note="from patient serum"
     CDS             <1. .>304
                     /codon_start=3
                     /product="nucleocapsid protein"
                     /protein_id="AAM96007.1"
                     /db_xref="GI:22384857"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              335           Length:        304
Score:                  94.00         Matches:       94
Percent Similarity:     94.95%        Conservative:  0
Best Local Similarity:  94.95%        Mismatches:    5
Query Match:            17.12%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AF296160 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTGAACTCCTATACCAATACACCTTATACTGGTGCTCTCGGCCTGCTCGACTTCGCGCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTCGTAATTTGACACCTGGTAATACAAACACGCGCGTTTCTCGTTATTCG 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||   |||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCAGTGCACGCCACAAATTGCGCCGAGGGGCCGACGGCACCGCTGAGCTAACTACTACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        186 GCTGCTACACGGTTTATGAAGGATCTTCATTTTACAGGGACTAATGGTGTTGGTGAGGTT 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGGATAGCGCTTACCTTGTTTAACCTTGCTGATACACTTCTCGGCGGGCTC 302

RESULT 546
AY052774
LOCUS       AY052774                304 bp    RNA     linear   VRL 01-SEP-2002
DEFINITION  Hepatitis E virus TW6345-1E nucleocapsid protein gene, partial cds.
ACCESSION   AY052774
VERSION     AY052774.1  GI:22651424
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   WU,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-AUG-2001) Department of Medicine, Institute of
            Clinical Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW6345-1E"
                     /db_xref="taxon:12461"
     CDS             <1. .>304
                     /codon_start=3
                     /product="nucleocapsid protein"
                     /protein_id="AAL14260.1"
                     /db_xref="GI:22651425"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              335           Length:        304
Score:                  94.00         Matches:       94
Percent Similarity:     94.95%        Conservative:  0
Best Local Similarity:  94.95%        Mismatches:    5
Query Match:            17.12%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AY052774 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTGAACTCCTATACCAATACACCTTATACTGGTGCCCTCGGCCTGCTCGACTTCGCGCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTCGTAATTTGACACCTGGTAATACAAACACGCGCGTTTCTCGTTATTCG 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||   |||||||||  ||||||||||||||||||||||||||||||||||||||||||||
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Db        126 AGCAGTGCACGCCACAAATTGCGCCGAGGGGCCGACGGCACCGCTGAGCTAACTACTACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||
Db        186 GCTGCTACACGGTTTATGAAGGATCTTCATTTTACAGGGACTAATGGTGTTGGTGAGGTT 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGGATAGCGCTTACCTTGTTTAACCTTGCTGATACACTTCTCGGCGGGCTC 302

RESULT 547
AY697426
LOCUS       AY697426                283 bp    DNA     linear   VRL 12-OCT-2004
DEFINITION  Hepatitis E virus isolate osh89-5 capsid protein gene, partial cds.
ACCESSION   AY697426
VERSION     AY697426.1  GI:53854289
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 283)
  AUTHORS   Lu,L., Drobeniuc,J., Kobylnikov,N., Usmanov,R.K., Robertson,B.H.,
            Favorov,M.O. and Margolis,H.S.
  TITLE     Complete sequence of a Kygyzstan swine hepatitis E virus (HEV)
            isolated from a piglet thought to be experimentally infected with
            human HEV
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 283)
  AUTHORS   Lu,L., Drobeniuc,J., Kobylnikov,N., Usmanov,R.K., Robertson,B.H.,
            Favorov,M.O. and Margolis,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-JUL-2004) Laboratory Branch, Division of Viral
            Hepatitis, National Center for Infectious Disease, Centers for
            Disease Control and Prevention, 1600 Clifton Road NE., MS A33,
            Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .283
                     /organism="Hepatitis E virus"
                     /mol_type="genomic DNA"
                     /isolate="osh89-5"
                     /isolation_source="Human fecal sample"
                     /db_xref="taxon:12461"
                     /country="Kyrgyzstan: 1989"
                     /note="genotype: I"
     CDS             <1. .>283
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAU95601.1"
                     /db_xref="GI:53854290"
                     /translation="TPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRG
                     ADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              337           Length:         283
Score:                  93.00         Matches:        93
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            16.94%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AY697426 (1-283)

Qy        180 ThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsn 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCTCTCGAACTTGAGTTCCGCAAC 62

Qy        200 LeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArg 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CTCACCCCCGGTAATACCAACACTCGGGTCTCCCGCTACTCCAGCACTGCTCGCCACCGT 122

Qy        220 LeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMet 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        123 CTCCGTCGTGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATG 182

Qy        240 LysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeu 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AAGGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTT 242

Qy        260 ThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||
Db        243 ACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTA 281

RESULT 548
AF324504
LOCUS       AF324504                299 bp    RNA     linear   VRL 26-AUG-2002
DEFINITION  Swine hepatitis E virus isolate IND-SW4 nucleocapsid protein gene,
            partial cds.
ACCESSION   AF324504
VERSION     AF324504.1  GI:22476832
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 299)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 299)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B.R. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-NOV-2000) Hepatitis Department, National Institute of
            Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune,
            Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .299
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW4"
                     /specific_host="swine"
                     /db_xref="taxon:63421"
                     /country="India"
     CDS             <1. .>299
                     /codon_start=1
                     /product="nucleocapsid protein"
                     /protein_id="AAM97327.1"
                     /db_xref="GI:22476833"
                     /translation="NTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRR
                     GADGTAELTTTAATRFMKDLHFTGTNGVGEVGCGIALTLFNLADTLLGGLPTELIS"

Alignment Scores:
Pred. No.:              338           Length:         299
Score:                  93.00         Matches:        93
Percent Similarity:     93.94%        Conservative:   0
Best Local Similarity:  93.94%        Mismatches:     6
Query Match:            16.94%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF324504 (1-299)

Qy        179 AsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArg 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATACACCTTACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGT 60

Qy        199 AsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHis 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACTTAACACCTGGCAATACGAACACCCGTGTGTCTCGTTACTCGAGCAGCGCGCGTCAT 120

Qy        219 ArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPhe 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGTTGCGCCGGGGGGCTGATGGCACTGCTGAGTTAACCACTACTGCTGCTACACGTTTT 180
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Qy        239 MetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAla 258
              ||||||||||||  ||||||  ||||||||||||||||||  |||  |||||||||
Db        181 ATGAAGGACCTCCATTTTACTGGGACCAACGGTGTTGGTGAAGTCGGTTGTGGTATAGCG 240

Qy        259 LeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGACCTTATTTAATCTTGCTGATACACTTCTCGGCGGGCTTCCGACAGAATTGATT 297

RESULT 549
HEE428852
LOCUS       HEE428852               300 bp    RNA     linear   VRL 12-JUL-2002
DEFINITION  Hepatitis E virus type 4 partial polyprotein gene for capsid
            protein, swine isolate SB2.
ACCESSION   AJ428852
VERSION     AJ428852.1  GI:18447771
KEYWORDS    capsid protein; polyprotein gene.
SOURCE      Hepatitis E virus type 4
  ORGANISM  Hepatitis E virus type 4
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Xia,N., Peng,G., Lan,H., Zhuang,H., Zhu,Y.,
            Li,S., Tian,K., Gu,W., Lin,J., Wu,X., Li,H. and Harrison,T.J.
  TITLE     Prevalence, isolation, and partial sequence analysis of hepatitis E
            virus from domestic animals in China
  JOURNAL   J. Med. Virol. 67 (4), 516-521 (2002)
  MEDLINE   22110701
   PUBMED   12115997
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2002) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Hepatitis E virus type 4"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="SB2"
                     /specific_host="Sus scrofa"
                     /db_xref="taxon:185580"
                     /country="China:Beijing"
     CDS             <1. .>300
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="CAD21788.1"
                     /db_xref="GI:18447772"
                     /db_xref="GOA:Q8UZ76"
                     /db_xref="UniProt/TrEMBL:Q8UZ76"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGG"

Alignment Scores:
Pred. No.:              338           Length:         300
Score:                  93.00         Matches:        93
Percent Similarity:     94.90%        Conservative:   0
Best Local Similarity:  94.90%        Mismatches:     5
Query Match:            16.94%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x HEE428852 (1-300)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTGAACTCTTATACCAATACACCCTATACCGGTGCCCTCGGCCTGCTCGACTTTGCGCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTCGTAATTTGACACCTGGCAATACGAATACGCGCGTCTCTCGCTACTCG 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||   |||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCAGTGCGCGCCACAAACTGCGCCGAGGGGCCGATGGTACTGCTGAGTTGACTACTACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        186 GCTGCTACACGGTTTATGAAGGACCTTCATTTTACAGGGACTAATGGTGTTGGTGAGGTT 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGly 271
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGGATTGCACTTACCTTGTTTAACCTTGCTGACACACTTCTCGGCGGG 299

RESULT 550
AF134812
LOCUS       AF134812                301 bp    RNA     linear   VRL 15-AUG-2002
DEFINITION  Hepatitis E virus capsid protein gene, partial cds.
ACCESSION   AF134812
VERSION     AF134812.1  GI:4530608
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Li,K., Zhuang,H. and Zhu,W.
  TITLE     Partial nucleotide sequencing of hepatitis E viruses detected in
            sera of patients with hepatitis E from 14 cities in China
  JOURNAL   Chin. Med. J. 115 (7), 1058-1063 (2002)
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Li,K., Zhuang,H. and Zhu,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAR-1999) Department of Microbiology, Beijing Medical
            University, 38 Xueyuan Road, Beijing 100083, P.R.China
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="HF-044"
                     /db_xref="taxon:12461"
                     /country="China"
     CDS             <1. .>301
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAD22115.1"
                     /db_xref="GI:4530609"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              339           Length:         301
Score:                  93.00         Matches:        93
Percent Similarity:     94.90%        Conservative:   0
Best Local Similarity:  94.90%        Mismatches:     5
Query Match:            16.94%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF134812 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTGAACTCCTACACTAATACACCCTACACTGGTGCCCTTGGCCTGCTCGATTTTGCGCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTCGCAATTTGACACCTGGTAATACAAACACGCGCGTCTCTCGTTATTCG 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||   |||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        126 AGTAGTGCGCGCCATAAACTGCGCCGAGGGGCTGACGGCACTGCTGAGCTGACTACCACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        186 GCTGCTACACGATTTATGAAGGATCTTCATTTTACAGGGACTAATGGCGTTGGTGAGGTT 245
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Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGly 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGCGGGATAGCGCTTACCCTGTTTAACCTTGCTGATACACTTCTCGGCGGG 299

RESULT 551
AF134917
LOCUS       AF134917                 301 bp ss-RNA     linear   VRL 15-AUG-2002
DEFINITION  Hepatitis E virus strain HF-054/China capsid protein gene, partial
            cds.
ACCESSION   AF134917
VERSION     AF134917.1  GI:4836760
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Li,K., Zhuang,H. and Zhu,W.
  TITLE     Partial nucleotide sequencing of hepatitis E viruses detected in
            sera of patients with hepatitis E from 14 cities in China
  JOURNAL   Chin. Med. J. 115 (7), 1058-1063 (2002)
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Li,K., Zhuang,H. and Zhu,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-1999) Department of Microbiology, Beijing Medical
            University, 38 Xueyuan Road, Beijing 100083, P.R.China
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="HF-054/China"
                     /db_xref="taxon:12461"
     CDS             <1. .>301
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAD30543.1"
                     /db_xref="GI:4836761"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              339          Length:         301
Score:                  93.00        Matches:        93
Percent Similarity:     94.90%       Conservative:   0
Best Local Similarity:  94.90%       Mismatches:     5
Query Match:            16.94%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AF134917 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTGAACTCCTACACCAATACACCCTATACCGGTGCTCTTGGCCTGCTCGATTTTGCGCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTCGTAATTTGACACCTGGCAATACGAATACGCGCGTCTCTCGTTACTCG 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||  |||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCAGTGCGCGCCACAAACTGCGTCGAGGGGCCGATGGTACCGCTGAGTTAACTACTACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||
Db        186 GCTGCTACACGGTTTATGAAGGACCTTCATTTTACAGGGACTAATGGCGTTGGCGAGGTT 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGly 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGGATAGCACTTACCTTGTTTAACCTTGCTGACACACTTCTCGGCGGG 299

RESULT 552
AY621101
LOCUS       AY621101                 302 bp    RNA     linear   VRL 27-JUN-2004
DEFINITION  Swine hepatitis E virus isolate swCH103 capsid protein gene,
            partial cds.
ACCESSION   AY621101
VERSION     AY621101.1  GI:49036124
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 302)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 302)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .302
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="swCH103"
                     /isolation_source="pig feces"
                     /db_xref="taxon:63421"
     CDS             <1. .>302
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT48735.1"
                     /db_xref="GI:49036125"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLA"

Alignment Scores:
Pred. No.:              339          Length:         302
Score:                  93.00        Matches:        93
Percent Similarity:     93.00%       Conservative:   0
Best Local Similarity:  93.00%       Mismatches:     7
Query Match:            16.94%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AY621101 (1-302)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||  ||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db          1 GTCATGTTTTGCATACATGGCTCACCTGTGAATTCTTACACTAATACACCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCCTACTTGATTTCGCACTTGAGCTTGAGTTCCGTAATTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||  |||||||||  ||||||||||||||||
Db        121 ACTAATACGCGTGTTTCTCGTTACTCGAGTAGCGCGCGACACAAATTGCGCCGAGGGGCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        181 GATGGTACTGCTGAGCTTACTACCACTGCTGCCACACGTTTTATGAAAGACCTTCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||  ||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db        241 ACGGGAACTAATGGTGTTGGCGAGGTCGGTCGTGGTATAGCGTTAACCCTGTTTAATCTT 300

RESULT 553
AY621102
LOCUS       AY621102                 302 bp    RNA     linear   VRL 27-JUN-2004
DEFINITION  Swine hepatitis E virus isolate swCH100 capsid protein gene,
            partial cds.
ACCESSION   AY621102
VERSION     AY621102.1  GI:49036126
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KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 302)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 302)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .302
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="swCH100"
                     /isolation_source="pig feces"
                     /db_xref="taxon:63421"
     CDS             <1. .>302
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT48736.1"
                     /db_xref="GI:49036127"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLA"

Alignment Scores:
Pred. No.:              339             Length:         302
Score:                  93.00           Matches:        93
Percent Similarity:     93.00%          Conservative:   0
Best Local Similarity:  93.00%          Mismatches:     7
Query Match:            16.94%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AY621102 (1-302)

Qy        165 ValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 GTCATGTTTTGCATACATGGCTCACCTGTGAATTCTTACACTAATACACCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCTCGGCCTACTTGATTTCGCACTTGAGCTTGAGTTCCGTAATTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||||||
Db        121 ACTAATACGCGTGTTTCTCGTTACTCGAGTAGCGCGCGACACAAATTGCGCCGAGGGGCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGTACTGCTGAGCTTACTACCACTGCTGCCACACGTTTTATGAAAGACCTTCACTTT 240

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||   ||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        241 ACGGGAACTAATGGTGTTGGCGAGGTCGGTCGTGGTATAGCGTTAACCCTGTTTAATCTT 300

RESULT 554
AF302068
LOCUS       AF302068                304 bp    mRNA    linear   VRL 02-DEC-2001
DEFINITION  Hepatitis E virus strain TW11SW capsid protein mRNA, partial cds.
ACCESSION   AF302068
VERSION     AF302068.1  GI:17224601
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.C.
  TITLE     Hepatitis E virus cross-species infection in human and swine
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-AUG-2000) Division of Gastroenterology, Taipei
            Veterans General Hospital & Institute of Clinical Medicine,
            National Yang-Ming University, 201 Shih-Pai Road, Sec. 2, Taipei
            112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="TW11SW"
                     /db_xref="taxon:12461"
                     /note="isolated from swine stool"
     CDS             <1. .>304
                     /note="ORF2"
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAL37038.1"
                     /db_xref="GI:17224602"
                     /translation="PVNSYTNTPYTGALGLLDSALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              339             Length:         304
Score:                  93.00           Matches:        93
Percent Similarity:     93.94%          Conservative:   0
Best Local Similarity:  93.94%          Mismatches:     6
Query Match:            16.94%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF302068 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          6 GTGAACTCCTATACCAATACACCTTATACCGGTGCCCTCGGCCTGCTCGACTCCGCGCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTCGTAATTTGACACCTGGTAATACAAACACGCGCGTTTCTCGTTATTCG 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||   |||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCAGTGCACGCCACAAATTGCGCCGAGGGGCCGACGGCACCGCTGAGCTAACTACTACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        186 GCTGCTACACGGTTTATGAAGGATCTTCATTTTACAGGGACTAATGGTGTTGGTGAGGTT 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGGATAGCGCTTACCTTGTTTAACCTTGCTGATACACTTCTCGGCGGGCTC 302

RESULT 555
HEE428853
LOCUS       HEE428853               300 bp    RNA     linear   VRL 12-JUL-2002
DEFINITION  Hepatitis E virus type 4 partial polyprotein gene for capsid
            protein, swine isolate G6.
ACCESSION   AJ428853
VERSION     AJ428853.1  GI:18447773
KEYWORDS    capsid protein; polyprotein gene.
SOURCE      Hepatitis E virus type 4
  ORGANISM  Hepatitis E virus type 4
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Xia,N., Peng,G., Lan,H., Zhuang,H., Zhu,Y.,
            Li,S., Tian,K., Gu,W., Lin,J., Wu,X., Li,H. and Harrison,T.J.
  TITLE     Prevalence, isolation, and partial sequence analysis of hepatitis E
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          virus from domestic animals in China
  JOURNAL   J. Med. Virol. 67 (4), 516-521 (2002)
  MEDLINE   22110701
   PUBMED   12115997
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2002) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Hepatitis E virus type 4"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="G6"
                     /specific_host="Sus scrofa"
                     /db_xref="taxon:185580"
                     /country="China:Beijing"
     CDS             <1. .>300
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="CAD21789.1"
                     /db_xref="GI:18447774"
                     /db_xref="GOA:Q8UZ75"
                     /db_xref="UniProt/TrEMBL:Q8UZ75"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGG"

Alignment Scores:
Pred. No.:                343           Length:         300
Score:                    92.00         Matches:        92
Percent Similarity:       93.88%        Conservative:   0
Best Local Similarity:    93.88%        Mismatches:     6
Query Match:              16.76%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x HEE428853 (1-300)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTGAATTCTTACACTAATACACCCTACACCGGTGCCCTCGGCTTACTTGATTTTGCACTC 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTCGAGTTCCGCAATTTAACACCTGGTAACACTAACACGCGCGTTTCTCGCTACTCG 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||   |||||||||   ||||||||||||   |||||||||||||||||||||||||||
Db        126 AGTAGCGCACGTCACAAATTGCGCCGAGGGCCTGATGGTACTGCTGAGTTAACTACTACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        186 GCTGCCACACGCTTTATGAAAGACCTCCATTTCACGGGGACTAATGGTGTTGGTGAGGTC 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGly 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGTCGTGGTATAGCGCTGACCTTGTTTAATCTTGCTGATACGCTTCTCGGCGGG 299

RESULT 556
HEE428854
LOCUS       HEE428854               300 bp    RNA     linear   VRL 12-JUL-2002
DEFINITION  Hepatitis E virus type 4 partial polyprotein gene for capsid
            protein, swine isolate G8.
ACCESSION   AJ428854
VERSION     AJ428854.1  GI:18447775
KEYWORDS    capsid protein; polyprotein gene.
SOURCE      Hepatitis E virus type 4
  ORGANISM  Hepatitis E virus type 4
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Xia,N., Peng,G., Lan,H., Zhuang,H., Zhu,Y.,
            Li,S., Tian,K., Gu,W., Lin,J., Wu,X., Li,H. and Harrison,T.J.
  TITLE     Prevalence, isolation, and partial sequence analysis of hepatitis E
            virus from domestic animals in China
  JOURNAL   J. Med. Virol. 67 (4), 516-521 (2002)
  MEDLINE   22110701
   PUBMED   12115997
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2002) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Hepatitis E virus type 4"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="G8"
                     /specific_host="Sus scrofa"
                     /db_xref="taxon:185580"
                     /country="China:Beijing"
     CDS             <1. .>300
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="CAD21790.1"
                     /db_xref="GI:18447776"
                     /db_xref="GOA:Q8UZ74"
                     /db_xref="UniProt/TrEMBL:Q8UZ74"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGG"

Alignment Scores:
Pred. No.:                343           Length:         300
Score:                    92.00         Matches:        92
Percent Similarity:       93.88%        Conservative:   0
Best Local Similarity:    93.88%        Mismatches:     6
Query Match:              16.76%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-15 (1-549) x HEE428854 (1-300)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTGAATTCCTATACTAATACACCTTATACCGGTGCCCTCGGCTTACTTGACTTTGCACTC 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTCGAGTTTCGCAATTTGACACCTGGTAACACCAATACGCGCGTTTCTCGTTATTCG 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||   |||||||||   ||||||||||||   |||||||||||||||||||||||||||
Db        126 AGTAGCGCGCGTCACAAACTGCGCCGAGGGCCTGATGGTACCGCTGAGTTGACTACTACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        186 GCTGCCACACGTTTTATGAAAGACCTCCATTTTACGGGGACTAATGGTGTTGGTGAGGTC 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGly 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGTCGTGGTATAGCGTTAACTTTGTTTAATCTTGCTGATACGCTTCTCGGTGGG 299

RESULT 557
HEE428855
LOCUS       HEE428855               300 bp    RNA     linear   VRL 12-JUL-2002
DEFINITION  Hepatitis E virus type 4 partial polyprotein gene for capsid
            protein, swine isolate SH1.
ACCESSION   AJ428855
VERSION     AJ428855.1  GI:18447777
KEYWORDS    capsid protein; polyprotein gene.
SOURCE      Hepatitis E virus type 4
  ORGANISM  Hepatitis E virus type 4
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
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REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Xia,N., Peng,G., Lan,H., Zhuang,H., Zhu,Y.,
            Li,S., Tian,K., Gu,W., Lin,J., Wu,X., Li,H. and Harrison,T.J.
  TITLE     Prevalence, isolation, and partial sequence analysis of hepatitis E
            virus from domestic animals in China
  JOURNAL   J. Med. Virol. 67 (4), 516-521 (2002)
  MEDLINE   22110701
   PUBMED   12115997
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2002) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Hepatitis E virus type 4"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="SH1"
                     /specific_host="Sus scrofa"
                     /db_xref="taxon:185580"
                     /country="China:Henan"
     CDS             <1. .>300
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="CAD21791.1"
                     /db_xref="GI:18447778"
                     /db_xref="GOA:Q8UZ73"
                     /db_xref="UniProt/TrEMBL:Q8UZ73"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGG"

Alignment Scores:
Pred. No.:                343             Length:         300
Score:                    92.00           Matches:        92
Percent Similarity:       93.88%          Conservative:   0
Best Local Similarity:    93.88%          Mismatches:     6
Query Match:              16.76%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x HEE428855 (1-300)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTAAATTCTTATACTAATACGCCTTATACTGGCGCTCTTGGCTTGCTTGACTTCGCGCTC 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTCCGTAATTTGACACCTGGCAACACGAATACTCGTGTATCTCGTTACTCG 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||   |||||||||   ||||||||||   ||||||||||||||||||||||||||||
Db        126 AGTAGCGCGCGCCACAAGTTACGCCGTGGGCCCGATGGCACTGCTGAATTGACTACTACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        186 GCTGCTACACGCTTTATGAAGGACCTTCATTTCACGGGGACTAATGGTGTTGGTGAGGTC 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGly 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGTCGTGGCATAGCGTTAACCCTGTTTAACCTTGCTGATACGCTTCTCGGTGGG 299

RESULT 558
AF103940
LOCUS       AF103940                301 bp ss-RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus capsid protein gene, partial cds.
ACCESSION   AF103940
VERSION     AF103940.1  GI:4324410
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Li,K., Zhuang,H., Wang,Y., Zhu,W., Tang,R., Bi,Y., Wei,Q., Liao,D.,
            Guo,Q., Wei,F. and Huang,Y.
  TITLE     A variant of hepatitis E virus isolated from a hepatitis E patient
            with negative anti-HEV
  JOURNAL   Zhonghua Wei Sheng Wu Xue He Mian Yi Xue Za Zhi 20 (2), 164-166
            (2000)
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Li,K., Zhuang,H. and Zhu,W.
  TITLE     Partial nucleotide sequencing of hepatitis E viruses detected in
            sera of patients with hepatitis E from 14 cities in China
  JOURNAL   Chin. Med. J. 115 (7), 1058-1063 (2002)
REFERENCE   3  (bases 1 to 301)
  AUTHORS   Li,K., Zhuang,H., Wang,Y., Zhu,W., Tang,R., Bi,Y., Wei,Q., Liao,D.,
            Guo,Q., Wei,F. and Huang,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-NOV-1998) Dept. of Microbiology, Beijing Medical
            University, 38 Xueyuan Road, Beijing, Beijing 100083, China
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="LZ-105/China"
                     /db_xref="taxon:12461"
                     /country="China"
     CDS             <1. .>301
                     /note="ORF2"
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAD16876.1"
                     /db_xref="GI:4324411"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:                343             Length:         301
Score:                    92.00           Matches:        92
Percent Similarity:       93.88%          Conservative:   0
Best Local Similarity:    93.88%          Mismatches:     6
Query Match:              16.76%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AF103940 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTAAATTCTTACACTAACACACCTTACACCGGCGCCCTCGGTCTGCTTGACTTCGCACTC 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTCGAGTTTCGCAATTTGACACCTGGTAACACGAACACGCGCGTCTCCCGTTATTCG 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||   |||||||||   ||||||||||   ||||||||||||||||||||||||||||
Db        126 AGTAGCGCGCGTCATAAGCTGCGCCGAGGGCCTGACGGCACTGCGGAGCTAACTACCACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        186 GCTGCTACACGTTTTATGAAAGATCTTCATTTCACTGGGACTAATGGTGTTGGTGAAGTT 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGly 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGTCGTGGTATAGCACTGACCCTGTTTAATCTTGCTGATACGCTTCTCGGCGGG 299

RESULT 559
AF134916
LOCUS       AF134916                301 bp ss-RNA     linear   VRL 15-AUG-2002
DEFINITION  Hepatitis E virus strain HF-030/China capsid protein gene, partial
            cds.
ACCESSION   AF134916
VERSION     AF134916.1  GI:4836758
KEYWORDS    .
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SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Li,K., Zhuang,H. and Zhu,W.
  TITLE     Partial nucleotide sequencing of hepatitis E viruses detected in
            sera of patients with hepatitis E from 14 cities in China
  JOURNAL   Chin. Med. J. 115 (7), 1058-1063 (2002)
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Li,K., Zhuang,H. and Zhu,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-1999) Department of Microbiology, Beijing Medical
            University, 38 Xueyuan Road, Beijing 100083, P.R.China
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="HF-030/China"
                     /db_xref="taxon:12461"
     CDS             <1. .>301
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAD30542.1"
                     /db_xref="GI:4836759"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGADGTAELTTTAATRFMKDLHLTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:                343             Length:         301
Score:                    92.00           Matches:        92
Percent Similarity:       93.88%          Conservative:   0
Best Local Similarity:    93.88%          Mismatches:     6
Query Match:              16.76%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AF134916 (1-301)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTGAACTCTTACACCAATACACCCTATACCGGTGCTCTTGGCCTGCTCGATTTTGCGCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTCGAGTTTCGTAATTTGACACCTGGTAATACGAATACGCGCGTCTCTCGTTATTCG 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||   |||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGTAGTGCGCGCCACAAACTGCGCCGAGGGGCCGACGGTACTGCTGAGTTAACTACTACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||   |||   ||||||||||||||||||||
Db        186 GCTGCTACACGGTTTATGAAGGACCTTCATTTGACAGGGACTAATGGCGTTGGTGAGGTT 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGly 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGGATAGCGCTTACCCTGTTTAACCTTGCTGACACACTTCTCGGCGGG 299

RESULT 560
AF296161
LOCUS       AF296161                304 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus strain TW2896E nucleocapsid protein gene, partial
            cds.
ACCESSION   AF296161
VERSION     AF296161.1  GI:22384859
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2000) Department of Medicine, Division of
            Gastroenterology, Taipei Veterans General Hospital, Institute of
            Clinical Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW2896E"
                     /db_xref="taxon:12461"
                     /note="from patient serum"
     CDS             <1. .>304
                     /codon_start=3
                     /product="nucleocapsid protein"
                     /protein_id="AAM96008.1"
                     /db_xref="GI:22384860"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGHGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:                343             Length:         304
Score:                    92.00           Matches:        92
Percent Similarity:       92.93%          Conservative:   0
Best Local Similarity:    92.93%          Mismatches:     7
Query Match:              16.76%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AF296161 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTAAATTCTTATACTAATACACCCTATACTGGTGCTCTCGGTCTGCTTGATTTTGCACTC 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAACTTGAGTTTCGCAATTTGACACCTGGCAATACAAACACGCGTGTCTCTCGTTACTCG 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||   |||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGTAGCGCGCGCCACAAGCTACGCCGAGGACCTGATGGTACAGCAGAGCTAACCACTACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        186 GCTGCTACACGCTTTATGAAGGATCTTCATTTCACCGGGACTAACGGTGTTGGTGAGGTT 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGTCATGGTATAGCATTAACCCTGTTTAATCTTGCTGATACGCTTCTCGGCGGGCTT 302

RESULT 561
AF296162
LOCUS       AF296162                304 bp    RNA     linear   VRL 12-SEP-2001
DEFINITION  Hepatitis E virus strain TW6345E nonfunctional nucleocapsid protein
            gene, partial sequence.
ACCESSION   AF296162
VERSION     AF296162.1  GI:15558948
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2000) Department of Medicine, Division of
            Gastroenterology, Taipei Veterans General Hospital, Institute of
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           Clinical Medicine, National Yang-Ming University School of
           Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW6345E"
                     /db_xref="taxon:12461"
                     /note="from Taiwanese patient serum"
     misc_feature    <1. .>304
                     /note="nonfunctional nucleocapsid protein due to mutation"

Alignment Scores:
Pred. No.:              343             Length:         304
Score:                  92.00           Matches:        92
Percent Similarity:     92.93%          Conservative:   0
Best Local Similarity:  92.93%          Mismatches:     7
Query Match:            16.76%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF296162 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTGAACTCCTATACCAATACACCTTATACTGGTGCCCTCGGCCTGCTCGACTTCGCGCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTCGTAATTTGACACCTGGTAATACAAACACGCGCGTTTCTCGTTATTCG 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||   |||||||||   ||||||   ||||||||||||||||||||||||||||||||
Db        126 AGCAGTGCACGCCACAAATTGCGCTGAGGGGCCGACGGCACCGCTGAGCTAACTACTACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||   |||       ||||||||||||||||||||
Db        186 GCTGCTACACGGTTTATGAAGGATCTTCATTTTGCAGGGACTAATGGTGTTGGTGAGGTT 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGGATAGCGCTTACCTTGTTTAACCTTGCTGATACACTTCTCGGCGGGCTC 302

RESULT 562
AF296164
LOCUS       AF296164                304 bp    RNA     linear   VRL 12-SEP-2001
DEFINITION  Hepatitis E virus strain TW5856E nucleocapsid protein gene, partial
            cds.
ACCESSION   AF296164
VERSION     AF296164.1  GI:15558951
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2000) Department of Medicine, Division of
            Gastroenterology, Taipei Veterans General Hospital, Institute of
            Clinical Medicine, National Yang-Ming University School of
            Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW5856E"
                     /db_xref="taxon:12461"
                     /note="from Taiwanese patient serum"
     CDS             <1. .>304
                     /codon_start=3
                     /product="nucleocapsid protein"
                     /protein_id="AAL02058.1"
                     /db_xref="GI:15558952"
                     /translation="PVNSYTNTPYTGALGPLDFALELEFRNLTPGNTSTRVSRYSSSA
                     RHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              343             Length:         304
Score:                  92.00           Matches:        92
Percent Similarity:     92.93%          Conservative:   0
Best Local Similarity:  92.93%          Mismatches:     7
Query Match:            16.76%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF296164 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTGAACTCCTATACCAATACACCTTATACTGGTGCCCTCGGCCCGCTCGACTTCGCGCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTCGTAATTTGACACCTGGTAATACAAGCACGCGCGTTTCTCGTTATTCG 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||   |||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCAGTGCACGCCACAAATTGCGCCGAGGGGCCGACGGCACCGCTGAGCTAACTACTACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        186 GCTGCTACACGGTTTATGAAGGATCTTCATTTTACAGGGACTAATGGTGTTGGTGAGGTT 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGGATAGCGCTTACCTTGTTTAACCTTGCTGATACACTTCTCGGCGGGCTC 302

RESULT 563
AF296167
LOCUS       AF296167                304 bp    RNA     linear   VRL 12-SEP-2001
DEFINITION  Hepatitis E virus strain TW3SW nucleocapsid protein gene, partial
            cds.
ACCESSION   AF296167
VERSION     AF296167.1  GI:15558957
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2000) Department of Medicine, Division of
            Gastroenterology, Taipei Veterans General Hospital, Institute of
            Clinical Medicine, National Yang-Ming University School of
            Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW3SW"
                     /db_xref="taxon:12461"
                     /note="from 3 month old swine serum"
     CDS             <1. .>304
                     /codon_start=3
                     /product="nucleocapsid protein"
                     /protein_id="AAL02061.1"
                     /db_xref="GI:15558958"
                     /translation="PVNSYTNTPHNGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
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RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAYTLLGGLS"

Alignment Scores:

Pred. No.:	343	Length:	304
Score:	92.00	Matches:	92
Percent Similarity:	92.93%	Conservative:	0
Best Local Similarity:	92.93%	Mismatches:	7
Query Match:	16.76%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x AF296167 (1-304)

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Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||      ||||||||||||||||||||||||||||||
Db          6 GTTAATTCTTATACTAACACACCTCATAATGGCGCACTTGGACTTCTTGATTTTGCGCTG 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAATTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTTTCCCGATATACT 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGTACAGCCCGCCACCGACTGCGCCGTGGTGCAGACGGGACTGCTGAGCTTACAACTACA 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||  ||||||   ||||||||||||||||||||||
Db        186 GCAGCCACGCGCTTCATGAAAGACCTGCATTTTACAGGCACGAATGGGGTCGGCGAGGTG 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        246 GGCCGCGGTATTGCTCTTACATTGTTCAATCTTGCTTACACTCTCCTTGGTGGGTTG 302
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RESULT 564
HEE428856

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LOCUS       HEE428856                300 bp    RNA     linear   VRL 12-JUL-2002
DEFINITION  Hepatitis E virus type 4 partial polyprotein gene for capsid
            protein, swine isolate SJ14.
ACCESSION   AJ428856
VERSION     AJ428856.1  GI:18447779
KEYWORDS    capsid protein; polyprotein gene.
SOURCE      Hepatitis E virus type 4
  ORGANISM  Hepatitis E virus type 4
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Xia,N., Peng,G., Lan,H., Zhuang,H., Zhu,Y.,
            Li,S., Tian,K., Gu,W., Lin,J., Wu,X., Li,H. and Harrison,T.J.
  TITLE     Prevalence, isolation, and partial sequence analysis of hepatitis E
            virus from domestic animals in China
  JOURNAL   J. Med. Virol. 67 (4), 516-521 (2002)
  MEDLINE   22110701
   PUBMED   12115997
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2002) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Hepatitis E virus type 4"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="SJ14"
                     /specific_host="Sus scrofa"
                     /db_xref="taxon:185580"
                     /country="China:Zhejiang"
     CDS             <1. .>300
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="CAD21792.1"
                     /db_xref="GI:18447780"
                     /db_xref="GOA:Q8UZ72"
                     /db_xref="UniProt/TrEMBL:Q8UZ72"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
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Alignment Scores:

Pred. No.:	347	Length:	300
Score:	91.00	Matches:	91
Percent Similarity:	92.86%	Conservative:	0
Best Local Similarity:	92.86%	Mismatches:	7
Query Match:	16.58%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-15 (1-549) x HEE428856 (1-300)

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Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTAAATTCTTACACTAATACACCTTACACTGGCGCCCTCGGCCTGCTTGACTTTGCACTC 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTCGAGTTCCGCAACCTGACACCTGGTAATACGAACACGCGTGTCTCCCGTTATTCG 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||   |||||||||   ||||||||||||   ||||||||||||||||||||||||||
Db        126 AGTAGCGCGCGTCACAAGTTACGCCGAGGGCCTGACGGCACTGCGGAGCTAACTACTACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||  ||||||   |||  ||||||||||||
Db        186 GCTGCTACACGTTTCATGAAAGATCTTCATTTTACTGGGACTGATGGTGTTGGTGAAGTT 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGly 271
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GGCCGTGGTATAGCATTGACCTTGTTTAATCTTGCTGATACACTTCTCGGCGGG 299
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RESULT 565
AF296163

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LOCUS       AF296163                 304 bp    RNA     linear   VRL 12-SEP-2001
DEFINITION  Hepatitis E virus strain TW7924E nucleocapsid protein gene, partial
            cds.
ACCESSION   AF296163
VERSION     AF296163.1  GI:15558949
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2000) Department of Medicine, Division of
            Gastroenterology, Taipei Veterans General Hospital, Institute of
            Clinical Medicine, National Yang-Ming University School of
            Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW7924E"
                     /db_xref="taxon:12461"
                     /note="from Thai human"
     CDS             <1. .>304
                     /codon_start=3
                     /product="nucleocapsid protein"
                     /protein_id="AAL02057.1"
                     /db_xref="GI:15558950"
                     /translation="PVNSYTNTPYTSALGLLDFALELEFRNLTPGNTNTRVSCYSSSA
                     RHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVARGIALTLFNLADTLLGGLP"
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Alignment Scores:

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Pred. No.:              347          Length:        304
Score:                  91.00        Matches:       91
Percent Similarity:     91.92%       Conservative:  0
Best Local Similarity:  91.92%       Mismatches:    8
Query Match:            16.58%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AF296163 (1-304)

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db          6 GTGAACTCCTATACCAATACACCTTATACTAGTGCCCTCGGCCTGCTCGACTTCGCGCTT 65

Qy        194 GluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GAGCTTGAGTTTCGTAATTTGACACCTGGTAATACAAACACGCGCGTTTCTTGTTATTCG 125

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||   |||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        126 AGCAGTGCACGCCACAAATTGCGCCGAGGGGCCGACGGCACCGCTGAGCTAACTACTACT 185

Qy        234 AlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGlyValGlyGluIle 253
              ||||||||||||||||||||||||||   ||||||   ||||||||||||||||||||
Db        186 GCTGCTACACGGTTTATGAAGGATCTTCATTTTACAGGGACTAATGGTGTTGGTGAGGTT 245

Qy        254 GlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GCCCGTGGGATAGCGCTTACCTTGTTCAACCTTGCTGATACACTTCTCGGCGGGCTC 302

RESULT 566
AY697428
LOCUS       AY697428                 266 bp    DNA     linear   VRL 12-OCT-2004
DEFINITION  Hepatitis E virus isolate osh89-4 capsid protein gene, partial cds.
ACCESSION   AY697428
VERSION     AY697428.1  GI:53854293
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 266)
  AUTHORS   Lu,L., Drobeniuc,J., Kobylnikov,N., Usmanov,R.K., Robertson,B.H.,
            Favorov,M.O. and Margolis,H.S.
  TITLE     Complete sequence of a Kygyzstan swine hepatitis E virus (HEV)
            isolated from a piglet thought to be experimentally infected with
            human HEV
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 266)
  AUTHORS   Lu,L., Drobeniuc,J., Kobylnikov,N., Usmanov,R.K., Robertson,B.H.,
            Favorov,M.O. and Margolis,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-JUL-2004) Laboratory Branch, Division of Viral
            Hepatitis, National Center for Infectious Disease, Centers for
            Disease Control and Prevention, 1600 Clifton Road NE., MS A33,
            Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .266
                     /organism="Hepatitis E virus"
                     /mol_type="genomic DNA"
                     /isolate="osh89-4"
                     /isolation_source="Human fecal sample"
                     /db_xref="taxon:12461"
                     /country="Kyrgyzstan: 1989"
                     /note="genotype: I"
     CDS             <1. .>266
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAU95603.1"
                     /db_xref="GI:53854294"
                     /translation="ALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTA
                     ELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGL"

Alignment Scores:
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Pred. No.:              357          Length:        266
Score:                  88.00        Matches:       88
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0
Query Match:            16.03%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AY697428 (1-266)

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCCTCGGGCTGCTGGACTTTGCTCTCGAACTTGAGTTCCGCAACCTCACCCCCGGTAAT 61

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ACCAACACTCGGGTCTCCCGCTACTCCAGCACTGCTCGCCACCGTCTCCGTCGTGGTGCG 121

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GATGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAGGATCTCTATTTT 181

Qy        245 ThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 ACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTTACCCTGTTCAACCTT 241

Qy        265 AlaAspThrLeuLeuGlyGlyLeu 272
              |||||||||||||||||||||||||
Db        242 GCTGACACTCTGCTTGGCGGCCTA 265

RESULT 567
AY697427
LOCUS       AY697427                 265 bp    DNA     linear   VRL 12-OCT-2004
DEFINITION  Hepatitis E virus isolate osh89-3 capsid protein gene, partial cds.
ACCESSION   AY697427
VERSION     AY697427.1  GI:53854291
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 265)
  AUTHORS   Lu,L., Drobeniuc,J., Kobylnikov,N., Usmanov,R.K., Robertson,B.H.,
            Favorov,M.O. and Margolis,H.S.
  TITLE     Complete sequence of a Kygyzstan swine hepatitis E virus (HEV)
            isolated from a piglet thought to be experimentally infected with
            human HEV
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 265)
  AUTHORS   Lu,L., Drobeniuc,J., Kobylnikov,N., Usmanov,R.K., Robertson,B.H.,
            Favorov,M.O. and Margolis,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-JUL-2004) Laboratory Branch, Division of Viral
            Hepatitis, National Center for Infectious Disease, Centers for
            Disease Control and Prevention, 1600 Clifton Road NE., MS A33,
            Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .265
                     /organism="Hepatitis E virus"
                     /mol_type="genomic DNA"
                     /isolate="osh89-3"
                     /isolation_source="Human fecal sample"
                     /db_xref="taxon:12461"
                     /country="Kyrgyzstan: 1989"
                     /note="genotype: I"
     CDS             <1. .>265
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAU95602.1"
                     /db_xref="GI:53854292"
                     /translation="LGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAE
                     LTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
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Pred. No.:              361          Length:        265
Score:                  87.00        Matches:       87
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0
Query Match:            15.85%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AY697427 (1-265)

Qy        186 LeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThr 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CTCGGGCTGCTGGACTTTGCTCTCGAACTTGAGTTCCGCAACCTCACCCCCGGTAATACC 62

Qy        206 AsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAsp 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 AACACTCGGGTCTCCCGCTACTCCAGCACTGCTCGCCACCGTCTCCGTCGTGGTGCGGAT 122

Qy        226 GlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThr 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAGGATCTCTATTTTACT 182

Qy        246 SerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAla 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTTACCCTGTTCAACCTTGCT 242

Qy        266 AspThrLeuLeuGlyGlyLeu 272
              |||||||||||||||||||||
Db        243 GACACTCTGCTTGGCGGCCTA 263

RESULT 568
AF228533
LOCUS       AF228533                 255 bp    RNA     linear   VRL 02-FEB-2001
DEFINITION  Hepatitis E virus isolate 93-Dji 42031 structural protein gene,
            partial cds.
ACCESSION   AF228533
VERSION     AF228533.1  GI:12656044
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 255)
  AUTHORS   van Cuyck,H. and Viret,J.
  TITLE     Introduction for a modelization of Hepatitis E virus (HEV)
            evolution
  JOURNAL   Acta Biotheor. (2000) In press
REFERENCE   2  (bases 1 to 255)
  AUTHORS   Buisson,Y., Grandadam,M., Tsarev,S. and Masseron,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Transmissible Agents, CRSSA, 24 Ave des
            Maquis du Gresivaudan, BP87, La Tronche 38702, France
FEATURES             Location/Qualifiers
     source          1. .255
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="93-Dji 42031"
                     /db_xref="taxon:12461"
                     /country="Djibouti"
                     /note="isolated from sporadic case in 1993"
     CDS             <1. .>255
                     /note="ORF2"
                     /codon_start=1
                     /product="structural protein"
                     /protein_id="AAK00718.1"
                     /db_xref="GI:12656045"
                     /translation="FWEAGTTKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGA
                     GPVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECR"

Alignment Scores:
Pred. No.:              374          Length:        255
Score:                  84.00        Matches:       84
Percent Similarity:     98.82%       Conservative:  0
Best Local Similarity:  98.82%       Mismatches:    1
Query Match:            15.30%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AF228533 (1-255)

Qy        436 PheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSer 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTCTGGGAGGCGGGTACTACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGC 60

Qy        456 AspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThr 475
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACCAATTGCTCATCGAGAATGCCGCCGGACATCGGGTGGCTATTTCCACCTATACCACT 120

Qy        476 SerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAla 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCCTAGGTGCTGGCCCTGTTTCCATCTCCGCGGTCGCTGTTCTAGCCCCCCACTCTGCT 180

Qy        496 LeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPhe 515
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTAGCACTGCTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTC 240

Qy        516 CysProGluCysArg 520
              ||||||||||||||
Db        241 TGCCCGGAGTGCCGT 255

RESULT 569
AF228529
LOCUS       AF228529                 256 bp    RNA     linear   VRL 02-FEB-2001
DEFINITION  Hepatitis E virus isolate 93-Som structural protein gene, partial
            cds.
ACCESSION   AF228529
VERSION     AF228529.1  GI:12656036
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 256)
  AUTHORS   van Cuyck,H. and Viret,J.
  TITLE     Introduction for a modelization of Hepatitis E virus (HEV)
            evolution
  JOURNAL   Acta Biotheor. (2000) In press
REFERENCE   2  (bases 1 to 256)
  AUTHORS   Masseron,T., Buisson,Y., Grandadam,M. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Transmissible Agents, CRSSA, 24 Ave des
            Maquis du Gresivaudan, BP87, La Tronche 38702, France
FEATURES             Location/Qualifiers
     source          1. .256
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="93-Som"
                     /db_xref="taxon:12461"
     CDS             <1. .>256
                     /note="ORF2"
                     /codon_start=1
                     /product="structural protein"
                     /protein_id="AAK00714.1"
                     /db_xref="GI:12656037"
                     /translation="FWEAGTTKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGA
                     GPVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECR"

Alignment Scores:
Pred. No.:              374          Length:        256
Score:                  84.00        Matches:       84
Percent Similarity:     98.82%       Conservative:  0
Best Local Similarity:  98.82%       Mismatches:    1
Query Match:            15.30%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AF228529 (1-256)
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Qy        436 PheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSer 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTTTGGGAGGCGGGTACTACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGT 60

Qy        456 AspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThr 475
              |||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACCAATTGCTCATCGAGAATGCCGCCGGACATCGGGTGGCTATTTCCACCTATACCACT 120

Qy        476 SerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAla 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCCTAGGTGCTGGCCCTGTCTCCATCTCCGCGGTCGCTGTTCTAGCCCCCCACTCTGCT 180

Qy        496 LeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPhe 515
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTAGCGCTGCTTGAGGACACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTC 240

Qy        516 CysProGluCysArg 520
              ||||||||||||||||
Db        241 TGCCCGGAGTGCCGC 255

RESULT 570
AF228530
LOCUS       AF228530                256 bp    RNA     linear   VRL 02-FEB-2001
DEFINITION  Hepatitis E virus isolate 95-Alg Tan 11 structural protein gene,
            partial cds.
ACCESSION   AF228530
VERSION     AF228530.1  GI:12656038
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 256)
  AUTHORS   van Cuyck,H. and Viret,J.
  TITLE     Introduction for a modelization of Hepatitis E virus (HEV)
            evolution
  JOURNAL   Acta Biotheor. (2000) In press
REFERENCE   2  (bases 1 to 256)
  AUTHORS   Larouze,B., Buisson,Y., Grandadam,M., Nicand,E. and Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Transmissible Agents, CRSSA, 24 Ave des
            Maquis du Gresivaudan, BP87, La Tronche 38702, France
FEATURES             Location/Qualifiers
     source          1. .256
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="95-Alg Tan 11"
                     /db_xref="taxon:12461"
                     /country="Algeria: Tanedfou"
                     /note="isolated from 1995 epidemic outbreak case"
     CDS             <1. .>256
                     /note="ORF2"
                     /codon_start=1
                     /product="structural protein"
                     /protein_id="AAK00715.1"
                     /db_xref="GI:12656039"
                     /translation="FWEAGTTKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGA
                     GPVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECR"

Alignment Scores:
Pred. No.:              374           Length:         256
Score:                  84.00         Matches:        84
Percent Similarity:     98.82%        Conservative:   0
Best Local Similarity:  98.82%        Mismatches:     1
Query Match:            15.30%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF228530 (1-256)

Qy        436 PheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSer 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTCTGGGAGGCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGC 60

Qy        456 AspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThr 475
              |||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACCAATTGCTTATTGAGAACGCCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACT 120

Qy        476 SerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAla 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCCTAGGTGCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCATTCTGCT 180

Qy        496 LeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPhe 515
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTAGCACTGCTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTC 240

Qy        516 CysProGluCysArg 520
              ||||||||||||||||
Db        241 TGTCCGGAGTGCCGT 255

RESULT 571
AF228534
LOCUS       AF228534                256 bp    RNA     linear   VRL 02-FEB-2001
DEFINITION  Hepatitis E virus isolate 95-Dji 26-3 93393 structural protein
            gene, partial cds.
ACCESSION   AF228534
VERSION     AF228534.1  GI:12656046
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 256)
  AUTHORS   van Cuyck,H. and Viret,J.
  TITLE     Introduction for a modelization of Hepatitis E virus (HEV)
            evolution
  JOURNAL   Acta Biotheor. (2000) In press
REFERENCE   2  (bases 1 to 256)
  AUTHORS   Masseron,T., Buisson,Y., Grandadam,M. and Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Transmissible Agents, CRSSA, 24 Ave des
            Maquis du Gresivaudan, BP87, La Tronche 38702, France
FEATURES             Location/Qualifiers
     source          1. .256
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="95-Dji 26-3 93393"
                     /db_xref="taxon:12461"
                     /country="Djibouti"
                     /note="isolated from sporadic case in 1995; Djibouti
                     resident"
     CDS             <1. .>256
                     /note="ORF2"
                     /codon_start=1
                     /product="structural protein"
                     /protein_id="AAK00719.1"
                     /db_xref="GI:12656047"
                     /translation="FWEAGTTKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGA
                     GPVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECR"

Alignment Scores:
Pred. No.:              374           Length:         256
Score:                  84.00         Matches:        84
Percent Similarity:     98.82%        Conservative:   0
Best Local Similarity:  98.82%        Mismatches:     1
Query Match:            15.30%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF228534 (1-256)

Qy        436 PheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSer 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTCTGGGAGGCGGGTACTACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGT 60
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Qy        456 AspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThr 475
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACCAATTGCTCATTGAGAATGCCGCCGGACATCGGGTGGCTATTTCCACCTATACCACT 120

Qy        476 SerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAla 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCCTAGGTGCTGGCCCTGTTTCCATCTCCGCGGTCGCTGTTTTAGCCCCCCACTCTGCT 180

Qy        496 LeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPhe 515
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTAGCACTGCTTGAGGATACCCTGGATTACCCTGCCCGCGCTCACACTTTCGATGATTTC 240

Qy        516 CysProGluCysArg 520
              ||||||||||||||||
Db        241 TGCCCGGAGTGCCGC 255
```

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RESULT 572
AF228535
LOCUS       AF228535                256 bp    RNA     linear   VRL 02-FEB-2001
DEFINITION  Hepatitis E virus isolate 96-Dji 28-1 99402 structural protein
            gene, partial cds.
ACCESSION   AF228535
VERSION     AF228535.1  GI:12656048
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 256)
  AUTHORS   van Cuyck,H. and Viret,J.
  TITLE     Introduction for a modelization of Hepatitis E virus (HEV)
            evolution
  JOURNAL   Acta Biotheor. (2000) In press
REFERENCE   2  (bases 1 to 256)
  AUTHORS   Masseron,T., Buisson,Y., Grandadam,M. and Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Transmissible Agents, CRSSA, 24 Ave des
            Maquis du Gresivaudan, BP87, La Tronche 38702, France
FEATURES             Location/Qualifiers
     source          1. .256
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="96-Dji 28-1 99402"
                     /db_xref="taxon:12461"
                     /country="Djibouti"
                     /note="isolated from sporadic case in 1996; French
                     soldier"
     CDS             <1. .>256
                     /note="ORF2"
                     /codon_start=1
                     /product="structural protein"
                     /protein_id="AAK00720.1"
                     /db_xref="GI:12656049"
                     /translation="FWEAGTTKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGA
                     GPVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECR"

Alignment Scores:
Pred. No.:              374             Length:         256
Score:                  84.00           Matches:        84
Percent Similarity:     98.82%          Conservative:   0
Best Local Similarity:  98.82%          Mismatches:     1
Query Match:            15.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF228535 (1-256)

Qy        436 PheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSer 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTCTGGGAGGCGGGTACTACTAAAGCCGGGTACCCTTATAACTATAACACCACTGCTAGT 60

Qy        456 AspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThr 475
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACCAATTGCTCATTGAGAATGCCGCCGGACATCGGGTGGCTATTTCCACCTATACCACT 120

Qy        476 SerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAla 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCCTAGGTGCTGGCCCTGTTTCCATCTCCGCGGTCGCTGTTTTAGCCCCCCACTCTGCT 180

Qy        496 LeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPhe 515
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTAGCACTGCTTGAGGATACTCTGGATTACCCTGCCCGCGCTCACACTTTCGATGATTTC 240

Qy        516 CysProGluCysArg 520
              ||||||||||||||||
Db        241 TGCCCGGAGTGCCGC 255
```

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RESULT 573
AF228537
LOCUS       AF228537                256 bp    RNA     linear   VRL 02-FEB-2001
DEFINITION  Hepatitis E virus isolate 95-Alg Tan 4 10TE structural protein
            gene, partial cds.
ACCESSION   AF228537
VERSION     AF228537.1  GI:12656052
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 256)
  AUTHORS   van Cuyck,H. and Viret,J.
  TITLE     Introduction for a modelization of Hepatitis E virus (HEV)
            evolution
  JOURNAL   Acta Biotheor. (2000) In press
REFERENCE   2  (bases 1 to 256)
  AUTHORS   Larouze,B., Siriwardana,M.G., Buisson,Y., Grandadam,M. and
            Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Transmissible Agents, CRSSA, 24 Ave des
            Maquis du Gresivaudan, BP87, La Tronche 38702, France
FEATURES             Location/Qualifiers
     source          1. .256
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="95-Alg Tan 4 10TE"
                     /db_xref="taxon:12461"
                     /country="Algeria: Tanedfou"
                     /note="isolated from epidemic outbreak case in 1995"
     CDS             <1. .>256
                     /note="ORF2"
                     /codon_start=1
                     /product="structural protein"
                     /protein_id="AAK00722.1"
                     /db_xref="GI:12656053"
                     /translation="FWEAGTTKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGA
                     GPVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECR"

Alignment Scores:
Pred. No.:              374             Length:         256
Score:                  84.00           Matches:        84
Percent Similarity:     98.82%          Conservative:   0
Best Local Similarity:  98.82%          Mismatches:     1
Query Match:            15.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF228537 (1-256)

Qy        436 PheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSer 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTCTGGGAGGCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCCAGC 60

Qy        456 AspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThr 475
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACCAATTGCTTATTGAGAACGCCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACT 120
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```
Qy        476 SerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAla 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCCTAGGCGCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCT 180

Qy        496 LeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPhe 515
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTAGCACTGCTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTC 240

Qy        516 CysProGluCysArg 520
              ||||||||||||||
Db        241 TGTCCGGAGTGCCGT 255

RESULT 574
AX181955
LOCUS       AX181955                250 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 237 from Patent WO0146696.
ACCESSION   AX181955
VERSION     AX181955.1  GI:15133238
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 237 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="3p.pile {hpea} shown in Figure 9F-9G"

Alignment Scores:
Pred. No.:              378             Length:         250
Score:                  83.00           Matches:        83
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            15.12%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AX181955 (1-250)

Qy        258 AlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGCTTACCCTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGTGGCCAGCTGTTCTACTCTCGCCCCGTCGTCTCAGCCAATGGCGAGCCG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACTGTTAAGCTGTATACATCTGTGGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCG 181

Qy        318 HisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CATGACATCGACCTCGGGGAATCCCGTGTAGTTATTCAGGATTATGACAACCAACATGAG 241

Qy        338 GlnAspArg 340
              |||||||||
Db        242 CAGGACCGA 250

RESULT 575
AX181956
LOCUS       AX181956                250 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 238 from Patent WO0146696.
ACCESSION   AX181956
VERSION     AX181956.1  GI:15133239
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 238 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="3p.pile {hpeuigh} shown in Figure 9F-9G"

Alignment Scores:
Pred. No.:              378             Length:         250
Score:                  83.00           Matches:        83
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            15.12%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AX181956 (1-250)

Qy        258 AlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGCTTACCCTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGTGGCCAGCTGTTCTACTCTCGCCCCGTCGTCTCAGCCAATGGCGAGCCG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACTGTTAAGCTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCG 181

Qy        318 HisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CATGACATCGACCTCGGGGAATCTCGAGTTGTTATTCAGGATTATGACAACCAACATGAG 241

Qy        338 GlnAspArg 340
              |||||||||
Db        242 CAGGACCGG 250

RESULT 576
AX181957
LOCUS       AX181957                250 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 239 from Patent WO0146696.
ACCESSION   AX181957
VERSION     AX181957.1  GI:15133240
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 239 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="3p.pile {hpesvp} shown in Figure 9F-9G"

Alignment Scores:
Pred. No.:              378             Length:         250
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Score:                  83.00          Matches:       83
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            15.12%         Indels:        0
DB:                     1              Gaps:          0

US-09-769-066-15 (1-549) x AX181957 (1-250)

Qy        258 AlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCG 181

Qy        318 HisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CATGACATTGACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAA 241

Qy        338 GlnAspArg 340
              ||||||||
Db        242 CAAGATCGG 250

RESULT 577
BD077323
LOCUS       BD077323                  250 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077323
VERSION     BD077323.1  GI:22622926
KEYWORDS    JP 2001520384-A/202.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 250)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 202 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/202
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   3p.pile {hpea} shown in Figure 9C
            FH   Key             Location/Qualifiers
            FT   source          1. .250
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                                 virus)'.
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              378            Length:        250
Score:                  83.00          Matches:       83
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            15.12%         Indels:        0
DB:                     1              Gaps:          0

US-09-769-066-15 (1-549) x BD077323 (1-250)

Qy        258 AlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGCTTACCCTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGTGGCCAGCTGTTCTACTCTCGCCCCGTCGTCTCAGCCAATGGCGAGCCG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACTGTTAAGCTGTATACATCTGTGGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCG 181

Qy        318 HisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CATGACATCGACCTCGGGGAATCCCGTGTAGTTATTCAGGATTATGACAACCAACATGAG 241

Qy        338 GlnAspArg 340
              ||||||||
Db        242 CAGGACCGA 250

RESULT 578
BD077324
LOCUS       BD077324                  250 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077324
VERSION     BD077324.1  GI:22622927
KEYWORDS    JP 2001520384-A/203.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 250)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 203 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/203
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   3p.pile {hpeuigh} shown in Figure 9C
            FH   Key             Location/Qualifiers
            FT   source          1. .250
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                                 virus)'.
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              378            Length:        250
Score:                  83.00          Matches:       83
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            15.12%         Indels:        0
DB:                     1              Gaps:          0

US-09-769-066-15 (1-549) x BD077324 (1-250)

Qy        258 AlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db          2 GCGCTTACCCTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGTGGCCAGCTGTTCTACTCTCGCCCCGTCGTCTCAGCCAATGGCGAGCCG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACTGTTAAGCTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCG 181

Qy        318 HisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CATGACATCGACCTCGGGGAATCTCGAGTTGTTATTCAGGATTATGACAACCAACATGAG 241

Qy        338 GlnAspArg 340
              |||||||||
Db        242 CAAGGACCGG 250

RESULT 579
BD077325
LOCUS       BD077325                250 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077325
VERSION     BD077325.1  GI:22622928
KEYWORDS    JP 2001520384-A/204.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 250)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 204 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/204
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   3p.pile (hpesvp) shown in Figure 9C
            FH   Key             Location/Qualifiers
            FT   source          1. .250
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                        virus)'.
FEATURES              Location/Qualifiers
     source           1. .250
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              378           Length:         250
Score:                  83.00         Matches:        83
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            15.12%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x BD077325 (1-250)

Qy        258 AlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCG 181

Qy        318 HisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CATGACATTGACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAA 241

Qy        338 GlnAspArg 340
              |||||||||
Db        242 CAAGATCGG 250

RESULT 580
AF228538
LOCUS       AF228538                256 bp    RNA     linear   VRL 02-FEB-2001
DEFINITION  Hepatitis E virus isolate 95-Alg Tan 6 Al17 structural protein
            gene, partial cds.
ACCESSION   AF228538
VERSION     AF228538.1  GI:12656054
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 256)
  AUTHORS   van Cuyck,H. and Viret,J.
  TITLE     Introduction for a modelization of Hepatitis E virus (HEV)
            evolution
  JOURNAL   Acta Biotheor. (2000) In press
REFERENCE   2  (bases 1 to 256)
  AUTHORS   Larouze,B., Siriwardana,M.G., Buisson,Y., Grandadam,M. and
            Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Transmissible Agents, CRSSA, 24 Ave des
            Maquis du Gresivaudan, BP87, La Tronche 38702, France
FEATURES              Location/Qualifiers
     source           1. .256
                      /organism="Hepatitis E virus"
                      /virion
                      /mol_type="genomic RNA"
                      /isolate="95-Alg Tan 6 Al17"
                      /db_xref="taxon:12461"
                      /country="Algeria: Tanedfou"
                      /note="isolated from epidemic outbreak case in 1995"
     CDS              <1. .>256
                      /note="ORF2"
                      /codon_start=1
                      /product="structural protein"
                      /protein_id="AAK00723.1"
                      /db_xref="GI:12656055"
                      /translation="FWEAGTTKAGYPYNYNTTASDQLLIENVAGHRVAISTYTTSLGA
                      GPVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECR"

Alignment Scores:
Pred. No.:              379           Length:         256
Score:                  83.00         Matches:        83
Percent Similarity:     97.65%        Conservative:   0
Best Local Similarity:  97.65%        Mismatches:     2
Query Match:            15.12%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF228538 (1-256)

Qy        436 PheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSer 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTCTGGGAGGCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGC 60

Qy        456 AspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThr 475
              ||||||||||||  ||||||  ||||||||||||||||||||||||||||||||||||||
Db         61 GACCAATTGCTTATTGAGAACGTCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACT 120

Qy        476 SerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAlaProHisSerAla 495
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCCTAGGTGCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCT 180

Qy        496 LeuAlaLeuLeuGluAspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPhe 515
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTAGCACTGCTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTC 240

Qy        516 CysProGluCysArg 520
                ||||||||||||||||
Db        241 TGTCCGGAGTGCCGT 255

RESULT 581
AX181958
LOCUS       AX181958                250 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 240 from Patent WO0146696.
ACCESSION   AX181958
VERSION     AX181958.1  GI:15133241
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 240 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="3p.pile (hpenssp) shown in Figure 9F-9G"

Alignment Scores:
Pred. No.:              392             Length:         250
Score:                  80.00           Matches:        80
Percent Similarity:     96.39%          Conservative:   0
Best Local Similarity:  96.39%          Mismatches:     3
Query Match:            14.57%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AX181958 (1-250)

Qy        258 AlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
                ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTCTAACATTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCA 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIlePro 317
                ||||||||||||||||||||||||||||||||||||||||||||||||    |||||||||
Db        122 ACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCC 181

Qy        318 HisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
                ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        182 CACGATATCGATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAG 241

Qy        338 GlnAspArg 340
                |||||||||
Db        242 CAGGATCGG 250

RESULT 582
BD077326
LOCUS       BD077326                250 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077326
VERSION     BD077326.1  GI:22622929
KEYWORDS    JP 2001520384-A/205.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 250)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 205 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/205
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   3p.pile (hpenssp) shown in Figure 9C
            FH   Key             Location/Qualifiers
            FT   source          1. .250
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                        virus)'.
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644".

Alignment Scores:
Pred. No.:              392             Length:         250
Score:                  80.00           Matches:        80
Percent Similarity:     96.39%          Conservative:   0
Best Local Similarity:  96.39%          Mismatches:     3
Query Match:            14.57%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x BD077326 (1-250)

Qy        258 AlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
                ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTCTAACATTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCA 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIlePro 317
                ||||||||||||||||||||||||||||||||||||||||||||||||    |||||||||
Db        122 ACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCC 181

Qy        318 HisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
                ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        182 CACGATATCGATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAG 241

Qy        338 GlnAspArg 340
                |||||||||
Db        242 CAGGATCGG 250

RESULT 583
AF407560
LOCUS       AF407560                249 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW5 capsid protein gene, partial cds.
ACCESSION   AF407560
VERSION     AF407560.1  GI:22347436
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 249)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
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            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 249)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .249
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW5"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>249
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM95904.1"
                     /db_xref="GI:22347437"
                     /translation="YTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGAD
                     GTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNL"

Alignment Scores:
Pred. No.:              401           Length:         249
Score:                  78.00         Matches:        78
Percent Similarity:     93.98%        Conservative:   0
Best Local Similarity:  93.98%        Mismatches:     5
Query Match:            14.21%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF407560 (1-249)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGTAACTTAACA 60

Qy        202 ProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              |||||||||||||||||||||||||||||||||||||||||   |||||||||   ||||||
Db         61 CCTGGCAATACGAACACCCGTGTGTCTCGTTACTCGAGCAGCGCGCGTCATAAGTTGCGC 120

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGGGGCTGATGGCACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGAC 180

Qy        242 LeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeu 261
              |||   ||||||   ||||||||||||||||||   ||||||||||||||||||||||||||
Db        181 CTCCATTTTACTGGGACCAACGGTGTTGGTGAAGTTGGTCGTGGTATAGCGCTGACCTTA 240

Qy        262 PheAsnLeu 264
              |||||||||
Db        241 TTTAATCTA 249

RESULT 584
AF407567
LOCUS       AF407567                 249 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW12 capsid protein gene, partial cds.
ACCESSION   AF407567
VERSION     AF407567.1  GI:22347453
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 249)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 249)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .249
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW12"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>249
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM95908.1"
                     /db_xref="GI:22347454"
                     /translation="YTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGAD
                     GTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNL"

Alignment Scores:
Pred. No.:              401           Length:         249
Score:                  78.00         Matches:        78
Percent Similarity:     93.98%        Conservative:   0
Best Local Similarity:  93.98%        Mismatches:     5
Query Match:            14.21%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AF407567 (1-249)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGTAACTTAACA 60

Qy        202 ProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              |||||||||||||||||||||||||||||||||||||||||   |||||||||   ||||||
Db         61 CCTGGCAATACGAACACCCGTGTGTCTCGTTACTCGAGCAGCGCGCGTCATAAGTTGCGC 120

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGGGGCTGATGGCACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGAC 180

Qy        242 LeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeu 261
              |||   ||||||   ||||||||||||||||||   ||||||||||||||||||||||||||
Db        181 CTCCATTTTACTGGGACCAACGGTGTTGGTGAAGTTGGTCGTGGTATAGCGCTGACCTTA 240

Qy        262 PheAsnLeu 264
              |||||||||
Db        241 TTTAATCTA 249

RESULT 585
AF505860
LOCUS       AF505860                 249 bp ss-RNA     linear   VRL 01-MAY-2003
DEFINITION  Swine hepatitis E virus isolate IND-SW17 ORF2 gene, partial cds.
ACCESSION   AF505860
VERSION     AF505860.1  GI:30269361
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 249)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Walimbe,A.M., Yergolkar,P.N. and
            George,J.P.
  TITLE     Incidence of Swine HEV Infection in South India and Phylogenetic
            Analysis (1985-1999)
  JOURNAL   Unpublished
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REFERENCE   2  (bases 1 to 249)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Walimbe,A.M., Yergolkar,P.N. and
            George,J.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-2002) Hepatitis Department, National Institute of
            Virology, 20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .249
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW17"
                     /db_xref="taxon:63421"
                     /country="India: South"
     CDS             <1. .>249
                     /codon_start=1
                     /product="ORF2"
                     /protein_id="AAP29642.1"
                     /db_xref="GI:30269362"
                     /translation="YTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGAD
                     GTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNL"

Alignment Scores:
Pred. No.:                401             Length:         249
Score:                    78.00           Matches:        78
Percent Similarity:       93.98%          Conservative:   0
Best Local Similarity:    93.98%          Mismatches:     5
Query Match:              14.21%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AF505860 (1-249)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACACTGGCGCCCTCGGTCTGCTCGACTTTGCGCTTGAACTCGAGTTTCGTAATTTAACA 60

Qy        202 ProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              |||||||||||||||||||||||||||||||||||||||||   |||||||||   ||||||
Db         61 CCTGGCAATACGAATACCCGTGTGTCCCGTTATTCGAGCAGCGCACGTCACAAGTTGCGC 120

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGAGGGGCTGATGGTACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGAT 180

Qy        242 LeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeu 261
              |||   ||||||   ||||||||||||||||||   ||||||||||||||||||||||||||
Db        181 CTCCATTTTACTGGGACCAACGGTGTTGGTGAAGTTGGCCGTGGTATAGCGCTGACCTTA 240

Qy        262 PheAsnLeu 264
              |||||||||
Db        241 TTTAATCTC 249

RESULT 586
AF407562
LOCUS       AF407562                 244 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW7 capsid protein gene, partial cds.
ACCESSION   AF407562
VERSION     AF407562.1  GI:22347441
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 244)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 244)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .244
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW7"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>244
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM95905.1"
                     /db_xref="GI:22347442"
                     /translation="GALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGADGT
                     AELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNL"

Alignment Scores:
Pred. No.:                410             Length:         244
Score:                    76.00           Matches:        76
Percent Similarity:       93.83%          Conservative:   0
Best Local Similarity:    93.83%          Mismatches:     5
Query Match:              13.84%          Indels:         0.
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AF407562 (1-244)

Qy        184 GlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGly 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGTAACCTAACACCTGGC 61

Qy        204 AsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGly 223
              |||||||||||||||||||||||||||||||||||||||||   |||||||||   ||||||
Db         62 AATACGAACACCCGTGTGTCTCGTTACTCGAGCAGCGCGCGTCATAAGTTGCGCCGGGGG 121

Qy        224 AlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyr 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GCTGATGGCACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGACCTCCAT 181

Qy        244 PheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsn 263
              ||||||   ||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        182 TTTACTGGGACCAACGGTGTTGGTGAAGTTGGTCGTGGTATAGCGCTGACCTTATTTAAT 241

Qy        264 Leu 264
              |||
Db        242 CTA 244

RESULT 587
AF407561
LOCUS       AF407561                 246 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW6 nonfunctional capsid protein gene,
            partial sequence.
ACCESSION   AF407561
VERSION     AF407561.1  GI:22347439
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 246)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 246)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
```

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          20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .246
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW6"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     misc_feature    <1. .>246
                     /note="nonfunctional capsid protein due to mutation; ORF2"

Alignment Scores:
Pred. No.:              410           Length:        246
Score:                  76.00         Matches:       76
Percent Similarity:     93.83%        Conservative:  0
Best Local Similarity:  93.83%        Mismatches:    5
Query Match:            13.84%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AF407561 (1-246)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGTAACTTAACA 60

Qy        202 ProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              |||||||||||||||||||||||||||||||||||   |||||||||   ||||||
Db         61 CCTGGCAATACGAACACCCGTGTGTCTCGTTACTCGAGCAGCGCGCGTCATAAGTTGCGC 120

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGGGGCTGATGGCACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGAC 180

Qy        242 LeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeu 261
              |||   ||||||   ||||||||||||||||||   ||||||||||||||||||||||||
Db        181 CTCCATTTTACTGGGACCAACGGTGTTGGTGAAGTTGGTCGTGGTATAGCGCTGACCTTA 240

Qy        262 Phe 262
              |||
Db        241 TTT 243

RESULT 588
AF407564
LOCUS       AF407564                247 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW9 capsid protein gene, partial cds.
ACCESSION   AF407564
VERSION     AF407564.1  GI:22347447
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 247)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 247)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .247
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW9"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>247
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM95907.1"
                     /db_xref="GI:22347448"
                     /translation="YTGALGLLDFALELEFRSLTPGNTNTRVSRYSSSARHKLRRGAD
                     GTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFN"

Alignment Scores:
Pred. No.:              410           Length:        247
Score:                  76.00         Matches:       76
Percent Similarity:     92.68%        Conservative:  0
Best Local Similarity:  92.68%        Mismatches:    6
Query Match:            13.84%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AF407564 (1-247)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          1 TACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGTAGCTTAACA 60

Qy        202 ProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              |||||||||||||||||||||||||||||||||||   |||||||||   ||||||
Db         61 CCTGGCAATACGAACACCCGTGTGTCCCGTTACTCGAGCAGCGCGCGTCATAAGTTGCGC 120

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGGGGCCGATGGTACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGAC 180

Qy        242 LeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeu 261
              |||   ||||||   ||||||||||||||||||   ||||||||||||||||||||||||
Db        181 CTCCATTTTACTGGGACCAACGGTGTTGGTGAAGTTGGTCGTGGTATAGCGCTGACCTTA 240

Qy        262 PheAsn 263
              ||||||
Db        241 TTTAAT 246

RESULT 589
AF407569
LOCUS       AF407569                247 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW14 capsid protein gene, partial cds.
ACCESSION   AF407569
VERSION     AF407569.1  GI:22347459
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 247)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 247)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .247
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW14"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>247
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                /note="ORF2"
                /codon_start=2
                /product="capsid protein"
                /protein_id="AAM95910.1"
                /db_xref="GI:22347460"
                /translation="YTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGAD
                GTAELTTTAATRFMKDLHFTGTNGVGEVGCGIALTLFN"

Alignment Scores:
Pred. No.:              410             Length:         247
Score:                  76.00           Matches:        76
Percent Similarity:     92.68%          Conservative:   0
Best Local Similarity:  92.68%          Mismatches:     6
Query Match:            13.84%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF407569 (1-247)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TACACTGGCGCCCTCGGTCTGCTCGATTTTGCGCTTGAACTCGAGTTTCGTAATTTAACA 61

Qy        202 ProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              ||||||||||||||||||||||||||||||||||||  |||||||||  ||||||
Db         62 CCTGGTAATACGAACACCCGTGTGTCCCGTTATTCGAGCAGCGCGCGTCACAAGTTGCGC 121

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CGAGGGGCTGATGGTACTGCTGAGTTAACTACTACTGCTGCCACACGTTTTATGAAGGAC 181

Qy        242 LeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeu 261
              |||   ||||||   ||||||||||||||||||   |||   ||||||||||||||||||
Db        182 CTCCATTTTACTGGGACCAATGGTGTTGGTGAAGTTGGTTGTGGTATAGCGCTGACCTTA 241

Qy        262 PheAsn 263
              ||||||
Db        242 TTTAAT 247

RESULT 590
AF505861
LOCUS       AF505861                 249 bp ss-RNA     linear   VRL 01-MAY-2003
DEFINITION  Swine hepatitis E virus isolate IND-SW18 ORF2 gene, partial cds.
ACCESSION   AF505861
VERSION     AF505861.1  GI:30269363
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 249)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Walimbe,A.M., Yergolkar,P.N. and
            George,J.P.
  TITLE     Incidence of Swine HEV Infection in South India and Phylogenetic
            Analysis (1985-1999)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 249)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Walimbe,A.M., Yergolkar,P.N. and
            George,J.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-2002) Hepatitis Department, National Institute of
            Virology, 20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .249
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW18"
                     /db_xref="taxon:63421"
                     /country="India: South"
     CDS             <1. .>249
                     /codon_start=2
                     /product="ORF2"
                     /protein_id="AAP29643.1"
                     /db_xref="GI:30269364"
                     /translation="YTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGAD
                     GTAELTTTAATRFMKDPHFTGTNGVGEVGRGIALTLFNL"

Alignment Scores:
Pred. No.:              411             Length:         249
Score:                  76.00           Matches:        76
Percent Similarity:     92.68%          Conservative:   0
Best Local Similarity:  92.68%          Mismatches:     6
Query Match:            13.84%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AF505861 (1-249)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TACACTGGCGCCCTCGGTCTGCTCGATTTTGCGCTTGAACTCGAGTTTCGTAATTTAACA 61

Qy        202 ProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              ||||||||||||||||||||||||||||||||||||  |||||||||  ||||||
Db         62 CCTGGCAATACGAATACCCGTGTGTCCCGTTATTCGAGCAGCGCACGTCACAAGTTGCGC 121

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CGAGGGGCTGATGGTACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGAT 181

Qy        242 LeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeu 261
              ||||||   ||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        182 CCCCATTTTACTGGGACCAACGGTGTTGGTGAAGTTGGCCGTGGTATAGCGCTGACCTTA 241

Qy        262 PheAsn 263
              ||||||
Db        242 TTTAAT 247

RESULT 591
AF407570
LOCUS       AF407570                 250 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW15 capsid protein gene, partial cds.
ACCESSION   AF407570
VERSION     AF407570.1  GI:22347462
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 250)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 250)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW15"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>250
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM95911.1"
                     /db_xref="GI:22347463"
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                     GTAELTSTAATRFMKDLHFTGTNGVGEVGCGIALTLFNL"
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Alignment Scores:
Pred. No.:              411          Length:        250
Score:                  76.00        Matches:       76
Percent Similarity:     91.57%       Conservative:  0
Best Local Similarity:  91.57%       Mismatches:    7
Query Match:            13.84%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AF407570 (1-250)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGTAATTTAACA 61

Qy        202 ProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              ||||||||||||||||||||||||||||||||||||||   |||||||||   ||||||
Db         62 CCTGGTAATACGAACACCCGTGTGTCCCGTTATTCGAGCAGCGCGCGTCACAAGTTGCGC 121

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        122 CGAGGGGCTGATGGTACTGCTGAGTTAACCTCTACTGCTGCTACACGTTTTATGAAGGAT 181

Qy        242 LeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeu 261
              |||   ||||||   ||||||||||||||||||   |||   ||||||||||||||||||
Db        182 CTCCATTTTACTGGGACCAATGGTGTTGGTGAAGTTGGTTGTGGTATAGCGCTGACCTTA 241

Qy        262 PheAsnLeu 264
              |||||||||
Db        242 TTTAATCTA 250

RESULT 592
AF407563
LOCUS       AF407563                247 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW8 capsid protein gene, partial cds.
ACCESSION   AF407563
VERSION     AF407563.1  GI:22347444
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 247)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 247)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .247
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW8"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>247
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM95906.1"
                     /db_xref="GI:22347445"
                     /translation="YTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGAD
                     GTAELTTTAATRFMKDLHFTGTNGVGEVGCGLALTLFN"

Alignment Scores:
Pred. No.:              415          Length:        247
Score:                  75.00        Matches:       75
Percent Similarity:     91.46%       Conservative:  0
Best Local Similarity:  91.46%       Mismatches:    7
Query Match:            13.66%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-15 (1-549) x AF407563 (1-247)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGTAACTTAACA 60

Qy        202 ProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              ||||||||||||||||||||||||||||||||||||||   |||||||||   ||||||
Db         61 CCTGGCAATACGAACACCCGTGTGTCTCGTTACTCGAGCAGCGCGCGTCATAAGTTGCGC 120

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGGGGCTGATGGTACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGAC 180

Qy        242 LeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeu 261
              |||   ||||||   ||||||||||||||||||   |||   |||   ||||||||||||
Db        181 CTCCATTTTACTGGGACCAACGGTGTTGGTGAAGTCGGTTGTGGTCTAGCGCTGACCTTA 240

Qy        262 PheAsn 263
              ||||||
Db        241 TTTAAT 246

RESULT 593
AF407568
LOCUS       AF407568                239 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW13 capsid protein gene, partial cds.
ACCESSION   AF407568
VERSION     AF407568.1  GI:22347456
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 239)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 239)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .239
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW13"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>239
                     /note="ORF2"
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAM95909.1"
                     /db_xref="GI:22347457"
                     /translation="LGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGADGTAE
                     LTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNL"

Alignment Scores:
Pred. No.:              419          Length:        239
Score:                  74.00        Matches:       74
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Percent Similarity:     93.67%          Conservative:  0
Best Local Similarity:  93.67%          Mismatches:    5
Query Match:            13.48%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-15 (1-549) x AF407568 (1-239)

Qy        186 LeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThr 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CTCGGTCTGCTCGATTTTGCGCTTGAACTCGAGTTTCGTAATTTAACACCTGGTAATACG 62

Qy        206 AsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAsp 225
              |||||||||||||||||||||||||   |||||||||   ||||||||||||||||||||
Db         63 AACACCCGTGTGTCCCGTTACTCGAGCAGCGCGCGTCATAAGTTGCGCCGGGGGGCTGAT 122

Qy        226 GlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThr 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        123 GGCACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGACCTCCATTTTACT 182

Qy        246 SerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeuPheAsnLeu 264
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        183 GGGACCAACGGTGTTGGTGAAGTTGGTCGTGGTATAGCGCTGACCTTATTTAATCTA 239

RESULT 594
AY753554
LOCUS       AY753554                 227 bp    RNA     linear   VRL 12-OCT-2004
DEFINITION  Hepatitis E virus isolate Lucknow_Sw_208 capsid protein gene,
            partial cds.
ACCESSION   AY753554
VERSION     AY753554.1  GI:53854173
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 227)
  AUTHORS   Aggarwal,R., Shukla,P. and Naik,S.
  TITLE     Hepatitis E virus among swine in northern India
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 227)
  AUTHORS   Aggarwal,R., Shukla,P. and Naik,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-SEP-2004) Gastroenterology, Sanjay Gandhi
            Postgraduate Institute of Medical Sciences, Raebareli Road,
            Lucknow, UP 226014, India
FEATURES             Location/Qualifiers
     source          1. .227
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="Lucknow_Sw_208"
                     /specific_host="swine"
                     /db_xref="taxon:12461"
                     /country="India: Lucknow"
     CDS             <1. .>227
                     /note="Orf2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAU95557.1"
                     /db_xref="GI:53854174"
                     /translation="YTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGAD
                     GTAELTTTAATRFMKDLHFTGTNGVGEVGRG"

Alignment Scores:
Pred. No.:              438             Length:        227
Score:                  70.00           Matches:       70
Percent Similarity:     93.33%          Conservative:  0
Best Local Similarity:  93.33%          Mismatches:    5
Query Match:            12.75%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-15 (1-549) x AY753554 (1-227)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACACTGGCGCCCTCGGTCTGCTCGACTTTGCACTTGAGCTTGAGTTTCGTAATTTGACA 60

Qy        202 ProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              |||||||||||||||||||||||||||||||||||||||||   |||||||||   ||||||
Db         61 CCCGGGAATACCAACACACGTGTGTCTCGTTACTCGAGCAGTGCGCGCCACAAATTGCGT 120

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGGCGCTGATGGGACCGCCGAGTTAACCACTACAGCAGCTACTCGGTTTATGAAGGAT 180

Qy        242 LeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGly 256
              |||   ||||||   ||||||||||||||||||   |||||||||
Db        181 TTACATTTTACTGGGACTAATGGTGTTGGTGAGGTTGGGCGTGGT 225

RESULT 595
AF407566
LOCUS       AF407566                 249 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW11 nonfunctional capsid protein gene,
            partial sequence.
ACCESSION   AF407566
VERSION     AF407566.1  GI:22347451
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 249)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 249)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .249
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW11"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     misc_feature    <1. .>249
                     /note="nonfunctional capsid protein due to mutation; ORF2"

Alignment Scores:
Pred. No.:              445             Length:        249
Score:                  69.00           Matches:       69
Percent Similarity:     86.25%          Conservative:  0
Best Local Similarity:  86.25%          Mismatches:    11
Query Match:            12.57%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-15 (1-549) x AF407566 (1-249)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTTGAACTCGAGTTCCGTAATCTAACA 60

Qy        202 ProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              |||||||||||||||||||||||||||||||||||||||||   |||||||||   ||||||
Db         61 CCCGGTAATACGAACACCCGTGTGTCTCGTTATTCGAGCAGCGCGCGTCACAAGTTGCGC 120

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGAGGGGCTGATGGTACTGCTGAGTTAACCACTACTGCTGCTACACGCTTTATGAAGGAC 180
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Qy        242 LeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeu 261
              |||   ||||||   ||||||||||||||||||   |||                   |||
Db        181 CTTCATTTTACTGGGACCAACGGTGTTGGTGAAGTTGGTCTGTGGTATAGCGCTGACCTT 240

RESULT 596
AF407565
LOCUS       AF407565                 251 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW10 nonfunctional capsid protein gene,
            partial sequence.
ACCESSION   AF407565
VERSION     AF407565.1  GI:22347450
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 251)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 251)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .251
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW10"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     misc_feature    <1. .>251
                     /note="nonfunctional capsid protein due to mutation; ORF2"

Alignment Scores:
Pred. No.:              445           Length:        251
Score:                  69.00         Matches:       69
Percent Similarity:     86.25%        Conservative:  0
Best Local Similarity:  86.25%        Mismatches:    11
Query Match:            12.57%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AF407565 (1-251)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGTAACTTAACA 61

Qy        202 ProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              ||||||||||||||||||||||||||||||||||||   |||||||||   ||||||
Db         62 CCAGGCAACACGAACACCCGTGTGTCCCGTTACTCGAGCAGCGCGCGTCATAAGTTGCGC 121

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CGGGGGGCTGATGGTACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGAC 181

Qy        242 LeuTyrPheThrSerThrAsnGlyValGlyGluIleGlyArgGlyIleAlaLeuThrLeu 261
              |||   ||||||   ||||||||||||||||||   |||                   |||
Db        182 CTCCATTTTACTGGGACCAACGGTGTTGGTGAAGTTGGTCTGTGGTATAGCGCTGACCTT 241

RESULT 597
AF347692
LOCUS       AF347692                 212 bp    RNA     linear   VRL 01-NOV-2001
DEFINITION  Swine hepatitis E virus capsid protein gene, partial cds.
ACCESSION   AF347692
VERSION     AF347692.1  GI:16565781
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 212)
  AUTHORS   Yoo,D., Willson,P., Pei,Y., Hayes,M.A., Deckert,A., Dewey,C.E.,
            Friendship,R.M., Yoon,Y., Gottschalk,M., Yason,C. and Giulivi,A.
  TITLE     Prevalence of hepatitis E virus antibodies in Canadian swine herds
            and identification of a novel variant of swine hepatitis E virus
  JOURNAL   Clin. Diagn. Lab. Immunol. 8 (6), 1213-1219 (2001)
  MEDLINE   21546646
   PUBMED   11687465
REFERENCE   2  (bases 1 to 212)
  AUTHORS   Pei,Y. and Yoo,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-FEB-2001) Department of Pathobiology, University of
            Guelph, Guelph, Ontario N1G 2W1, Canada
FEATURES             Location/Qualifiers
     source          1. .212
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="SK3"
                     /db_xref="taxon:63421"
                     /country="Canada: Saskatchewan"
     CDS             <1. .>212
                     /note="ORF2"
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAL26294.1"
                     /db_xref="GI:16565782"
                     /translation="NPLLPLQDGTNTHIMATEASNYAQYRVVRATIRYRPLVPNAVGG
                     YAISISFWPQTTTTPTSVDMNSITST"

Alignment Scores:
Pred. No.:              446           Length:        212
Score:                  68.00         Matches:       68
Percent Similarity:     98.55%        Conservative:  0
Best Local Similarity:  98.55%        Mismatches:    1
Query Match:            12.39%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AF347692 (1-212)

Qy         51 ProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSerAsn 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 CCCCTTTTACCCCTCCAGGACGGAACCAATACTCATATCATGGCCACCGAGGCGTCCAAC 65

Qy         71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db         66 TATGCCCAGTATCGGGTCGTCCGAGCTACGATCCGTTACCGCCCGCTGGTGCCTAATGCT 125

Qy         91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GTTGGCGGTTACGCTATTTCTATTTCTTTCTGGCCCCAAACTACAACTACTCCTACTTCT 185

Qy        111 ValAspMetAsnSerIleThrSerThr 119
              ||||||||||||||||||||||||||
Db        186 GTTGATATGAATTCCATCACTTCTACT 212

RESULT 598
AF505859
LOCUS       AF505859                 217 bp ss-RNA     linear   VRL 01-MAY-2003
DEFINITION  Swine hepatitis E virus isolate IND-SW16 ORF2 gene, partial cds.
ACCESSION   AF505859
VERSION     AF505859.1  GI:30269359
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 217)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Walimbe,A.M., Yergolkar,P.N. and
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            George,J.P.
  TITLE     Incidence of Swine HEV Infection in South India and Phylogenetic
            Analysis (1985-1999)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 217)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Walimbe,A.M., Yergolkar,P.N. and
            George,J.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-2002) Hepatitis Department, National Institute of
            Virology, 20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .217
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW16"
                     /db_xref="taxon:63421"
                     /country="India: South"
     CDS             <1. .>217
                     /codon_start=1
                     /product="ORF2"
                     /protein_id="AAP29641.1"
                     /db_xref="GI:30269360"
                     /translation="TPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRG
                     ADGTAELTTTAATRFMKDLHFTGTNGVG"

Alignment Scores:
Pred. No.:                447             Length:         217
Score:                    68.00           Matches:        68
Percent Similarity:       94.44%          Conservative:   0
Best Local Similarity:    94.44%          Mismatches:     4
Query Match:              12.39%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AF505859 (1-217)

Qy        180 ThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsn 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACACCTTACACTGGCGCCCTCGGTCTGCTCGATTTTGCACTCGAACTCGAGTTTCGTAAT 60

Qy        200 LeuThrProGlyAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArg 219
              ||||||||||||||||||||||||||||||||||||||||||||    |||||||||
Db         61 TTGACACCTGGTAATACGAACACTCGTGTGTCTCGTTATTCGAGCAGCGCGCGTCATAAG 120

Qy        220 LeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMet 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTGCGCCGAGGGGCTGATGGTACTGCTGAGCTAACTACTACTGCTGCTACACGCTTTATG 180

Qy        240 LysAspLeuTyrPheThrSerThrAsnGlyValGly 251
              |||||||||   ||||||   ||||||||||||||
Db        181 AAGGACCTCCATTTTACTGGGACCAATGGTGTTGGT 216

RESULT 599
AX181959
LOCUS       AX181959                 250 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 241 from Patent WO0146696.
ACCESSION   AX181959
VERSION     AX181959.1  GI:15133242
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 241 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="3p.pile (840453p) shown in Figure 9F-9G"

Alignment Scores:
Pred. No.:                461             Length:         250
Score:                    66.00           Matches:        66
Percent Similarity:       79.52%          Conservative:   0
Best Local Similarity:    79.52%          Mismatches:     17
Query Match:              12.02%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-15 (1-549) x AX181959 (1-250)

Qy        258 AlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCCTGACTCTGTTTAATCTTGCTGATACGCTTCTTGGTGGTTTACCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              |||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCTGTTCAGAATTGATTTCGTCGGCTG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIlePro 317
                 |||         |||              ||||||||||||||||||||   ||||||
Db        122 GGGGTCAACTGTTTTACTCCCGCCCTGTTTGCGCAGCAAGACAAGGGCATCACCATTCCA 181

Qy        318 HisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        182 CACGACATAGATTTAGGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCACGAA 241

Qy        338 GlnAspArg 340
              |||||||||
Db        242 CAAGATCGA 250

RESULT 600
BD077327
LOCUS       BD077327                 250 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077327
VERSION     BD077327.1  GI:22622930
KEYWORDS    JP 2001520384-A/206.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 250)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 206 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/206
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   3p.pile (840453p) shown in Figure 9C
            FH   Key             Location/Qualifiers
            FT   source          1. .250
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                        virus)'.
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:                461             Length:         250
Score:                    66.00           Matches:        66
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Percent Similarity:     79.52%          Conservative:  0
Best Local Similarity:  79.52%          Mismatches:    17
Query Match:            12.02%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-15 (1-549) x BD077327 (1-250)

Qy        258 AlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCCTGACTCTGTTTAATCTTGCTGATACGCTTCTTGGTGGTTTACCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              |||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCTGTTCAGAATTGATTTCGTCGGCTG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyIleAlaIlePro 317
                  |||         |||             ||||||||||||||||||||   ||||||
Db        122 GGGGTCAACTGTTTTACTCCCGCCCTGTTTGCGCAGCAAGACAAGGGCATCACCATTCCA 181

Qy        318 HisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        182 CACGACATAGATTTAGGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCACGAA 241

Qy        338 GlnAspArg 340
              |||||||||
Db        242 CAAGATCGA 250

RESULT 601
AX181929
LOCUS       AX181929                197 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 211 from Patent WO0146696.
ACCESSION   AX181929
VERSION     AX181929.1  GI:15141762
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 211 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .197
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="1440o2.seq"
     CDS             <2. .>196
                     /note="unnamed protein product; Greek Isolate 2 Orf2"
                     /codon_start=1
                     /protein_id="CAC50185.1"
                     /db_xref="GI:15141763"
                     /translation="TELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIP
                     HDIDLGDSRVVIQDYDNQHEQ"

Alignment Scores:
Pred. No.:              465             Length:        197
Score:                  64.00           Matches:       64
Percent Similarity:     98.46%          Conservative:  0
Best Local Similarity:  98.46%          Mismatches:    1
Query Match:            11.66%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-15 (1-549) x AX181929 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTRATTTCGTCGGCTGGAGGTCAACTGTTCTACTCCCGCCCGGTTGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTTAAGTTATACACCTCTGTCGAGAATGCACAGCAGGATAAGGGC 121

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        122 ATTGCTATACCACATGATATAGACTTAGGGGATTCCCGTGTGGTTATACAAGATTATGAY 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCARCAYGAACAA 196

RESULT 602
AX181933
LOCUS       AX181933                197 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 215 from Patent WO0146696.
ACCESSION   AX181933
VERSION     AX181933.1  GI:15141766
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 215 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .197
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="2015o2.seq"
     CDS             <2. .>196
                     /note="unnamed protein product; Greek Isolate 2 Orf2"
                     /codon_start=1
                     /protein_id="CAC50187.1"
                     /db_xref="GI:15141767"
                     /translation="TELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIP
                     HDIDLGDSRVVIQDYDNQHEQ"

Alignment Scores:
Pred. No.:              465             Length:        197
Score:                  64.00           Matches:       64
Percent Similarity:     98.46%          Conservative:  0
Best Local Similarity:  98.46%          Mismatches:    1
Query Match:            11.66%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-15 (1-549) x AX181933 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTRATTTCGTCGGCTGGAGGCCAGCTCTTCTACTCCCGCCCAGTCGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTTAAATTGTATACATCCGTCGAGAATGCGCAGCAGGACAAGGGC 121

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        122 ATTGCCATACCACATGATATAGATCTAGGAGATTCCCGCGTGGTTATCCAGGATTATGAY 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCARCAYGAACAA 196

RESULT 603
AX181963
LOCUS       AX181963                197 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 245 from Patent WO0146696.
ACCESSION   AX181963
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VERSION     AX181963.1  GI:15141774
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 245 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .197
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="Aulo2-wlao2.pat"
     CDS             <2. .>196
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC50192.1"
                     /db_xref="GI:15141775"
                     /translation="TELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIP
                     HDIDLGDSRVVIQDYDNQHEQ"

Alignment Scores:
Pred. No.:              465          Length:         197
Score:                  64.00        Matches:        64
Percent Similarity:     98.46%       Conservative:   0
Best Local Similarity:  98.46%       Mismatches:     1
Query Match:            11.66%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AX181963 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTRATTTCGTCGGCTGGGGGACAGTTATTCTACTCCCGCCCTGTYGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTTAAATTATATACATCTGTAGAGAATGCGCAGCAGGACAAGGGG 121

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
              |||||||||||||||||||||||||||||||    |||||||||||||||||||||||||||
Db        122 ATTGCCATCCCACATGATATAGATCTGGGCGACTCTCGTGTGGTGATCCAGGATTATGAY 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCARCAYGAACAA 196

RESULT 604
AX181971
LOCUS       AX181971                 197 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 253 from Patent WO0146696.
ACCESSION   AX181971
VERSION     AX181971.1  GI:15141782
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 253 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .197
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="Ar2o2-f7702.pat"
     CDS             <2. .>196
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC50196.1"
                     /db_xref="GI:15141783"
                     /translation="TELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIP
                     HDIDLGDSRVVIQDYDNQHEQ"

Alignment Scores:
Pred. No.:              465          Length:         197
Score:                  64.00        Matches:        64
Percent Similarity:     98.46%       Conservative:   0
Best Local Similarity:  98.46%       Mismatches:     1
Query Match:            11.66%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-15 (1-549) x AX181971 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTRATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTTAAGTTGTATACATCTGTGGAGAATGCGCAGCAGGATAAAGGA 121

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
              |||||||||||||||||||||||||||||||    |||||||||||||||||||||||||||
Db        122 ATCGCCATCCCACACGACATAGATCTGGGCGATTCCCGTGTGGTTATTCAGGATTATGAY 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCARCAYGAACAA 196

RESULT 605
BD077306
LOCUS       BD077306                 197 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077306
VERSION     BD077306.1  GI:22622909
KEYWORDS    JP.2001520384-A/185.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 197)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 185 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/185
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   1440o2.seq
            CC   Xaa = Unknown or Other at position 3
            CC   Xaa = Unknown or Other at position 60
            CC   Xaa = Unknown or Other at positions 62-63
            FH   Key             Location/Qualifiers
            FT   CDS             (2). .(196).
FEATURES             Location/Qualifiers
     source          1. .197
                     /organism="unidentified"
                     /mol_type="genomic DNA"
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                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              465             Length:         197
Score:                  64.00           Matches:        64
Percent Similarity:     98.46%          Conservative:   0
Best Local Similarity:  98.46%          Mismatches:     1
Query Match:            11.66%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x BD077306 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTRATTTCGTCGGCTGGAGGTCAACTGTTCTACTCCCGCCCGGTTGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTTAAGTTATACACCTCTGTCGAGAATGCACAGCAGGATAAGGGC 121

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
              |||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        122 ATTGCTATACCACATGATATAGACTTAGGGGATTCCCGTGTGGTTATACAAGATTATGAY 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCARCAYGAACAA 196

RESULT 606
BD077308
LOCUS       BD077308                197 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077308
VERSION     BD077308.1  GI:22622911
KEYWORDS    JP 2001520384-A/187.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 197)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 187 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/187
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   2015o2.seq
            CC   Xaa = Unknown or Other at position 3
            CC   Xaa = Unknown or Other at position 60
            CC   Xaa = Unknown or Other at positions 62-63
            FH   Key             Location/Qualifiers
            FT   CDS             (2). .(196).
FEATURES            Location/Qualifiers
     source         1. .197
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              465             Length:         197
Score:                  64.00           Matches:        64
Percent Similarity:     98.46%          Conservative:   0
Best Local Similarity:  98.46%          Mismatches:     1
Query Match:            11.66%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x BD077308 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTRATTTCGTCGGCTGGAGGCCAGCTCTTCTACTCCCGCCCAGTCGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTTAAATTGTATACATCCGTCGAGAATGCGCAGCAGGACAAGGGC 121

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
              |||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        122 ATTGCCATACCACATGATATAGATCTAGGAGATTCCCGCGTGGTTATCCAGGATTATGAY 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCARCAYGAACAA 196

RESULT 607
AX181869
LOCUS       AX181869                197 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 151 from Patent WO0146696.
ACCESSION   AX181869
VERSION     AX181869.1  GI:15133190
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 151 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES            Location/Qualifiers
     source         1. .197
                    /organism="Hepatitis E virus"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:12461"
                    /note="us2-orf2"

Alignment Scores:
Pred. No.:              471             Length:         197
Score:                  63.00           Matches:        63
Percent Similarity:     96.92%          Conservative:   0
Best Local Similarity:  96.92%          Mismatches:     2
Query Match:            11.48%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-15 (1-549) x AX181869 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTGATTTCGTCGGCTGGGGGCCAACTGTTTTACTCCCGCCCGGTTGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCAACAGTAAAGTTATATACATCTGTTGAGAATGCGCAGCAAGACAAGGGC 121

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
              |||   |||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        122 ATCACCATTCCACATGATATAGACCTGGGTGACTCCCGTGTGGTTATCCAGGATTATGAT 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCAGCAYGAGCAA 196

RESULT 608
AX181899
LOCUS       AX181899                197 bp    DNA     linear   PAT 07-AUG-2001
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DEFINITION  Sequence 181 from Patent WO0146696.
ACCESSION   AX181899
VERSION     AX181899.1  GI:15133209
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 181 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .197
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="z12-orf2.con"

Alignment Scores:
Pred. No.:              471           Length:         197
Score:                  63.00         Matches:        63
Percent Similarity:     96.92%        Conservative:   0
Best Local Similarity:  96.92%        Mismatches:     2
Query Match:            11.48%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x AX181899 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTAATTTCGTCGGCTGGGGGTCAACTGTTCTACTCCCGCCCTGTCGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTCAAGTTATACACATCTGTTGAGAATGCACAGCAGGATAAGGGG 121

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
              |||||||||||||||||||||||||||||    ||||||    ||||||||||||||||||
Db        122 ATAGCTATTCCACATGACATAGATTTGGGCGACTCTCGTTTGGTAATCCAGGATTATGAT 181

Qy        334 AsnGlnHisGluGln 338
              ||||||||||||||||
Db        182 AACCAACACGAACAA 196

RESULT 609
BD077269
LOCUS       BD077269                197 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077269
VERSION     BD077269.1  GI:22622872
KEYWORDS    JP 2001520384-A/148.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 197)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 148 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/148
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   us2-orf2
            FH   Key             Location/Qualifiers
            FT   source          1. .197
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                 virus)'.
FEATURES             Location/Qualifiers
     source          1. .197
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              471           Length:         197
Score:                  63.00         Matches:        63
Percent Similarity:     96.92%        Conservative:   0
Best Local Similarity:  96.92%        Mismatches:     2
Query Match:            11.48%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-15 (1-549) x BD077269 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTGATTTCGTCGGCTGGGGGCCAACTGTTTTACTCCCGCCCGGTTGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCAACAGTAAAGTTATATACATCTGTTGAGAATGCGCAGCAAGACAAGGGC 121

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
              |||    ||||||||||||||||||||||    ||||||||||||||||||||||||||||
Db        122 ATCACCATTCCACATGATATAGACCTGGGTGACTCCCGTGTGGTTATCCAGGATTATGAT 181

Qy        334 AsnGlnHisGluGln 338
              ||||||||||||||||
Db        182 AACCAGCAYGAGCAA 196

RESULT 610
BD077288
LOCUS       BD077288                197 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077288
VERSION     BD077288.1  GI:22622891
KEYWORDS    JP 2001520384-A/167.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 197)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 167 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/167
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   z12-orf2.con
            FH   Key             Location/Qualifiers
            FT   source          1. .197
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                 virus)'.
FEATURES             Location/Qualifiers
     source          1. .197
                     /organism="unidentified"
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              471           Length:        197
Score:                  63.00         Matches:       63
Percent Similarity:     96.92%        Conservative:  0
Best Local Similarity:  96.92%        Mismatches:    2
Query Match:            11.48%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x BD077288 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
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Db          2 ACAGAATTAATTTCGTCGGCTGGGGGTCAACTGTTCTACTCCCGCCCTGTCGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
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Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
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Db        122 ATAGCTATTCCACATGACATAGATTTGGGCGACTCTCGTTTGGTAATCCAGGATTATGAT 181

Qy        334 AsnGlnHisGluGln 338
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Db        182 AACCAACACGAACAA 196

RESULT 611
AY626041
LOCUS       AY626041                 189 bp    RNA     linear   VRL 12-JUN-2004
DEFINITION  Hepatitis E virus isolate MP13 structural protein gene, partial
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ACCESSION   AY626041
VERSION     AY626041.1  GI:48374467
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 189)
  AUTHORS   Mansuy,J.M., Peron,J.M., Bureau,C., Alric,L., Vinel,J.P. and
            Izopet,J.
  TITLE     Immunologically silent autochthonous acute hepatitis E virus
            infection in France
  JOURNAL   J. Clin. Microbiol. 42 (2), 912-913 (2004)
   PUBMED   14766888
REFERENCE   2  (bases 1 to 189)
  AUTHORS   Mansuy,J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-MAY-2004) Virology Laboratory, University Hospital
            Purpan, Palce du Dr Baylac TSA 40031, Toulouse 31059, France
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Best Local Similarity:  98.39%        Mismatches:    1
Query Match:            11.11%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-15 (1-549) x AY626041 (1-189)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
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Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
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Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
              |||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||
Db        122 ATCGCTATACCACATGATATAGATTTAGGGGATTCCCGCGTGGTTATACAGGATTATGAC 181

Qy        334 AsnGln 335
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Db        182 AACCAR 187

RESULT 612
AY626042
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DEFINITION  Hepatitis E virus isolate MP14 structural protein gene, partial
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ACCESSION   AY626042
VERSION     AY626042.1  GI:48374469
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 189)
  AUTHORS   Mansuy,J.M., Peron,J.M., Bureau,C., Alric,L., Vinel,J.P. and
            Izopet,J.
  TITLE     Immunologically silent autochthonous acute hepatitis E virus
            infection in France
  JOURNAL   J. Clin. Microbiol. 42 (2), 912-913 (2004)
   PUBMED   14766888
REFERENCE   2  (bases 1 to 189)
  AUTHORS   Mansuy,J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-MAY-2004) Virology Laboratory, University Hospital
            Purpan, Palce du Dr Baylac TSA 40031, Toulouse 31059, France
FEATURES             Location/Qualifiers
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US-09-769-066-15 (1-549) x AY626042 (1-189)

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Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
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Db          2 ACAGAATTGATTTCGTCGGCTGGAGGTCAACTGTTCTACTCCCGCCCGGTTGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
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Db         62 AATGGCGAGCCGACTGTTAAGTTATACACCTCTGTCGAGAATGCACAGCAGGACAAGGGC 121

Qy        314 IleAlaIleProHisAspIleAspLeuGlyGluSerArgValValIleGlnAspTyrAsp 333
              |||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        122 ATCGCTATACCACATGATATAGATTTAGGGGATTCCCGCGTGGTTATACAGGATTATGAC 181

Qy        334 AsnGln 335
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Db        182 AACCAR 187
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Search completed: July 26, 2005, 08:54:17
Job time : 279 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2005, 09:17:43 ; Search time 137 Seconds
(without alignments)
2.335 Million cell updates/sec

Title: US-09-769-066-16
Perfect score: 549
Sequence: 1 AVAPAHDTSPVPDVDSRGAI.....QSTVAELQRLKVKVGKTREL 549

Scoring table: UNITARY_AA
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 612 seqs, 291396 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 612 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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431	114	20.8	449	1	AR207637	ACCESSION:AR207637
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433	110	20.0	348	1	AY621100	ACCESSION:AY621100
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457	108	19.7	348	1	AY596318	ACCESSION:AY596318
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465	107	19.5	346	1	AF117281	ACCESSION:AF117281
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519	94	17.1	301	1	AF466676	ACCESSION:AF466676
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522	94	17.1	304	1	AF296160	ACCESSION:AF296160
523	94	17.1	304	1	AY052774	ACCESSION:AY052774
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526	93	16.9	299	1	AF324503	ACCESSION:AF324503
527	93	16.9	300	1	HEE428852	ACCESSION:AJ428852
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529	93	16.9	301	1	AF134917	ACCESSION:AF134917
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555	92	16.8	304	1	AF296161	ACCESSION:AF296161
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557	92	16.8	304	1	AF296164	ACCESSION:AF296164
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577	78	14.2	256	1	AF228529	ACCESSION:AF228529
578	78	14.2	256	1	AF228530	ACCESSION:AF228530
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582	77	14.0	249	1	AF407560	ACCESSION:AF407560
583	77	14.0	249	1	AF407567	ACCESSION:AF407567
584	77	14.0	249	1	AF505860	ACCESSION:AF505860
585	77	14.0	256	1	AF228538	ACCESSION:AF228538
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591	75	13.7	250	1	AF407570	ACCESSION:AF407570
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594	70	12.8	227	1	AY753554	ACCESSION:AY753554
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597	68	12.4	212	1	AF347692	ACCESSION:AF347692
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ALIGNMENTS

RESULT 1
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LOCUS AR170407 1644 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 4 from patent US 6291641.
ACCESSION AR170407
VERSION AR170407.1 GI:17908366
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1644)
AUTHORS Fuerst,T.R., McAtee,C.Patrick., Yarbough,P.O. and Zhang,Y.-F.
TITLE Hepatitis E virus antigens and uses therefor
JOURNAL Patent: US 6291641-A 4 18-SEP-2001;
FEATURES Location/Qualifiers
source 1. .1644
/organism="unknown"
/mol_type="unassigned DNA"

Alignment Scores:

Pred. No.:	0.64	Length:	1644
Score:	535.50	Matches:	546
Percent Similarity:	99.45%	Conservative:	0
Best Local Similarity:	99.45%	Mismatches:	2
Query Match:	97.54%	Indels:	1
DB:	1	Gaps:	1

US-09-769-066-16 (1-549) x AR170407 (1-1644)

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Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
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Db          1 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 60

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
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Db         61 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 120

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
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Db        121 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 180

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 240

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db        241 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 300

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        301 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 360

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Db        361 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 420

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Db        421 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 480

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
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Db        481 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 540

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Db        541 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 600

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

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Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

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Db        718 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 777

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Db        778 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 837

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db        838 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 897

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320

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Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db        958 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1017

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1018 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1077

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

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Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420

Db       1198 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1257

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

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Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460

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Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480

Db       1378 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1437

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500

Db       1438 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1497

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Db       1498 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1557

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1558 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1617

Qy        541 ValLysValGlyLysThrArgGluLeu 549

Db       1618 GTTAAGGTGGGTAAAACTCGGGAGTTG 1644

RESULT 2
I73140
LOCUS       I73140                  1980 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 2 from patent US 5686239.
ACCESSION   I73140
VERSION     I73140.1  GI:3009279
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1980)
  AUTHORS   Reyes,G.R., Tam,A.W. and Yarbough,P.O.
  TITLE     Hepatitis E virus peptides and methods
  JOURNAL   Patent: US 5686239-A 2 11-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .1980
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Alignment Scores:
Pred. No.:              0.646          Length:          1980
Score:                  535.50         Matches:         546
Percent Similarity:     99.45%         Conservative:    0
Best Local Similarity:  99.45%         Mismatches:      2
Query Match:            97.54%         Indels:          1
DB:                     1              Gaps:            1

US-09-769-066-16 (1-549) x I73140 (1-1980)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20

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Db        394 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60

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Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

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Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

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Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

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Db        814 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        874 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Db       1051 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1110

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Db       1111 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1170

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

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Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

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Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480

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Db       1831 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1890

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

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Qy        541 ValLysValGlyLysThrArgGluLeu 549

Db       1951 GTTAAGGTGGGTAAAACTCGGGAGTTG 1977

RESULT 3
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LOCUS       AR002161               2055 bp    DNA     linear   PAT 04-DEC-1998

DEFINITION  Sequence 4 from patent US 5741490.
ACCESSION   AR002161
VERSION     AR002161.1  GI:3963715
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2055)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.D.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 5741490-A 4 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .2055
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Alignment Scores:
Pred. No.:                0.647        Length:          2055
Score:                    535.50       Matches:         546
Percent Similarity:       99.45%       Conservative:    0
Best Local Similarity:    99.45%       Mismatches:      2
Query Match:              97.54%       Indels:          1
DB:                       1            Gaps:            1

US-09-769-066-16 (1-549) x AR002161 (1-2055)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20

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Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40

Db        394 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60

Db        454 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 513

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Db        514 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        574 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        634 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db        694 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

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Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180

Db        814 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        874 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db        934 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCAC---TCC 990

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Db        991 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1050

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1110

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1170

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1230

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1290

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1291 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1350

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1410

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1411 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1470

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1471 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1530

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1531 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1590

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1591 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1650

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1651 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1710

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1711 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1770

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1771 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1830

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1831 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1890

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1891 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1950

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1951 GTTAAGGTGGGTAAAACTCGGGAGTTG 1977

RESULT 4
AR170405
LOCUS       AR170405               2055 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 2 from patent US 6291641.
ACCESSION   AR170405
VERSION     AR170405.1  GI:17908364
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2055)
  AUTHORS   Fuerst,T.R., McAtee,C.Patrick., Yarbough,P.O. and Zhang,Y.-F.
  TITLE     Hepatitis E virus antigens and uses therefor
  JOURNAL   Patent: US 6291641-A 2 18-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .2055
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:              0.647          Length:          2055
Score:                  535.50         Matches:         546
Percent Similarity:     99.45%         Conservative:    0
Best Local Similarity:  99.45%         Mismatches:      2
Query Match:            97.54%         Indels:          1
DB:                     1              Gaps:            1

US-09-769-066-16 (1-549) x AR170405 (1-2055)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCAC---TCC 990

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1050

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
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Db       1051 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1110
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Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db       1111 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1170

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1230

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1290

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Db       1291 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1350

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1410

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1411 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1470

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1471 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1530

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1531 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1590

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1591 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1650

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1651 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1710

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1711 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1770

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1771 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1830

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1831 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1890

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1891 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1950

Qy        541 ValLysValGlyLysThrArgGluLeu 549
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Db       1951 GTTAAGGTGGGTAAAACTCGGGAGTTG 1977
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RESULT 5
AR232466
LOCUS       AR232466                2055 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 4 from patent US 6455492.
ACCESSION   AR232466
VERSION     AR232466.1  GI:27274535
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2055)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.O.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 6455492-A 4 24-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .2055
                     /organism="unknown"
                     /mol_type="mRNA"
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Alignment Scores:
Pred. No.:                0.647          Length:              2055
Score:                    535.50         Matches:             546
Percent Similarity:       99.45%         Conservative:        0
Best Local Similarity:    99.45%         Mismatches:          2
Query Match:              97.54%         Indels:              1
DB:                       1              Gaps:                1

US-09-769-066-16 (1-549) x AR232466 (1-2055)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCAC---TCC 990

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1050

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1110

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1170
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Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1230

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1290

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1291 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1350

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1410

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1411 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1470

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1471 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1530

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1531 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1590

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1591 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1650

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1651 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1710

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1711 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1770

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1771 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1830

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1831 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1890

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1891 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1950

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1951 GTTAAGGTGGGTAAAACTCGGGAGTTG 1977

RESULT 6
AR002159
LOCUS       AR002159               2100 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 2 from patent US 5741490.
ACCESSION   AR002159
VERSION     AR002159.1  GI:3963713
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2100)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.D.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 5741490-A 2 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .2100
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Alignment Scores:
Pred. No.:              0.648          Length:          2100
Score:                  535.50         Matches:         546
Percent Similarity:     99.45%         Conservative:    0
Best Local Similarity:  99.45%         Mismatches:      2
Query Match:            97.54%         Indels:          1
DB:                     1              Gaps:            1

US-09-769-066-16 (1-549) x AR002159 (1-2100)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 438

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
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Db        439 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 498

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
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Db        499 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 558

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
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Db        559 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 618

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db        619 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 678

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        679 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 738

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
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Db        859 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 918

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Db        919 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 978

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Db        979 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCAC---TCC 1035

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Db       1036 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1095

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
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Db       1216 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1275
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Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
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Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Db       1336 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1395

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Db       1396 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1455

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Db       1456 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1515

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       1516 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1575

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
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Db       1576 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1635

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Db       1636 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1695

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
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Db       1696 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1755

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Db       1816 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1875

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
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Db       1876 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1935

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
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Db       1936 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1995

Qy        541 ValLysValGlyLysThrArgGluLeu 549
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LOCUS       AR232464               2100 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 2 from patent US 6455492.
ACCESSION   AR232464
VERSION     AR232464.1  GI:27274533
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2100)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.O.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 6455492-A 2 24-SEP-2002;
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:                0.648          Length:          2100
Score:                    535.50         Matches:         546
Percent Similarity:       99.45%         Conservative:    0
Best Local Similarity:    99.45%         Mismatches:      2
Query Match:              97.54%         Indels:          1
DB:                       1              Gaps:            1

US-09-769-066-16 (1-549) x AR232464 (1-2100)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
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Db        379 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 438

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 498

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
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Db        499 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 558

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
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Db        619 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 678

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        679 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 738

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Db        739 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 798

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Db        799 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 858

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
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Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Db        979 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCAC---TCC 1035

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Db       1036 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1095

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
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Db       1096 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1155

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db       1156 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1215

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Db       1216 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1275

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
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Db       1276 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1335
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Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Db       1336 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1395

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Db       1396 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1455

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Db       1456 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1515

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       1516 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1575

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
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Db       1576 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1635

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Db       1636 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1695

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
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Db       1696 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1755

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
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Db       1756 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1815

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
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Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
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Db       1876 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1935

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
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Db       1936 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1995

Qy        541 ValLysValGlyLysThrArgGluLeu 549
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Db       1996 GTTAAGGTGGGTAAAACTCGGGAGTTG 2022

RESULT 8
E17105
LOCUS       E17105                  1647 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  DNA encoding HEV hollow particle.
ACCESSION   E17105
VERSION     E17105.1  GI:5711788
KEYWORDS    JP 1998234383-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1647)
  AUTHORS   Takeda,N., Ri,T. and Miyamura,T.
  TITLE     HEPATITIS E VIRUS HOLLOW PARTICLE, GENE ENCODING THE SAME AND
            PREPARATION OF RECOMBINATION VECTOR CONTAINING THE GENE AND
            UTILIZATION OF THE RECOMBINATION VECTOR
  JOURNAL   Patent: JP 1998234383-A 1 08-SEP-1998;
            DENKA SEIKEN CO LTD, KOKURITSU KANSENSHIYOU KENKYUSHO
COMMENT     OS   Hepatitis E virus
            PN   JP 1998234383-A/1
            PD   08-SEP-1998
            PF   28-FEB-1997 JP 1997062445
            PI   TAKEDA NAOKAZU, RI TENSEI, MIYAMURA TATSUO
            PC   C12N15/09,C07K14/08,C12N5/10,C12P21/02;
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            CC   topology: Linear;
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FEATURES             Location/Qualifiers
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Alignment Scores:
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Percent Similarity:     94.90%         Conservative:    0
Best Local Similarity:  94.90%         Mismatches:      28
Query Match:            94.90%         Indels:          0
DB:                     1              Gaps:            0

US-09-769-066-16 (1-549) x E17105 (1-1647)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
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Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
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Db         61 TTGCGCCGGCAGTATAATCTATCAACATCTCCCCTCACCTCTTCCGTGGCCACCGGCACT 120

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
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Db        121 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAAT 180

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
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Db        181 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 240

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        301 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 360

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Db        361 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 420

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Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 600

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 660

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAG 720

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||   ||||||      ||||||||||||||   ||||||||||||||||||||
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Db        721 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 780

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db        781 CTGTTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 840

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db        841 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCGGCCAATGGCGAGCCGACTGTTAAG 900

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320

Db        901 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 960

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db        961 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGG 1020

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1021 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1080

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1081 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1140

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1141 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1200

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420

Db       1201 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1260

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1261 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1320

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460

Db       1321 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1380

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480

Db       1381 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1440

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500

Db       1441 CCCGTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1500

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1501 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1560

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1561 CCTCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1620

Qy        541 ValLysValGlyLysThrArgGluLeu 549

Db       1621 ATGAAGGTGGGTAAAACTCGGGAGTTA 1647

RESULT 9
AR278920
LOCUS       AR278920               1686 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 19 from patent US 6514690.
ACCESSION   AR278920
VERSION     AR278920.1  GI:29713554
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1686)
  AUTHORS   Li,F., Hui,Z., Anderson,D.A., Logarnini,S.A. and Torresi,J.
  TITLE     Immunoreactive antigens of Hepatitis E Virus
  JOURNAL   Patent: US 6514690-A 19 04-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .1686
                     /organism="unknown"
                     /mol_type="genomic DNA"

Alignment Scores:
Pred. No.:                0.793          Length:          1686
Score:                    521.00         Matches:         521
Percent Similarity:       94.90%         Conservative:    0
Best Local Similarity:    94.90%         Mismatches:      28
Query Match:              94.90%         Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-16 (1-549) x AR278920 (1-1686)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20

Db         38 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 97

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40

Db         98 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 157

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60

Db        158 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 217

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

Db        218 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 277

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        278 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 337

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        338 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 397

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db        398 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 457

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db        458 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 517

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180

Db        518 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 577

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        578 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 637

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db        638 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 697

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db        698 CGTCGCGGTGCAGATGGGACTGCCGAGCTTACCACCACGGCTGCTACCCGCTTCATGAAG 757

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260

Db        758 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 817

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db        818 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 877
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Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        878 GGTGGCCAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 937

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db        938 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 997

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        998 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1057

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1058 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1117

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1118 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1177

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1178 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1237

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||  |||||||||||||||||||||||||||  |||      |||
Db       1238 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1297

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1298 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1357

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              |||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db       1358 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1417

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db       1418 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1477

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||  |||||||||  ||||||||||||||  ||||||||||||||||||||||||
Db       1478 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCCGCGCTAGCATTGCTTGAG 1537

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||  |||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db       1538 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1597

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1598 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1657

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1658 ATGAAGGTGGGTAAAACTCGGGAGTTA 1684

RESULT 10
E17107
LOCUS       E17107                  1983 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Hepatitis E virus ORF2.
ACCESSION   E17107
VERSION     E17107.1  GI:5711790
KEYWORDS    JP 1998234383-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1983)
  AUTHORS   Takeda,N., Ri,T. and Miyamura,T.
  TITLE     HEPATITIS E VIRUS HOLLOW PARTICLE, GENE ENCODING THE SAME AND
            PREPARATION OF RECOMBINATION VECTOR CONTAINING THE GENE AND
            UTILIZATION OF THE RECOMBINATION VECTOR
  JOURNAL   Patent: JP 1998234383-A 3 08-SEP-1998;
            DENKA SEIKEN CO LTD, KOKURITSU KANSENSHIYOU KENKYUSHO
COMMENT     OS   Hepatitis E virus
            PN   JP 1998234383-A/3
            PD   08-SEP-1998
            PF   28-FEB-1997 JP 1997062445
            PI   TAKEDA NAOKAZU, RI TENSEI, MIYAMURA TATSUO
            PC   C12N15/09,C07K14/08,C12N5/10,C12P21/02;
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .1983
            FT                   /organism='Hepatitis E virus' FT   CDS
                 1. .1983
            FT                   /product='structural protein'.
FEATURES              Location/Qualifiers
     source           1. .1983
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              0.799          Length:          1983
Score:                  521.00         Matches:         521
Percent Similarity:     94.90%         Conservative:    0
Best Local Similarity:  94.90%         Mismatches:      28
Query Match:            94.90%         Indels:          0
DB:                     1              Gaps:            0

US-09-769-066-16 (1-549) x E17107 (1-1983)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db        334 GCGGTCGCTCCAGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCTCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        394 TTGCGCCGGCAGTATAATCTATCAACATCTCCCCTCACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||  |||  ||||||||||||||||||||||||
Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAACACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||      ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db        994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAG 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260

Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db       1114 CTGTTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCGGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320

Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420

Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460

Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480

Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500

Db       1774 CCCGTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1894 CCTCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 ValLysValGlyLysThrArgGluLeu 549

Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTA 1980

RESULT 11
AR278906
LOCUS       AR278906               1984 bp    DNA     linear   PAT 10-APR-2003

DEFINITION  Sequence 1 from patent US 6514690.
ACCESSION   AR278906
VERSION     AR278906.1  GI:29713540
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1984)
  AUTHORS   Li,F., Hui,Z., Anderson,D.A., Logarnini,S.A. and Torresi,J.
  TITLE     Immunoreactive antigens of Hepatitis E Virus
  JOURNAL   Patent: US 6514690-A 1 04-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .1984
                     /organism="unknown"
                     /mol_type="genomic DNA"

Alignment Scores:
Pred. No.:                0.799          Length:          1984
Score:                    521.00         Matches:         521
Percent Similarity:       94.90%         Conservative:    0
Best Local Similarity:    94.90%         Mismatches:      28
Query Match:              94.90%         Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-16 (1-549) x AR278906 (1-1984)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20

Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40

Db        394 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60

Db        454 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

Db        514 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        574 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db        754 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180

Db        814 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        874 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db        934 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db        994 CGTCGCGGTGCAGATGGGACTGCCGAGCTTACCACCACGGCTGCTACCCGCTTCATGAAG 1053
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Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||  ||||||      ||||||||||||||   ||||||||||||||||||||
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGTGGCCAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              |||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db       1234 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              |||||||||||||   |||||||||||||||||||||||||   |||       |||
Db       1534 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db       1654 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||  |||||||||  ||||||||||||||  |||||||||||||||||||||||||
Db       1774 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCCGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||  |||||||||  ||||||||||||||||||||||||||||||||||||||||
Db       1834 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1893

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||
Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTA 1980

RESULT 12
AR170406
LOCUS       AR170406               1647 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 3 from patent US 6291641.
ACCESSION   AR170406
VERSION     AR170406.1  GI:17908365
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1647)
  AUTHORS   Fuerst,T.R., McAtee,C.Patrick., Yarbough,P.O. and Zhang,Y.-F.
  TITLE     Hepatitis E virus antigens and uses therefor
  JOURNAL   Patent: US 6291641-A 3 18-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .1647
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                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:                0.804          Length:          1647
Score:                    520.00         Matches:         520
Percent Similarity:       94.72%         Conservative:    0
Best Local Similarity:    94.72%         Mismatches:      29
Query Match:              94.72%         Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-16 (1-549) x AR170406 (1-1647)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
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Db          1 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 60

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db         61 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 120

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||  |||  ||||||||||||||||||||||||||
Db        121 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 180

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 240

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 300

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 360

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 420

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 480

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        481 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 540

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 600

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 660

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 720

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||  ||||||      ||||||||||||||   ||||||||||||||||||||
Db        721 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 780
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Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
Db        781 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 840

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
Db        841 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 900

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
Db        901 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 960

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
Db        961 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1020

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
Db       1021 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1080

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
Db       1081 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1140

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
Db       1141 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1200

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
Db       1201 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1260

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
Db       1261 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1320

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
Db       1321 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1380

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
Db       1381 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1440

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
Db       1441 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1500

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
Db       1501 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1560

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
Db       1561 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1620

Qy        541 ValLysValGlyLysThrArgGluLeu 549
Db       1621 ATGAAGGTGGGTAAAACTCGGGAGTTG 1647

RESULT 13
I73139
LOCUS       I73139                  1983 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 1 from patent US 5686239.
ACCESSION   I73139
VERSION     I73139.1  GI:3009278
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1983)
  AUTHORS   Reyes,G.R., Tam,A.W. and Yarbough,P.O.
  TITLE     Hepatitis E virus peptides and methods
  JOURNAL   Patent: US 5686239-A 1 11-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .1983
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:                0.811          Length:          1983
Score:                    520.00         Matches:         520
Percent Similarity:       94.72%         Conservative:    0
Best Local Similarity:    94.72%         Mismatches:      29
Query Match:              94.72%         Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-16 (1-549) x I73139 (1-1983)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
Db        394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
Db        754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
Db        874 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
Db        934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
Db        994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
Db       1114 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320

Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420

Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460

Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480

Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500

Db       1774 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1894 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 ValLysValGlyLysThrArgGluLeu 549

Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTG 1980

RESULT 14
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LOCUS       AF124407                1983 bp    RNA     linear   VRL 24-JUL-1999
DEFINITION  Hepatitis E virus isolate AKL-90 ORF-2 gene, complete cds.
ACCESSION   AF124407
VERSION     AF124407.1  GI:5579229
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 1983)
  AUTHORS   Arankalle,V.A., Paranjape,S., Emerson,S.U., Purcell,R.H. and
            Walimbe,A.M.
  TITLE     Phylogenetic analysis of hepatitis E virus isolates from India
            (1976-1993)
  JOURNAL   J. Gen. Virol. 80 (Pt 7), 1691-1700 (1999)
  MEDLINE   99350000
    PUBMED  10423137
REFERENCE   2  (bases 1 to 1983)
  AUTHORS   Arankalle,V.A., Paranjape,S., Emerson,S.U., Purcell,R.H. and
            Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JAN-1999) Hepatitis, National Institute of Virology,
            20-A Dr. Ambedkar Road, Pune, Maharashtra 411001, India
FEATURES             Location/Qualifiers
     source          1. .1983
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                     /mol_type="genomic RNA"
                     /isolate="AKL-90"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             1. .1983
                     /codon_start=1
                     /product="ORF-2"
                     /protein_id="AAD45493.1"
                     /db_xref="GI:5579230"
                     /translation="MRPRPILLLLLMFLPMLPAPPPGQPSGRRRGRRSGGSGGGFWGD
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                     PTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLV
                     MLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRG
                     ADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAG
                     GQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQD
                     RPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQ
                     AVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTAS
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Alignment Scores:
Pred. No.:                0.811          Length:          1983
Score:                    520.00         Matches:         520
Percent Similarity:       94.72%         Conservative:    0
Best Local Similarity:    94.72%         Mismatches:      29
Query Match:              94.72%         Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-16 (1-549) x AF124407 (1-1983)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20

Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCGGTGCCTGATGTCGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40

Db        394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60

Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGCCCGCTTTTACCCCTTCAGGACGGCACCAAC 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

Db        514 ACTCATATAATGGCCACGGAAGCTTCTAATTATGCCCAATACCGAGTTGCCCGTGCCACG 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        574 ATCCGTTACCGCCCGCTGGTCCCCAACGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140

Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGCGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db        754 CACTATCGTAACCAGGGTTGGCGCTCTGTCGAGACCTCCGGGGTGGCCGAGGAGGAGGCC 813
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Qy       161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
Db       814 ACCTCCGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAATACA 873

Qy       181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
Db       874 CCTTACACCGGTGCCCTTGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy       201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
Db       934 ACCCCCGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy       221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
Db       994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCCACCCGCTTTATGAAG 1053

Qy       241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy       261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
Db       1114 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy       281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy       301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
Db       1234 CTATATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy       321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGACCGG 1353

Qy       341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy       361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
Db       1414 TGGCTCTCCCTCACCGCTGCCGAGTATGACCAGTCCACCTATGGCTCTTCGACTGGCCCA 1473

Qy       381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTCAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy       401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy       421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy       441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTACAACACCACTGCTAGCGACCAATTGCTTGTC 1713

Qy       461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
Db       1714 GAGAATGCCGCCGGGCACCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy       481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
Db       1774 CCCGTCTCTATTTCTGCGGTTGCAGTCTTCGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy       501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
Db       1834 GATACCTTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy       521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
Db       1894 CCCCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy       541 ValLysValGlyLysThrArgGluLeu 549
Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTG 1980
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RESULT 15
AR002160

LOCUS	AR002160 2049 bp DNA linear PAT 04-DEC-1998
DEFINITION	Sequence 3 from patent US 5741490.
ACCESSION	AR002160
VERSION	AR002160.1 GI:3963714
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
	Unclassified.
REFERENCE	1 (bases 1 to 2049)
AUTHORS	Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W., Krawczynski,K.Z. and Yarbough,P.D.
TITLE	Hepatitis E virus vaccine and method
JOURNAL	Patent: US 5741490-A 3 21-APR-1998;
FEATURES	Location/Qualifiers
source	1. .2049
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	/mol_type="unassigned DNA"

Alignment Scores:

Pred. No.:	0.812	Length:	2049
Score:	520.00	Matches:	520
Percent Similarity:	94.72%	Conservative:	0
Best Local Similarity:	94.72%	Mismatches:	29
Query Match:	94.72%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AR002160 (1-2049)

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Qy         1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
Db       334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 393

Qy        21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
Db       394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy        41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
Db       454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 513

Qy        61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
Db       514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy        81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
Db       574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy       101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
Db       634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy       121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
Db       694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy       141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
Db       754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy       161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
Db       814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873
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Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
Db        874 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
Db        934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
Db        994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
Db       1114 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
Db       1774 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
Db       1894 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 ValLysValGlyLysThrArgGluLeu 549
Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTG 1980

RESULT 16
AR170404
LOCUS       AR170404               2049 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 1 from patent US 6291641.
ACCESSION   AR170404
VERSION     AR170404.1  GI:17908363
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2049)
  AUTHORS   Fuerst,T.R., McAtee,C.Patrick., Yarbough,P.O. and Zhang,Y.-F.
  TITLE     Hepatitis E virus antigens and uses therefor
  JOURNAL   Patent: US 6291641-A 1 18-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .2049
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:              0.812          Length:          2049
Score:                  520.00         Matches:         520
Percent Similarity:     94.72%         Conservative:    0
Best Local Similarity:  94.72%         Mismatches:      29
Query Match:            94.72%         Indels:          0
DB:                     1              Gaps:            0

US-09-769-066-16 (1-549) x AR170404 (1-2049)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
Db        394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
Db        754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
Db        874 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933
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Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||   ||||||       ||||||||||||||||   ||||||||||||||||||||||
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              |||||||||||||   |||||||||||||||||||||||||||||   |||      |||
Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
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Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||  |||||||||  ||||||||||||||||  ||||||||||||||||||||||||
Db       1774 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||  |||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 ValLysValGlyLysThrArgGluLeu 549
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Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTG 1980

RESULT 17
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AR232465
LOCUS       AR232465                2049 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 3 from patent US 6455492.
ACCESSION   AR232465
VERSION     AR232465.1  GI:27274534
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2049)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.O.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 6455492-A 3 24-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .2049
                     /organism="unknown"
                     /mol_type="mRNA"

Alignment Scores:
Pred. No.:                0.812          Length:          2049
Score:                    520.00         Matches:         520
Percent Similarity:       94.72%         Conservative:    0
Best Local Similarity:    94.72%         Mismatches:      29
Query Match:              94.72%         Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-16 (1-549) x AR232465 (1-2049)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
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Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||||||
Db        394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              |||||||||||||||||||||||||   |||   ||||||||||||||||||||||||||
Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993
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Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Db        994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
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Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              |||||||||||||   |||||||||||||||||||||||||||||   |||      |||
Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
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Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||   |||||||||   ||||||||||||||   |||||||||||||||||||||||
Db       1774 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||   |||||||||   ||||||||||||||||||||||||||||||||||||||||
Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 ValLysValGlyLysThrArgGluLeu 549
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Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTG 1980

RESULT 18
AR278918
LOCUS       AR278918               1658 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 15 from patent US 6514690.
ACCESSION   AR278918
VERSION     AR278918.1  GI:29713552
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1658)
  AUTHORS   Li,F., Hui,Z., Anderson,D.A., Logarnini,S.A. and Torresi,J.
  TITLE     Immunoreactive antigens of Hepatitis E Virus
  JOURNAL   Patent: US 6514690-A 15 04-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .1658
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Alignment Scores:
Pred. No.:                0.891          Length:          1658
Score:                    513.00         Matches:         513
Percent Similarity:       95.00%         Conservative:    0
Best Local Similarity:    95.00%         Mismatches:      27
Query Match:              93.44%         Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-16 (1-549) x AR278918 (1-1658)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
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Db         38 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 97

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db         98 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 157

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||   |||   ||||||||||||||||||||||||
Db        158 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 217

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
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Db        218 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 277

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db        278 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 337

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        338 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 397

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Db        398 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 457

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Db        458 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGGTGGCGGAGGAGGAGGCC 517

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
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Db        518 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 577

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Db        578 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 637

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Db        638 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 697

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Db        698 CGTCGCGGTGCAGATGGGACTGCCGAGCTTACCACCACGGCTGCTACCCGCTTCATGAAG 757

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
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Db        758 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 817

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db        818 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 877

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db        878 GGTGGCCAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 937

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320

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Db        998 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1057

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1058 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1117

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1118 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1177

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1178 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1237

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420

Db       1238 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1297

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1298 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1357

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460

Db       1358 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1417

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480

Db       1418 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1477

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500

Db       1478 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCCGCGCTAGCATTGCTTGAG 1537

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1538 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1597

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1598 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1657
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RESULT 19
AB082545
LOCUS       AB082545               1666 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, complete cds,
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ACCESSION   AB082545
VERSION     AB082545.1  GI:22759586
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
  PUBMED    12202555
REFERENCE   2  (bases 1 to 1666)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp,. Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              0.959          Length:          1666
Score:                  508.00         Matches:         508
Percent Similarity:     92.70%         Conservative:    0
Best Local Similarity:  92.70%         Mismatches:      40
Query Match:            92.53%         Indels:          0
DB:                     1              Gaps:            0

US-09-769-066-16 (1-549) x AB082545 (1-1666)

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Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40

Db         70 CTACGCCGCCAGTATAATCTATCAACATCCCCGCTCACGTCTACCATCGCTACCGGCACC 129

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60

Db        130 AATCTTGTTTTATATGCTGCTCCCCTGAGCCCTTTGCTTCCGCTTCAAGATGGGACTAAC 189

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

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Db        250 ATCCGGTATCGCCCACTCGTGCCGAACGCTGTTGGCGGGTACGCTATATCTATTTCTTTC 309
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Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
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Db        310 TGGCCCCAGACTACAACCACCCCGACATCTGTCGATATGAATTCTATTACCTCTACTGAT 369

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Db        370 GTTCGGATTCTTGTTCAGCCTGGTATCGCCTCCGAGCTTGTGATTCCCAGTGAGCGCCTG 429

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
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Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
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Db        490 ACCTCCGGCCTTGTTATGCTCTGCATCCATGGATCACCTGTGAACTCTTACACTAATACG 549

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
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Db        550 CCTTATACTGGTGCTCTTGGCTTGCTTGATTTTGCACTCGAACTTGAGTTCCGCAATTTG 609

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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Db        610 ACACCCGGTAATACGAATACGCGTGTTTCCCGTTATTCGAGTAGCGCGCGCCACAAGCTA 669

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
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Db        730 GATCTTCACTTCACAGGGACCAATGGTGTTGGTGAGGTCGGTCGCGGTATAGCGCTAACC 789

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAATTGATTTCGTCGGCT 849

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
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Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
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Db        910 CTTTACACTTCAGTCGAGAACGCCCAGCAGGATAAGGGTATAGCTATTCCACATGATATC 969

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
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Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
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Db       1030 CCCACCCCGTCTCCAGCCCCTTCCCGCCCTTTTTCTGTCCTCCGCGCTAATGATGTGCTT 1089

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
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Db       1090 TGGCTTTCACTTACAGCTGCTGAGTATGATCAGACTACTTATGGTTCTTCCACTAATCCT 1149

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
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Db       1150 ATGTATGTTTCTGATACTGTGACATTTGTTAATGTGGCGACTGGTGCTCAGGGGGTCTCT 1209

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
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Db       1210 CGCTCTCTGGACTGGTCTAAAGTCACCCTTGATGGGCGTCCACTTACTACTATCCAGCAG 1269

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
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Db       1270 TATTCTAAGACCTTCTTTGTTTTGCCCCTCCGTGGCAAGCTCTCTTTCTGGGAGGCTGGC 1329

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
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Db       1330 ACCACTAAGGCCGGCTACCCTTATAATTATAACACCACCGCCAGTGACCAGATCTTGATT 1389

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
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Db       1390 GAAAATGCAGCCGGTCACCGTGTTTGCATCTCGACCTACACTACTAATCTTGGCTCTGGC 1449

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
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Db       1450 CCTGTTTCTATTTCTGCTGTCGGTGTCCTTGCACCTCATTCCGCACTGGCCGCTTTAGAG 1509

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||    |||||||||   ||||||||||||||||||||||||||||||||||||||||
Db       1510 GACACTGTTGATTACCCTGCTCGCGCCCACACCTTTGATGATTTCTGCCCTGAGTGCCGT 1569

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1570 ACGCTCGGCCTTCAGGGCTGTGCTTTTCAGTCAACTGTTGCTGAGCTGCAGCGCCTTAAA 1629

Qy        541 ValLysValGlyLysThrArgGlu 548
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Db       1630 ATGAAGGTGGGTAAAACCCGGGAG 1653
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RESULT 20
HPEPPG
LOCUS HPEPPG 1649 bp RNA linear VRL 24-JAN-2003
DEFINITION Hepatitis E virus gene for polyprotein, partial cds.
ACCESSION D90274
VERSION D90274.1 GI:221702
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Uchida,T., Suzuki,K., Hayashi,N., Iida,F., Hara,T., Oo,S.S., Wang,C., Shikata,T., Ichikawa,M., Rikihisa,T., Mizuno,K. and Win,K.M.
TITLE Hepatitis E virus: cDNA cloning and expression
JOURNAL Microbiol. Immunol. 36 (1), 67-79 (1992)
MEDLINE 92261377
PUBMED 1584074
REFERENCE 2 (bases 1 to 1649)
AUTHORS Uchida,T.
TITLE Direct Submission
JOURNAL Submitted (25-DEC-1990) Toshikazu Uchida, Nihon University School of Medicine, 1st Department of Pathology; 30-1 Oyaguchi-Kamimachi, Itabashi-ku, Tokyo 173, Japan (Tel:81-3-3972-8111, Fax:81-3-3972-8830)

FEATURES Location/Qualifiers
source 1. .1649
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/mol_type="genomic RNA"
/isolate="HT-4"
/isolation_source="from infected monkey bile"
/db_xref="taxon:12461"
/note="clones #35, #38 and #41"
CDS <1. .>1456
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/translation="RRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMA
TEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRI
LVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTP
YTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFM
KDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSAHGEP
TVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLR
ANDVLWLSLTAAEYDQSTYGSSTAPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGR
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TYTTSLGAGPVSISAVAVLAPHSALALLEDTLDYP"

Alignment Scores:
Pred. No.: 1.14 Length: 1649
Score: 496.00 Matches: 496
Percent Similarity: 93.94% Conservative: 0
Best Local Similarity: 93.94% Mismatches: 32

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Query Match:          90.35%      Indels:      0
DB:                   1           Gaps:        0

US-09-769-066-16 (1-549) x HPEPPG (1-1649)

Qy         22 ArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThrAsn 41
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||
Db          3 CGCCGGCAGTATAATCTATCAACATCTCCCCTCACTTCTTCCGTGGCCACCGGCACTAAC 62

Qy         42 LeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsnThr 61
              ||||||||||||||||||||||||    |||   ||||||||||||||||||||||||||
Db         63 CTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAATACC 122

Qy         62 HisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIle 81
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||
Db        123 CATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGTCCGTGCCACAATC 182

Qy         82 ArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrp 101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 CGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTCTGG 242

Qy        102 ProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAspVal 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 CCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGATGTT 302

Qy        122 ArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeuHis 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACAC 362

Qy        142 TyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaThr 161
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Db        363 TATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCTACC 422

Qy        162 SerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrPro 181
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Db        423 TCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAACACACCC 482

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
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Db        483 TATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTTACC 542

Qy        202 ThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
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Db        543 CCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGT 602

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
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Db        603 CGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAGGAC 662

Qy        242 LeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeu 261
              |||   ||||||      ||||||||||||||||   ||||||||||||||||||||||||
Db        663 CTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTG 722

Qy        262 LeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGly 281
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Db        723 TTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGT 782

Qy        282 GlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeu 301
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Db        783 GGCCAGCTGTTCTACTCCCGTCCCGTCGTCTCGGCCCATGGCGAGCCGACTGTTAAGTTG 842

Qy        302 TyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAsp 321
              ||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        843 TATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGAC 902

Qy        322 LeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgPro 341
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGGCCG 962

Qy        342 ThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrp 361
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Db        963 ACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGG 1022

Qy        362 LeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProVal 381
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Db       1023 CTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGCCCCAGTT 1082

Qy        382 TyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArg 401
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1083 TATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGG 1142

Qy        402 SerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyr 421
              ||||||||||||   ||||||||||||||||||||||||||||   |||   ||||||
Db       1143 TCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAGTAC 1202

Qy        422 SerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThr 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1203 CCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACA 1262

Qy        442 ThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGlu 461
              ||||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db       1263 ACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAG 1322

Qy        462 AsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyPro 481
              ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||
Db       1323 AATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCC 1382

Qy        482 ValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAsp 501
              |||   |||||||||   ||||||||||||||||   ||||||||||||||||||||||||
Db       1383 GTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGAT 1442

Qy        502 ThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAla 521
              |||   ||||||||      ||||||||||||||||||||||||||||||||||||||||
Db       1443 ACCTTGGACTACCCTGCCTGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCT 1502

Qy        522 LeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysVal 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1503 CTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATG 1562

Qy        542 LysValGlyLysThrArgGluLeu 549
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Db       1563 AAGGTGGGTAAAACTCGGGAGTTA 1586

RESULT 21
E03815
LOCUS       E03815                  1643 bp    RNA     linear   PAT 29-SEP-1997
DEFINITION  cDNA encoding a part of type non-A non-B hepatitis virus genome.
ACCESSION   E03815
VERSION     E03815.1  GI:2172029
KEYWORDS    JP 1992200388-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1643)
  AUTHORS   Uchida,T., Shikata,T., Ichikawa,M., Araki,M., Rikihisa,T. and
            Mizuno,K.
  TITLE     EPIDEMIC NON-A NON-B HEPATITIS VIRUS ANTIGEN PEPTIDE AND NUCLEIC
            ACID FRAGMENT CODING THE SAME
  JOURNAL   Patent: JP 1992200388-A 1 21-JUL-1992;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Type non-A non-B hepatitis virus
            PN   JP 1992200388-A/1
            PD   21-JUL-1992
            PF   29-NOV-1990 JP 1990334835
            PI   UCHIDA TOSHIKAZU, SHIKATA TOSHIO, ICHIKAWA MUNETAKA, PI
            ARAKI MASAYASU,
            PI   RIKIHISA TETSUJI, MIZUNO KYOSUKE
            PC   C12N15/51,C07K13/00,C12P21/02,C12Q1/68,C12Q1/70,G01N33/569, PC
              G01N33/576//
            PC   A61K39/29,(C12P21/02,C12R1:19);
            CC   strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            CC   *source: clone=HT-4;
            FH   Key             Location/Qualifiers
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            FT                   /note='a part of type non-A non-B hepatitis
            FT                   virus genome'.
FEATURES             Location/Qualifiers
     source          1. .1643
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Alignment Scores:
Pred. No.:              1.92          Length:         1643
Score:                  460.50        Matches:        484
Percent Similarity:     91.67%        Conservative:   0
Best Local Similarity:  91.67%        Mismatches:     43
Query Match:            83.88%        Indels:         2
DB:                     1             Gaps:           1

US-09-769-066-16 (1-549) x E03815 (1-1643)

Qy         22 ArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThrAsn 41
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Db          3 CGCCGGCAGTATAATCTATCAACATCTCCCCTCACTTCTTCCGTGGCCACCGGCACTAAC 62

Qy         42 LeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsnThr 61
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Db         63 CTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAATACC 122

Qy         62 HisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIle 81
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Db        123 CATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGTCCGTGCCACAATC 182

Qy         82 ArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrp 101
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Db        183 CGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTCTGG 242

Qy        102 ProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAspVal 121
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Db        243 CCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGATGTT 302

Qy        122 ArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeuHis 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACAC 362

Qy        142 TyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaThr 161
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Db        363 TATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCTACC 422

Qy        162 SerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrPro 181
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Db        423 TCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAACACACCC 482

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
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Db        483 TATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTTACC 542

Qy        202 ThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
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Db        543 CCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGT 602

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
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Db        603 CGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAGGAC 662

Qy        242 LeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeu 261
              |||   ||||||      ||||||||||||||   ||||||||||||||||||||||||
Db        663 CTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTG 722

Qy        262 LeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGly 281
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Db        723 TTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGT 782

Qy        282 GlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeu 301
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Db        783 GGCCAGCTGTTCTACTCCCGTCCCGTCGTCTCGGCCCATGGCGAGCCGACTGTTAAGTTG 842

Qy        302 TyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAsp 321
              ||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        843 TATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGAC 902

Qy        322 LeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgPro 341
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGGCCG 962

Qy        342 ThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrp 361
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Db        963 ACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGG 1022

Qy        362 LeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProVal 381
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Db       1023 CTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTT 1082

Qy        382 TyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArg 401
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1083 TATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGG 1142

Qy        402 SerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyr 421
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Db       1143 TCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCTCTCCA---CCATCCAGCAGT 1199

Qy        422 SerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThr 441
                                          ||||||||||||||||||||||||||||||||||
Db       1200 ACCCGAAGACCTTCTTTGTCCTGCGCTCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACA 1259

Qy        442 ThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGlu 461
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db       1260 ACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAG 1319

Qy        462 AsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyPro 481
              ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||
Db       1320 AATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCC 1379

Qy        482 ValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAsp 501
              |||   |||||||||   ||||||||||||||   ||||||||||||||||||||||||||
Db       1380 GTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGAT 1439

Qy        502 ThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAla 521
              |||   ||||||||      ||||||||||||||||||||||||||||||||||||||||
Db       1440 ACCTTGGACTACCCTGCCTGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCT 1499

Qy        522 LeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysVal 541
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1500 CTTGGCCTCCA-GGGTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGANN 1558

Qy        542 LysValGlyLysThrArgGluLeu 549
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Db       1559 NAGGTGGGTAAAACTCGGGAGTTA 1582

RESULT 22
AF151962
LOCUS       AF151962               1497 bp    RNA     linear   VRL 30-JUN-1999
DEFINITION  Hepatitis E virus strain Ch-T11 ORF2 gene, partial cds.
ACCESSION   AF151962
VERSION     AF151962.1  GI:5281444
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 1497)
  AUTHORS   Yang,J., Zhang,H., Wang,Y. and Li,H.
  TITLE     Identification of a Novel Hepatitis E virus Responsible for
            Sporadic Acute Hepatitis in China
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1497)
  AUTHORS   Yang,J., Zhang,H., Wang,Y. and Li,H.
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  TITLE     Direct Submission
  JOURNAL   Submitted (17-MAY-1999) Department of Hepatitis, National Institute
            for the Control of Pharmaceutical and Biological Products, 2 Tian
            Tan Xi Li, Beijing, Hebei 100050, P. R. China
FEATURES             Location/Qualifiers
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     CDS             <1. .1463
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                     RPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQTTYGSSTNPMYVSDTVTFVNVATGAQ
                     GVSRSLDWSKVTLDGRPLTTIQQYSKTFYVLPLRGKLSFWEAGTTKAGYPYNYNTTAS
                     DQILIENAAGHRVCISTYTTNLGSGPVSISAVGVLAPHSALAALEDTVDYHARAHTFD
                     DFCPECRALGLQGCAFQSTVAELQRLKMKVGKTREY"
     3'UTR           1464. .>1497

Alignment Scores:
Pred. No.:                2.17          Length:          1497
Score:                    452.00        Matches:         452
Percent Similarity:       93.20%        Conservative:    0
Best Local Similarity:    93.20%        Mismatches:      33
Query Match:              82.33%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x AF151962 (1-1497)

Qy         64 MetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyr 83
              ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db          3 ATGGCTACTGAAGCCTCAAATTATGCCCAATACCGTGTTGTCCGTGCCACCATCCGGTAT 62

Qy         84 ArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGln 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGCCCTCTGGTGCCGAATGCTGTGGGTGGGTATGCTATTTCTATTTCTTTTTGGCCCCAA 122

Qy        104 ThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAspValArgIle 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACGACGACCACCCCGACGTCTGTGGACATGAATTCCATCACGTCCACCGATGTCCGTATT 182

Qy        124 LeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeuHisTyrArg 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 TTAGTTCAACCCGGCATAGCCTCCGAGCTGGTGATTCCCAGTGAGCGCCTGCATTACCGC 242

Qy        144 AsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaThrSerGly 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AACCAGGGCTGGCGCTCGGTTGAGACCTCCGGTGTCGCCGAGGAGGAGGCTACCTCCGGT 302

Qy        164 LeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThr 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CTTGTTATGCTTTGTATCCATGGGTCACCTGTGAATTCTTATACTAATACACCTTATACT 362

Qy        184 GlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCys 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GGCGCCCTTGGCTTGCTTGATTTTGCGCTTGAGCTTGAGTTCCGCAATTTGACACCCGGT 422

Qy        204 AsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGly 223
              ||||||||||||||||||||||||||||||||||  |||||||||  ||||||||||||||
Db        423 AATACAAACACGCGTGTTTCTCGTTATTCGAGTAGCGCACGTCACAAATTGCGCCGAGGG 482

Qy        224 AlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHis 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 GCCGATGGTACTGCTGAGTTAACTACTACTGCTGCTACACGGTTTATGAAGGATCTCCAT 542

Qy        244 PheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsn 263
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||  |||
Db        543 TTTACAGGGACTAACGGAGTTGGTGAGGTTGGCCGTGGTATAGCGCTTACCCTGTTTAAT 602

Qy        264 LeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGln 283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 CTTGCTGACACACTTCTCGGCGGGCTCCCGACAGAATTGATTTCGTCGGCTGGTGGTCAG 662

Qy        284 LeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThr 303
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Db        663 TTGTTTTATTCCCGCCCCGTCGTCTCGGCCAATGGCGAGCCGACAGTGAAACTTTACACC 722

Qy        304 SerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeuGly 323
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        723 TCAGTCGAGAATGCTCAGCAGGATAAAGGGATTGCTATTCCACATGACATTGATCTTGGT 782

Qy        324 AspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrPro 343
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GAGTCCCGAGTTGTTATCCAAGATTATGATAATCAACATGAGCAAGACCGCCCTACTCCT 842

Qy        344 SerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSer 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 TCCCCCGCCCCTTCTCGTCCCTTTTCTGTGCTCCGTGCTAATGATGTACTTTGGCTCTCT 902

Qy        364 LeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrIle 383
              ||||||||||||||||||||||||  ||||||||||||||||||  |||  |||
Db        903 CTTACAGCTGCTGAGTATGACCAGACTACCTATGGTTCCTCTACTAATCCTATGTATGTC 962

Qy        384 SerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeu 403
              ||||||  ||||||  ||||||||||||||||||||||  |||  |||||||||
Db        963 TCTGATACTGTGACGTTTGTCAATGTGGCTACCGGTGCCCAGGGGGTTTCGCGCTCTTTG 1022

Qy        404 AspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLys 423
              ||||||||||||||||||||||||||||||||||||  |||  ||||||||||||
Db       1023 GACTGGTCTAAGGTCACCCTTGACGGGCGCCCACTTACTACTATCCAGCAATACTCTAAG 1082

Qy        424 ThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLys 443
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1083 ACTTTCTATGTTTTGCCCCTTCGTGGTAAGCTTTCTTTCTGGGAGGCTGGCACCACTAAG 1142

Qy        444 AlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAla 463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1143 GCCGGTTACCCTTATAATTACAACACTACTGCTAGTGATCAGATTCTGATTGAGAATGCA 1202

Qy        464 AlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProValAla 483
              ||||||||||||||  ||||||||||||||||||  ||||||  |||||||||
Db       1203 GCCGGACACCGTGTCTGCATCTCTACTTACACTACTAATCTGGGCTCTGGACCCGTCTCT 1262

Qy        484 IleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPhe 503
              |||||||||  ||||||||||||  ||||||||||||  ||||||||||||||||||||||
Db       1263 ATCTCGGCCGTCGGTGTCCTCGCACCTCATTCTGCATTAGCCGCTTTAGAGGACACTGTC 1322

Qy        504 AspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeuGly 523
              ||||||      ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1323 GATTATCATGCTCGCGCTCACACCTTTGATGACTTCTGCCCTGAGTGCCGTGCACTCGGC 1382

Qy        524 LeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLysVal 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db       1383 CTTCAGGGTTGTGCTTTCCAGTCAACTGTTGCTGAGCTGCAGCGTCTCAAAATGAAGGTG 1442

Qy        544 GlyLysThrArgGlu 548
              ||||||||||||||
Db       1443 GGTAAAACTCGGGAG 1457

RESULT 23
AF151963
LOCUS       AF151963               1402 bp    RNA     linear   VRL 30-JUN-1999
DEFINITION  Hepatitis E virus strain Ch-T21 ORF2 gene, partial cds.
ACCESSION   AF151963
VERSION     AF151963.1  GI:5281446
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
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            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 1402)
  AUTHORS   Yang,J., Zhang,H., Wang,Y. and Li,H.
  TITLE     Identification of a Novel Hepatitis E virus Responsible for
            Sporadic Acute Hepatitis in China
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1402)
  AUTHORS   Yang,J., Zhang,H., Wang,Y. and Li,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-MAY-1999) Department of Hepatitis, National Institute
            for the Control of Pharmaceutical and Biological Products, 2 Tian
            Tan Xi Li, Beijing, Hebei 100050, P. R. China
FEATURES             Location/Qualifiers
     source          1. .1402
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="Ch-T21"
                     /db_xref="taxon:12461"
                     /country="China"
     CDS             <1. .>1402
                     /codon_start=3
                     /product="ORF2"
                     /protein_id="AAD41519.1"
                     /db_xref="GI:5281447"
                     /translation="YRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQ
                     PGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTPYTG
                     ALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGADGTAELTTTAATRFMKDL
                     HFTGTNGVGEVGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK
                     LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRAND
                     VLWLSLTAAEYDQTTYGSSTNPMYVSDTVTFVNVATGAQGVSRSLDWSKVTLDGRPLT
                     TIQQYSKTFYVLPLRGKLSFWETGTTKAGYPYNYNTTASDQILIENAAGHRVCISTYT
                     TNLGSGPVSISAVGVLAPHSALAALEDTVDYPARAHTFDDFCPECRALGLQGCAFQST
                     VAELQRLKMKVGKTRE"

Alignment Scores:
Pred. No.:                2.82          Length:          1402
Score:                    434.00        Matches:         434
Percent Similarity:       93.13%        Conservative:    0
Best Local Similarity:    93.13%        Mismatches:      32
Query Match:              79.05%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x AF151963 (1-1402)

Qy          83 TyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpPro 102
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           3 TATCGTCCTTTGGTGCCGAATGCTGTCGGTGGGTATGCTATATCTATTTCTTTTTGGCCC 62

Qy         103 GlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAspValArg 122
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          63 CAAACAACTACCACCCCGACGTCCGTGGATATGAACTCCATCACTTCCACTGATGTCCGT 122

Qy         123 IleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeuHisTyr 142
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         123 ATTCTTGTCCAACCCGGTATAGCCTCCGAGTTGGTGATCCCCAGTGAGCGCTTGCATTAT 182

Qy         143 ArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaThrSer 162
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         183 CGCAATCAGGGCTGGCGCTCAGTTGAGACCTCTGGCGTTGCTGAGGAGGAGGCTACTTCC 242

Qy         163 GlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyr 182
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         243 GGTCTTGTTATGCTTTGTATACATGGGTCACCTGTGAACTCCTACACTAATACACCTTAT 302

Qy         183 ThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThr 202
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         303 ACTGGTGCTCTCGGCCTGCTCGATTTTGCACTTGAGCTTGAGTTTCGTAATCTGACACCT 362

Qy         203 CysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArg 222
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         363 GGCAATACAAACACGCGCGTCTCTCGTTATTCGAGCAGTGCGCGCCATAAACTGCGCCGA 422

Qy         223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         423 GGGGCCGACGGCACTGCTGAGCTAACTACTACTGCTGCTACACGGTTTATGAAGGATCTT 482

Qy         243 HisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeu 262
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         483 CATTTTACAGGGACTAATGGCGTTGGTGAGGTTGGCCGTGGGATAGCGCTTACCTTGTTT 542

Qy         263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         543 AACCTTGCTGACACACTTCTCGGCGGGCTCCCGACAGAATTGATTTCGTCGGCTGGTGGT 602

Qy         283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         603 CAGTTGTTTTATTCCCGCCCCGTCGTCTCGGCCAATGGCGAGCCGACAGTGAAACTTTAC 662

Qy         303 ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu 322
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         663 ACCTCAGTCGAGAATGCTCAGCAGGATAAAGGGATTGCTATTCCACATGACATTGATCTT 722

Qy         323 GlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         723 GGTGAGTCCCGAGTTGTTATCCAAGATTATGATAATCAACATGAGCAAGACCGCCCTACT 782

Qy         343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         783 CCTTCCCCCGCCCCTTCTCGTCCCTTTTCTGTGCTCCGTGCTAATGATGTACTTTGGCTC 842

Qy         363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         843 TCTCTTACAGCTGCTGAGTATGACCAGACTACCTATGGTTCCTCTACTAATCCTATGTAT 902

Qy         383 IleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         903 GTCTCTGATACTGTGACGTTTGTCAATGTGGCTACCGGTGCCCAGGGGGTTTCGCGCTCT 962

Qy         403 LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer 422
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         963 TTGGACTGGTCTAAGGTCACCCTTGACGGGCGCCCACTTACTACTATCCAGCAATACTCT 1022

Qy         423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1023 AAGACTTTCTATGTTTTGCCCCTTCGTGGTAAGCTTTCTTTCTGGGAGACTGGCACCACT 1082

Qy         443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1083 AAGGCCGGTTACCCTTATAATTACAACACTACTGCTAGTGATCAGATTCTGATTGAGAAT 1142

Qy         463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1143 GCAGCCGGACACCGTGTCTGCATCTCTACTTACACTACTAATCTGGGCTCTGGACCCGTC 1202

Qy         483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1203 TCTATCTCGGCCGTCGGTGTCCTCGCACCTCATTCTGCATTAGCCGCTTTAGAGGACACT 1262

Qy         503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1263 GTCGATTATCCTGCTCGCGCTCACACCTTTGATGACTTCTGCCCTGAGTGCCGTGCACTC 1322

Qy         523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLys 542
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1323 GGCCTTCAGGGCTGTGCTTTCCAGTCAACTGTTGCTGAGCTGCAGCGTCTCAAAATGAAG 1382

Qy         543 ValGlyLysThrArgGlu 548
               ||||||||||||||||
Db        1383 GTGGGTAAAACTCGGGAG 1400

RESULT 24
AR002167
LOCUS       AR002167               1308 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 10 from patent US 5741490.
ACCESSION   AR002167
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VERSION     AR002167.1  GI:3963721
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1308)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.D.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 5741490-A 10 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .1308
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                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:                3.32          Length:          1308
Score:                    422.50        Matches:         433
Percent Similarity:       99.31%        Conservative:    0
Best Local Similarity:    99.31%        Mismatches:      2
Query Match:              76.96%        Indels:          1
DB:                       1             Gaps:            1

US-09-769-066-16 (1-549) x AR002167 (1-1308)

Qy        114 AsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGluLeu 133
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Db          1 AATTCCATTACTTCCACTGATGTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTG 60

Qy        134 ValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThrSer 153
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Db         61 GTCATCCCAAGCGAGCGCCTTCACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCT 120

Qy        154 GlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerPro 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTGTTGCTGAGGAGGAAGCCACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCA 180

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTTAACTCCTATACCAATACCCCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTA 240

Qy        194 GluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGCTTGAGTTTCGCAATCTCACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCC 300

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||||||||||||||          ||||||||||||||||||||||||||||||||||
Db        301 AGCACTGCTCGTCAC---TCCGCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACT 357

Qy        234 AlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluVal 253
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Db        358 GCAGCCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTC 417

Qy        254 GlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 GGCCGCGGGATAGCTCTAACATTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCG 477

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
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Db        478 ACAGAATTAATTTCGTCGGCTGGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCC 537

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
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Db        538 AATGGCGAGCCAACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGT 597

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
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Qy        334 AsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgProPheSerVal 353
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Qy        354 LeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThr 373
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Db        718 CTCCGAGCAAATGATGTACTTTGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACT 777

Qy        374 TyrGlySerSerThrGlyProValTyrIleSerAspSerValThrLeuValAsnValAla 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 TACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCG 837

Qy        394 ThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArg 413
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Db        838 ACTGGCGCGCAGGCCGTAGCCCGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGG 897

Qy        414 ProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLys 433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 CCCCTCCCGACTGTTGAGCAATATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAG 957

Qy        434 LeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThr 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 CTCTCCTTTTGGGAGGCCGGCACAACAAAAGCAGGTTATCCTTATAATTATAATACTACT 1017

Qy        454 AlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyr 473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 GCTAGTGACCAGATTCTGATTGAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTAT 1077

Qy        474 ThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArg 493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1078 ACCACCAGGCTTGGGGCCGGTCCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGC 1137

Qy        494 SerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAsp 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 TCCGCCCTGGCTCTGCTGGAGGATACTTTTGATTATCCGGGGCGGGCGCACACATTTGAT 1197

Qy        514 AspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrVal 533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1198 GACTTCTGCCCTGAATGCCGCGCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTC 1257

Qy        534 AlaGluLeuGlnArgLeuLysValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1258 GCTGAGCTCCAGCGCCTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTG 1305

RESULT 25
AR232472
LOCUS       AR232472                1308 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 10 from patent US 6455492.
ACCESSION   AR232472
VERSION     AR232472.1  GI:27274541
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1308)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.O.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 6455492-A 10 24-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .1308
                     /organism="unknown"
                     /mol_type="mRNA"

Alignment Scores:
Pred. No.:                3.32          Length:          1308
Score:                    422.50        Matches:         433
Percent Similarity:       99.31%        Conservative:    0
Best Local Similarity:    99.31%        Mismatches:      2
Query Match:              76.96%        Indels:          1
DB:                       1             Gaps:            1

US-09-769-066-16 (1-549) x AR232472 (1-1308)

Qy        114 AsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGluLeu 133
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Db          1 AATTCCATTACTTCCACTGATGTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTG 60
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Qy        134 ValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThrSer 153
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Db         61 GTCATCCCAAGCGAGCGCCTTCACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCT 120

Qy        154 GlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerPro 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTGTTGCTGAGGAGGAAGCCACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCA 180

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTTAACTCCTATACCAATACCCCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTA 240

Qy        194 GluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGCTTGAGTTTCGCAATCTCACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCC 300

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              |||||||||||||||         ||||||||||||||||||||||||||||||||||||
Db        301 AGCACTGCTCGTCAC---TCCGCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACT 357

Qy        234 AlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluVal 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 GCAGCCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTC 417

Qy        254 GlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 GGCCGCGGGATAGCTCTAACATTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCG 477

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 ACAGAATTAATTTCGTCGGCTGGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCC 537

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AATGGCGAGCCAACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGT 597

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 GTTGCTATCCCCCACGATATCGATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGAC 657

Qy        334 AsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgProPheSerVal 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 AACCAGCATGAGCAGGATCGGCCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTT 717

Qy        354 LeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThr 373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 CTCCGAGCAAATGATGTACTTTGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACT 777

Qy        374 TyrGlySerSerThrGlyProValTyrIleSerAspSerValThrLeuValAsnValAla 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 TACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCG 837

Qy        394 ThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArg 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 ACTGGCGCGCAGGCCGTAGCCCGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGG 897

Qy        414 ProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLys 433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 CCCCTCCCGACTGTTGAGCAATATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAG 957

Qy        434 LeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThr 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 CTCTCCTTTTGGGAGGCCGGCACAACAAAAGCAGGTTATCCTTATAATTATAATACTACT 1017

Qy        454 AlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyr 473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 GCTAGTGACCAGATTCTGATTGAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTAT 1077

Qy        474 ThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArg 493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1078 ACCACCAGGCTTGGGGCCGGTCCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGC 1137

Qy        494 SerAlaLeuAlaLeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAsp 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 TCCGCCCTGGCTCTGCTGGAGGATACTTTTGATTATCCGGGGCGGGCGCACACATTTGAT 1197

Qy        514 AspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrVal 533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1198 GACTTCTGCCCTGAATGCCGCGCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTC 1257

Qy        534 AlaGluLeuGlnArgLeuLysValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1258 GCTGAGCTCCAGCGCCTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTG 1305

RESULT 26
AR002166
LOCUS       AR002166                1311 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 9 from patent US 5741490.
ACCESSION   AR002166
VERSION     AR002166.1  GI:3963720
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1311)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.D.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 5741490-A 9 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .1311
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:              3.93          Length:          1311
Score:                  411.00        Matches:         411
Percent Similarity:     94.27%        Conservative:    0
Best Local Similarity:  94.27%        Mismatches:      25
Query Match:            74.86%        Indels:          0
DB:                     1             Gaps:            0

US-09-769-066-16 (1-549) x AR002166 (1-1311)

Qy        114 AsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGluLeu 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTT 60

Qy        134 ValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThrSer 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCT 120

Qy        154 GlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerPro 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGGTGGCTGAGGAGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTC 180

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTT 240

Qy        194 GluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||         ||||||||||||||||||||||||||||||
Db        241 GAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCC 300

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACG 360

Qy        234 AlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluVal 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 420

Qy        254 GlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCG 480
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Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCC 540

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGT 600

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
                 |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Db        601 ATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGAT 660

Qy        334 AsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgProPheSerVal 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACCAACATGAACAAGATCGGCCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTC 720

Qy        354 LeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThr 373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCGAGCTAATGATGTGCTTTGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACT 780

Qy        374 TyrGlySerSerThrGlyProValTyrIleSerAspSerValThrLeuValAsnValAla 393
              ||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        781 TATGGCTCTTCGACTGGCCCAGTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCG 840

Qy        394 ThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArg 413
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        841 ACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGC 900

Qy        414 ProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLys 433
              ||||||   |||      ||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAG 960

Qy        434 LeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThr 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTCTCTTTCTGGGAGGCAGGCACAACTAAAGCCGGGTACCCTTATAATTATAACACCACT 1020

Qy        454 AlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyr 473
              ||||||||||||   |||  ||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTAC 1080

Qy        474 ThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArg 493
              ||||||   ||||||||||||||||||   |||||||||   ||||||||||||||||||
Db       1081 ACCACTAGCCTGGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCAC 1140

Qy        494 SerAlaLeuAlaLeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAsp 513
              ||||||||||||||||||||||||||||   |||||||||   ||||||||||||||||||
Db       1141 TCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGAT 1200

Qy        514 AspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrVal 533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GATTTCTGCCCAGAGTGCCGCCCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTC 1260

Qy        534 AlaGluLeuGlnArgLeuLysValLysValGlyLysThrArgGluLeu 549
              ||||||||||||||||||||||   ||||||||||||||||||||||||
Db       1261 GCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTG 1308
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RESULT 27
AR232471
LOCUS       AR232471                1311 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 9 from patent US 6455492.
ACCESSION   AR232471
VERSION     AR232471.1  GI:27274540
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1311)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.O.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 6455492-A 9 24-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .1311
                     /organism="unknown"
                     /mol_type="mRNA"

Alignment Scores:
Pred. No.:              3.93          Length:          1311
Score:                  411.00        Matches:         411
Percent Similarity:     94.27%        Conservative:    0
Best Local Similarity:  94.27%        Mismatches:      25
Query Match:            74.86%        Indels:          0
DB:                     1             Gaps:            0

US-09-769-066-16 (1-549) x AR232471 (1-1311)

Qy        114 AsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGluLeu 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTT 60

Qy        134 ValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThrSer 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCT 120

Qy        154 GlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerPro 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGGTGGCTGAGGAGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTC 180

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTT 240

Qy        194 GluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        241 GAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCC 300

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACG 360

Qy        234 AlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluVal 253
              ||||||||||||||||||||||||||||  ||||||      ||||||||||||||||
Db        361 GCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 420

Qy        254 GlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        421 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCG 480

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCC 540

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGT 600

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
                 |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Db        601 ATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGAT 660

Qy        334 AsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgProPheSerVal 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACCAACATGAACAAGATCGGCCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTC 720

Qy        354 LeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThr 373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTCGAGCTAATGATGTGCTTTGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACT 780

Qy        374 TyrGlySerSerThrGlyProValTyrIleSerAspSerValThrLeuValAsnValAla 393
              ||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        781 TATGGCTCTTCGACTGGCCCAGTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCG 840

Qy        394 ThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArg 413
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        841 ACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGC 900
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Qy        414 ProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLys 433
              ||||||   |||      ||||||||||||||||||||||||||||||||||||||||||
Db        901 CCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAG 960

Qy        434 LeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThr 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTCTCTTTCTGGGAGGCAGGCACAACTAAAGCCGGGTACCCTTATAATTATAACACCACT 1020

Qy        454 AlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyr 473
              ||||||||||||   |||   ||||||||||||||||||||||||||||||||||||||
Db       1021 GCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTAC 1080

Qy        474 ThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArg 493
              ||||||   ||||||||||||||||   |||||||||   ||||||||||||||||
Db       1081 ACCACTAGCCTGGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCAC 1140

Qy        494 SerAlaLeuAlaLeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAsp 513
              ||||||||||||||||||||||||||   |||||||||   ||||||||||||||||||
Db       1141 TCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGAT 1200

Qy        514 AspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrVal 533
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db       1201 GATTTCTGCCCAGAGTGCCGCCCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTC 1260

Qy        534 AlaGluLeuGlnArgLeuLysValLysValGlyLysThrArgGluLeu 549
              ||||||||||||||||||   ||||||||||||||||||||||
Db       1261 GCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTG 1308

RESULT 28
AF141652
LOCUS       AF141652               1309 bp    RNA     linear   VRL 01-JUN-1999
DEFINITION  Hepatitis E virus structural protein gene, partial cds.
ACCESSION   AF141652
VERSION     AF141652.1  GI:4929147
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 1309)
  AUTHORS   Jiang,L., Yang,G. and Shen,X.L.
  TITLE     Cloning and sequence analysis of the 1.3Kb cDNA fragment from open
            reading frame 2 (ORF2) of hepatitis E virus (HEV)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1309)
  AUTHORS   Jiang,L., Yang,G. and Shen,X.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-APR-1999) Fourth Lab, Lanzhou Institute of Biological
            Products, Yanchang Road, Lanzhou, Gansu 730046, P.R.China
FEATURES             Location/Qualifiers
     source          1. .1309
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="China"
                     /db_xref="taxon:12461"
                     /note="isolated from patient serum"
     CDS             <1. .>1309
                     /function="viral particle assembly"
                     /note="ORF2; capsid protein homolog"
                     /codon_start=2
                     /product="structural protein"
                     /protein_id="AAD33878.1"
                     /db_xref="GI:4929148"
                     /translation="NSINSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAE
                     EEATSGLVMLCIHGSPVNSYTNTPYTGALGLSDFALELEFRNLTPGNTNTRVSRYSST
                     ARHRLRRGTDGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP
                     TELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDVGESRVVIQD
                     YDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTL
                     VNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAWYP
                     YNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLEDTMDY
                     PARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTREL"
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Alignment Scores:
Pred. No.:              4.17          Length:          1309
Score:                  407.00        Matches:         407
Percent Similarity:     93.35%        Conservative:    0
Best Local Similarity:  93.35%        Mismatches:      29
Query Match:            74.13%        Indels:          0
DB:                     1             Gaps:            0

US-09-769-066-16 (1-549) x AF141652 (1-1309)

Qy        114 AsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAlaSerGluLeu 133
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 AATTCAATAAACTCGACGGATGTCCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTT 61

Qy        134 ValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThrSer 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 GTTATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCC 121

Qy        154 GlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerPro 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GGGGTGGCGGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCT 181

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||
Db        182 GTAAATTCTTATACTAACACACCTTATACCGGTGCCCTTGGGCTGTCGGACTTTGCCCTC 241

Qy        194 GluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||      ||||||||||||||||||||||||||||||
Db        242 GAACTTGAGTTCCGCAACCTCACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCC 301

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 AGCACTGCCCGTCACCGCCTTCGTCGCGGTACAGATGGGACTGCCGAGCTCACCACCACG 361

Qy        234 AlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluVal 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 GCTGCTACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 421

Qy        254 GlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GGCCGCGGGATAGCGCTTACCCTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCG 481

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 ACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCTCGCCCCGTCGTCTCAGCC 541

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 AATGGCGAGCCGACTGTTAAGCTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGT 601

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
                  ||||||||||||||||||||   |||   ||||||||||||||||||||||||||||
Db        602 ATTGCAATCCCGCATGACATCGACGTCGGGGAATCTCGAGTTGTTATTCAGGATTATGAC 661

Qy        334 AsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgProPheSerVal 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 AACCAACATGAGCAGGACCGACCGACACCTTCCCCAGCCCCATCGCGTCCTTTTTCTGTC 721

Qy        354 LeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThr 373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 CTCCGAGCTAATGATGTGCTGTGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACT 781

Qy        374 TyrGlySerSerThrGlyProValTyrIleSerAspSerValThrLeuValAsnValAla 393
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        782 TACGGCTCTTCGACCGGCCCAGTCTATGTCTCCGACTCTGTGACCTTGGTTAATGTTGCG 841

Qy        394 ThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArg 413
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        842 ACCGGCGCGCAGGCCGTTGCCCGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGC 901

Qy        414 ProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLys 433
              ||||||   |||      ||||||||||||||||||||||||||||||||||||||||||
Db        902 CCCCTTTCCACCATCCAGCAGTATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAG 961
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Qy        434 LeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThr 453
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        962 CTCTCCTTTTGGGAGGCAGGTACTACTAAAGCCTGGTACCCTTATAATTATAATACCACT 1021

Qy        454 AlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyr 473
              ||||||||||||    |||   ||||||||||||||||||||||||||||||||||||||
Db       1022 GCTAGTGACCAACTGCTCGTTGAGAATGCCGCCGGGCATCGGGTTGCTATTTCCACTTAT 1081

Qy        474 ThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArg 493
              ||||||   ||||||||||||||||||   |||||||||   ||||||||||||||||
Db       1082 ACCACTAGCCTGGGTGCTGGCCCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCAC 1141

Qy        494 SerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAsp 513
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||||||||
Db       1142 TCTGCGCTAGCATTGCTTGAGGATACCATGGACTACCCTGCCCGCGCCCATACTTTCGAT 1201

Qy        514 AspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrVal 533
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db       1202 GACTTCTGCCCGGAGTGCCGCCCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTC 1261

Qy        534 AlaGluLeuGlnArgLeuLysValLysValGlyLysThrArgGluLeu 549
              ||||||||||||||||||||   ||||||||||||||||||||||||
Db       1262 GCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTA 1309

RESULT 29
AR170409
LOCUS       AR170409                 984 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 6 from patent US 6291641.
ACCESSION   AR170409
VERSION     AR170409.1  GI:17908368
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Fuerst,T.R., McAtee,C.Patrick., Yarbough,P.O. and Zhang,Y.-F.
  TITLE     Hepatitis E virus antigens and uses therefor
  JOURNAL   Patent: US 6291641-A 6 18-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:              13.2          Length:         984
Score:                  327.00        Matches:        327
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            59.56%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AR170409 (1-984)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAAGATCTC 60

Qy        243 HisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeu 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACATTACTT 120

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCTGGCGGG 180

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTAT 240

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATCGATCTT 300

Qy        323 GlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGGCCCACC 360

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTTTGGCTG 420

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTAT 480

Qy        383 IleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCCCGATCG 540

Qy        403 LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAATATTCC 600

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGCACAACA 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATTGAAAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGTCCGGTC 780

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAGGATACT 840

Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGCGCTTTA 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||
Db        961 GTGGGTAAAACTCGGGAGTTG 981

RESULT 30
I73146
LOCUS       I73146                   984 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 8 from patent US 5686239.
ACCESSION   I73146
VERSION     I73146.1  GI:3009285
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Reyes,G.R., Tam,A.W. and Yarbough,P.O.
  TITLE     Hepatitis E virus peptides and methods
  JOURNAL   Patent: US 5686239-A 8 11-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:              13.2          Length:         984
Score:                  327.00        Matches:        327
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
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Query Match:           59.56%        Indels:        0
DB:                    1             Gaps:          0

US-09-769-066-16 (1-549) x I73146 (1-984)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAAGATCTC 60

Qy        243 HisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeu 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACATTACTT 120

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCTGGCGGG 180

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTAT 240

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATCGATCTT 300

Qy        323 GlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGGCCCACC 360

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTTTGGCTG 420

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTAT 480

Qy        383 IleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCCCGATCG 540

Qy        403 LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAATATTCC 600

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGCACAACA 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATTGAAAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGTCCGGTC 780

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAGGATACT 840

Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGCGCTTTA 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||
Db        961 GTGGGTAAAACTCGGGAGTTG 981
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RESULT 31
AR002165
LOCUS       AR002165                981 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 8 from patent US 5741490.
ACCESSION   AR002165
VERSION     AR002165.1  GI:3963719
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 981)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.D.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 5741490-A 8 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .981
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:              13.4          Length:         981
Score:                  326.00        Matches:        326
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            59.38%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AR002165 (1-981)

Qy        224 AlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHis 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAAGATCTCCAC 60

Qy        244 PheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsn 263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACATTACTTAAC 120

Qy        264 LeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGln 283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCTGGCGGGCAA 180

Qy        284 LeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThr 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTATACA 240

Qy        304 SerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeuGly 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATCGATCTTGGT 300

Qy        324 AspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrPro 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGGCCCACCCCG 360

Qy        344 SerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSer 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTTTGGCTGTCC 420

Qy        364 LeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrIle 383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATC 480

Qy        384 SerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeu 403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCCCGATCGCTT 540

Qy        404 AspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLys 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAATATTCCAAG 600

Qy        424 ThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLys 443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGCACAACAAAA 660
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Qy        444 AlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAla 463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATTGAAAATGCT 720

Qy        464 AlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProValAla 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGTCCGGTCGCC 780

Qy        484 IleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPhe 503
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAGGATACTTTT 840

Qy        504 AspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeuGly 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGCGCTTTAGGC 900

Qy        524 LeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLysVal 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTG 960

Qy        544 GlyLysThrArgGluLeu 549
              |||||||||||||||||
Db        961 GGTAAAACTCGGGAGTTG 978
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RESULT 32
AR232470
LOCUS AR232470 981 bp mRNA linear PAT 20-DEC-2002
DEFINITION Sequence 8 from patent US 6455492.
ACCESSION AR232470
VERSION AR232470.1 GI:27274539
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 981)
AUTHORS Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W., Krawczynski,K.Z. and Yarbough,P.O.
TITLE Hepatitis E virus vaccine and method
JOURNAL Patent: US 6455492-A 8 24-SEP-2002;
FEATURES Location/Qualifiers
source 1. .981
/organism="unknown"
/mol_type="mRNA"

Alignment Scores:

Pred. No.:	13.4	Length:	981
Score:	326.00	Matches:	326
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	59.38%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AR232470 (1-981)

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Qy        224 AlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHis 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAAGATCTCCAC 60

Qy        244 PheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsn 263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACATTACTTAAC 120

Qy        264 LeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGln 283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCTGGCGGGCAA 180

Qy        284 LeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThr 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTATACA 240

Qy        304 SerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeuGly 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATCGATCTTGGT 300

Qy        324 AspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrPro 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGGCCCACCCCG 360

Qy        344 SerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSer 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTTTGGCTGTCC 420

Qy        364 LeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrIle 383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATC 480

Qy        384 SerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeu 403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCCCGATCGCTT 540

Qy        404 AspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLys 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAATATTCCAAG 600

Qy        424 ThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLys 443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGCACAACAAAA 660

Qy        444 AlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAla 463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATTGAAAATGCT 720

Qy        464 AlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProValAla 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGTCCGGTCGCC 780

Qy        484 IleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPhe 503
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAGGATACTTTT 840

Qy        504 AspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeuGly 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGCGCTTTAGGC 900

Qy        524 LeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLysVal 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTG 960

Qy        544 GlyLysThrArgGluLeu 549
              |||||||||||||||||
Db        961 GGTAAAACTCGGGAGTTG 978
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RESULT 33
AX181847
LOCUS AX181847 1020 bp DNA linear PAT 07-AUG-2001
DEFINITION Sequence 129 from Patent WO0146696.
ACCESSION AX181847
VERSION AX181847.1 GI:15133167
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and Mushahwar,I.K.
TITLE Methods and compositions for detecting hepatitis e virus
JOURNAL Patent: WO 0146696-A 129 28-JUN-2001;
ABBOTT LABORATORIES (US)
FEATURES Location/Qualifiers
source 1. .1020
/organism="Hepatitis E virus"
/mol_type="unassigned DNA"
/db_xref="taxon:12461"
/note="us2-1019"

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Alignment Scores:
Pred. No.:                14.1          Length:          1020
Score:                    323.00        Matches:         323
Percent Similarity:       95.85%        Conservative:    0
Best Local Similarity:    95.85%        Mismatches:      14
Query Match:              58.83%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x AX181847 (1-1020)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              |||||||   |||||||   |||||||   ||||||||||||||||||||||||||||||
Db          9 GCCGTGTCACCGGCTCCTGACACAGCCCCTGTACCTGATGTTGACTCACGTGGTGCTATT 68

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 CTGCGCCGGCAGTACAATTTGTCCACGTCCCCGCTCACGTCATCTGTCGCTTCGGGTACT 128

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        129 AATTTGGTCCTCTATGCTGCCCCGCTGAATCCCCTCTTGCCTCTCCAGGATGGTACCAAC 188

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||    ||||||||
Db        189 ACTCATATTATGGCTACTGAGGCATCCAATTATGCCCAGTATCGGGTTGTTCGAGCTACA 248

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 ATCCGTTATCGCCCGCTGGTGCCGAATGCCGTTGGTGGCTATGCCATTTCCATTTCTTTC 308

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TGGCCCCAAACTACAACTACCCCTACTTCTGTCGATATGAATTCTATTACTTCCACYGAT 368

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GTTAGGATTTTGGTTCAGCCCGGTATTGCCTCCGAGCTAGTCATCCCCAGTGAGCGCCTT 428

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        429 CATTACCGTAATCAAGGCTGGCGCTCTGTTGAGACCACGGGTGTGGCTGAGGAGGAGGCT 488

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 ACTTCCGGTCTGGTAATGCTTTGCATTCATGGCTCTCCTGTTAATTCCTACACTAATACA 548

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCACTAGAGCTTGAATTTAGGAATTTG 608

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||      ||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        609 ACACCCGGGAACACCAACACCCGTGTTTCCCGGTATACCAGCACAGCCCGCCACCGGCTG 668

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CGCCGTGGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCCACACGTTTCATGAAG 728

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||   |||   ||||||||||||||||||||||||||||||||||||||
Db        729 GACCTGCACTTCGCTGGCACGAATGGCGTTGGTGAGGTGGGTCGTGGTATCGCCCTGACA 788

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 CTGTTCAATCTCGCTGATACGCTTCTCGGCGGTTTACCGACAGAATTGATTTCGTCGGCT 848

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 GGGGGCCAACTGTTTTACTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAG 908

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||      ||||||||||||||||
Db        909 TTATATACATCTGTTGAGAATGCGCAGCAAGACAAGGGCATCACCATTCCACATGATATA 968

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 GACCTGGGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCAYGAA 1019

RESULT 34
BD077247
LOCUS       BD077247                1020 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077247
VERSION     BD077247.1  GI:22622850
KEYWORDS    JP 2001520384-A/126.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1020)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 126 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/126
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   us2-1019
            FH   Key             Location/Qualifiers
            FT   source          1. .1020
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                                 virus)'.
FEATURES             Location/Qualifiers
     source          1. .1020
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:                14.1          Length:          1020
Score:                    323.00        Matches:         323
Percent Similarity:       95.85%        Conservative:    0
Best Local Similarity:    95.85%        Mismatches:      14
Query Match:              58.83%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x BD077247 (1-1020)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              |||||||   |||||||   |||||||   ||||||||||||||||||||||||||||||
Db          9 GCCGTGTCACCGGCTCCTGACACAGCCCCTGTACCTGATGTTGACTCACGTGGTGCTATT 68

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 CTGCGCCGGCAGTACAATTTGTCCACGTCCCCGCTCACGTCATCTGTCGCTTCGGGTACT 128

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        129 AATTTGGTCCTCTATGCTGCCCCGCTGAATCCCCTCTTGCCTCTCCAGGATGGTACCAAC 188

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||    ||||||||
Db        189 ACTCATATTATGGCTACTGAGGCATCCAATTATGCCCAGTATCGGGTTGTTCGAGCTACA 248

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 ATCCGTTATCGCCCGCTGGTGCCGAATGCCGTTGGTGGCTATGCCATTTCCATTTCTTTC 308
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Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TGGCCCCAAACTACAACTACCCCTACTTCTGTCGATATGAATTCTATTACTTCCACYGAT 368

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GTTAGGATTTTGGTTCAGCCCGGTATTGCCTCCGAGCTAGTCATCCCCAGTGAGCGCCTT 428

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        429 CATTACCGTAATCAAGGCTGGCGCTCTGTTGAGACCACGGGTGTGGCTGAGGAGGAGGCT 488

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 ACTTCCGGTCTGGTAATGCTTTGCATTCATGGCTCTCCTGTTAATTCCTACACTAATACA 548

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCACTAGAGCTTGAATTTAGGAATTTG 608

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||      ||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        609 ACACCCGGGAACACCAACACCCGTGTTTCCCGGTATACCAGCACAGCCCGCCACCGGCTG 668

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CGCCGTGGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCCACACGTTTCATGAAG 728

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||   |||   ||||||||||||||||||||||||||||||||||||||||
Db        729 GACCTGCACTTCGCTGGCACGAATGGCGTTGGTGAGGTGGGTCGTGGTATCGCCCTGACA 788

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 CTGTTCAATCTCGCTGATACGCTTCTCGGCGGTTTACCGACAGAATTGATTTCGTCGGCT 848

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 GGGGGCCAACTGTTTTACTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAG 908

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        909 TTATATACATCTGTTGAGAATGCGCAGCAAGACAAGGGCATCACCATTCCACATGATATA 968

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 GACCTGGGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCAYGAA 1019
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RESULT 35
HEU40044
LOCUS HEU40044 1117 bp DNA linear VRL 26-JAN-1999
DEFINITION Hepatitis E virus structural protein 2 (orf2) mRNA, partial cds.
ACCESSION U40044
VERSION U40044.1 GI:4096791
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 1117)
AUTHORS Van Cuyck-Gandre,H., Clements,N.J., Zhang,H.Y., Caudill,J.C., Cohen,S.G., Coursaget,P., Buisson,Y., Warren,R.L. and Longer,C.F.
TITLE Partial Sequence of HEV Isolates from North Africa and Pakistan: Comparison with Known HEV Sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1117)
AUTHORS Van Cuyck-Gandre,H., Clements,N.J., Zhang,H.Y., Caudill,J.C., Cohen,S.G., Coursaget,P., Buisson,Y., Warren,R.L. and Longer,C.F.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-1995) Helene Van Cuyck-Gandre, Virus Disease, Walter Reed Army Institute of Research, BLD 40, Washington, DC 20307-5100, USA

FEATURES Location/Qualifiers
source 1. .1117
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/mol_type="genomic DNA"
/strain="2B Abbottabad, Pakistan"
/db_xref="taxon:12461"
CDS <1. .1035
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/product="structural protein 2"
/protein_id="AAD09445.1"
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/translation="NTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNG
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TFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGP
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KMKVGKTREL"

Alignment Scores:

Pred. No.:	14.3	Length:	1117
Score:	322.00	Matches:	322
Percent Similarity:	93.60%	Conservative:	0
Best Local Similarity:	93.60%	Mismatches:	22
Query Match:	58.65%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x HEU40044 (1-1117)

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Qy        206 AsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAsp 225
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Db          1 AATACGCGGGTCTCGCGTTACTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGAC 60

Qy        226 GlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThr 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGGACTGCCGAGCTCACCACCACGGCTGCTACCCGTTTTATGAAGGACCTCTATTTCACT 120

Qy        246 GlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAla 265
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Db        121 AGTACCAATGGTGTCGGTGAGATCGGCCGCGGGATAGCTCTCACCCTGTTCAACCTTGCT 180

Qy        266 AspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPhe 285
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Db        181 GACACTCTGCTTGGTGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTC 240

Qy        286 TyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerVal 305
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Db        241 TACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAGCTGTATACATCTGTA 300

Qy        306 GluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeuGlyAspSer 325
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Db        301 GAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGGGAATCT 360

Qy        326 ArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerPro 345
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Db        361 CGTGTGGTTATTCAGGACTATGATAACCAACATGAACAGGACCGGCCGACGCCTTCGCCA 420

Qy        346 AlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThr 365
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Db        421 GCTCCATCGCGCCCTTTTTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTCTCTCTCACC 480

Qy        366 AlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrIleSerAsp 385
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Db        481 GCTGCCGAGTATGACCAATCCACTTATGGCTCTTCGACTGGCCCAGTTTATGTCTCTGAC 540

Qy        386 SerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrp 405
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Db        541 TCTGTGACCTTGGTTAATGTCGCGACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGG 600

Qy        406 SerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhe 425
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Db        601 ACCAAGGTCACACTTGACGGCCGCCCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTC 660
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Qy        426 PheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGly 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACAACTAAAGCCGGG 720

Qy        446 TyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGly 465
              ||||||||||||||||||||||||||||||||||    |||    ||||||||||||||||
Db        721 TACCCTTATAATTATAATACCACTGCTAGCGACCAACTGCTCGTCGAGAATGCCGCCGGG 780

Qy        466 HisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSer 485
              |||||||||||||||||||||||||||||    ||||||||||||||||    ||||||
Db        781 CACCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGACCCGTTTCCATTTCT 840

Qy        486 AlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyr 505
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Db        841 GCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGATTAC 900

Qy        506 ProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuGln 525
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Db        901 CCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCCTTGGCCTCCAG 960

Qy        526 GlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLysValGlyLys 545
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Db        961 GGCTGTGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGTCTTAAGATGAAGGTGGGTAAA 1020

Qy        546 ThrArgGluLeu 549
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Db       1021 ACTCGGGAGTTA 1032
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RESULT 36
AR002164
LOCUS       AR002164                984 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 7 from patent US 5741490.
ACCESSION   AR002164
VERSION     AR002164.1  GI:3963718
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.D.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 5741490-A 7 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .984
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Alignment Scores:
Pred. No.:              18.2          Length:         984
Score:                  305.00        Matches:        305
Percent Similarity:     93.27%        Conservative:   0
Best Local Similarity:  93.27%        Mismatches:     22
Query Match:            55.56%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AR002164 (1-984)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTC 60

Qy        243 HisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeu 262
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Db         61 TATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTC 120

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
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Db        121 AACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGC 180

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
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Db        181 CAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTAT 240

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu 322
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Db        241 ACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTC 300

Qy        323 GlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
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Db        301 GGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGGCCGACG 360

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
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Db        361 CCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTC 420

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
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Db        421 TCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTTAT 480

Qy        383 IleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
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Db        481 GTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCG 540

Qy        403 LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer 422
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Db        541 CTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAGTACTCG 600

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
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Db        601 AAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACAACT 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
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Db        661 AAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482
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Db        721 GCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTC 780

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502
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Db        781 TCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACC 840

Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522
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Db        841 TTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCCTT 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLys 542
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Db        901 GGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549
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Db        961 GTGGGTAAAACTCGGGAGTTG 981
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RESULT 37
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LOCUS       AR170408                984 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 5 from patent US 6291641.
ACCESSION   AR170408
VERSION     AR170408.1  GI:17908367
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Fuerst,T.R., McAtee,C.Patrick., Yarbough,P.O. and Zhang,Y.-F.
  TITLE     Hepatitis E virus antigens and uses therefor
  JOURNAL   Patent: US 6291641-A 5 18-SEP-2001;
FEATURES             Location/Qualifiers
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Pred. No.:                18.2          Length:          984
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Percent Similarity:       93.27%        Conservative:    0
Best Local Similarity:    93.27%        Mismatches:      22
Query Match:              55.56%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x AR170408 (1-984)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
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Db          1 GGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTC 60

Qy        243 HisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeu 262
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Db         61 TATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTC 120

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
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Db        121 AACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGC 180

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTAT 240

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        241 ACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTC 300

Qy        323 GlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGGCCGACG 360

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTC 420

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
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Db        421 TCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTTAT 480

Qy        383 IleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
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Db        481 GTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCG 540

Qy        403 LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer 422
              |||||||||   ||||||||||||||||||||||||||||||   |||   |||||||||
Db        541 CTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAGTACTCG 600

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
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Db        601 AAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACAACT 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
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Db        661 AAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482
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Db        721 GCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTC 780

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502
              |||||||||   ||||||||||||||   ||||||||||||||||||||||||||||||||
Db        781 TCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACC 840

Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||   |||
Db        841 TTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCCTT 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        901 GGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549
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Db        961 GTGGGTAAAACTCGGGAGTTG 981

RESULT 38
I73145
LOCUS       I73145                   984 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 7 from patent US 5686239.
ACCESSION   I73145
VERSION     I73145.1  GI:3009284
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Reyes,G.R., Tam,A.W. and Yarbough,P.O.
  TITLE     Hepatitis E virus peptides and methods
  JOURNAL   Patent: US 5686239-A 7 11-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .984
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Alignment Scores:
Pred. No.:                18.2          Length:          984
Score:                    305.00        Matches:         305
Percent Similarity:       93.27%        Conservative:    0
Best Local Similarity:    93.27%        Mismatches:      22
Query Match:              55.56%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x I73145 (1-984)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
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Db          1 GGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTC 60

Qy        243 HisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeu 262
                  ||||||      ||||||||||||||||   ||||||||||||||||||||||||
Db         61 TATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTC 120

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGC 180

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTAT 240

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        241 ACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTC 300

Qy        323 GlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGGCCGACG 360

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTC 420

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTTAT 480

Qy        383 IleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCG 540

Qy        403 LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer 422
              |||||||||   ||||||||||||||||||||||||||||||   |||   |||||||||
Db        541 CTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAGTACTCG 600
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Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACAACT 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||    |||    ||||||
Db        661 AAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db        721 GCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTC 780

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502
                  |||||||||    ||||||||||||||    |||||||||||||||||||||||||||
Db        781 TCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACC 840

Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522
                  |||||||||    ||||||||||||||||||||||||||||||||||||    |||
Db        841 TTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCCTT 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db        901 GGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549
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Db        961 GTGGGTAAAACTCGGGAGTTG 981

RESULT 39
AR232469
LOCUS       AR232469                984 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 7 from patent US 6455492.
ACCESSION   AR232469
VERSION     AR232469.1  GI:27274538
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,
            Krawczynski,K.Z. and Yarbough,P.O.
  TITLE     Hepatitis E virus vaccine and method
  JOURNAL   Patent: US 6455492-A 7 24-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="unknown"
                     /mol_type="mRNA"

Alignment Scores:
Pred. No.:              18.2          Length:         984
Score:                  305.00        Matches:        305
Percent Similarity:     93.27%        Conservative:   0
Best Local Similarity:  93.27%        Mismatches:     22
Query Match:            55.56%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AR232469 (1-984)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTC 60

Qy        243 HisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeu 262
              ||||||      ||||||||||||||    ||||||||||||||||||||||||||||||
Db         61 TATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTC 120

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
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Db        121 AACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGC 180

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTAT 240

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        241 ACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTC 300

Qy        323 GlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGGCCGACG 360

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTC 420

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTTAT 480

Qy        383 IleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCG 540

Qy        403 LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer 422
              ||||||||    ||||||||||||||||||||||||    |||      |||||||||
Db        541 CTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAGTACTCG 600

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACAACT 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||    |||    ||||||
Db        661 AAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db        721 GCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTC 780

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502
                  |||||||||    ||||||||||||||    |||||||||||||||||||||||||||
Db        781 TCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACC 840

Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522
                  |||||||||    ||||||||||||||||||||||||||||||||||||    |||
Db        841 TTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCCTT 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db        901 GGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549
              |||||||||||||||||||
Db        961 GTGGGTAAAACTCGGGAGTTG 981

RESULT 40
AX181910
LOCUS       AX181910                1026 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 192 from Patent WO0146696.
ACCESSION   AX181910
VERSION     AX181910.1  GI:15133216
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 192 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .1026
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                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
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                     /note="cksorf2m-2.seq"

Alignment Scores:
Pred. No.:                19.7          Length:          1026
Score:                    300.00        Matches:         300
Percent Similarity:       92.02%        Conservative:    0
Best Local Similarity:    92.02%        Mismatches:      26
Query Match:              54.64%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x AX181910 (1-1026)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCCACACGTTTCATGAAGGACCTG 69

Qy        243 HisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeu 262
              ||||||   |||  ||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CACTTCGCTGGCACGAATGGCGTTGGTGAGGTGGGTCGTGGTATCGCCCTGACACTGTTC 129

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 AATCTCGCTGATACGCTTCTCGGCGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGC 189

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CAACTGTTTTACTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATAT 249

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ACATCTGTTGAGAATGCGCAGCAAGACAAGGGCATCACCATTCCACATGATATAGACCTG 309

Qy        323 GlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCATGAGCAAGACCGACCTACT 369

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CCGTCACCTGCCCCCTCTCGCCCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTT 429

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||   |||||||||||||||||||   |||   |||
Db        430 TCCCTCACTGCCGCTGAGTATGACCAGACTACGTATGGGTCGTCCACCAACCCTATGTAT 489

Qy        383 IleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
                  ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GTCTCTGACACAGTTACGCTTGTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCC 549

Qy        403 LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer 422
              ||||||||||||||||||||||||||||||||||||   |||       |||||||||
Db        550 CTTGATTGGTCTAAAGTTACTCTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCT 609

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 AAGACATTTTATGTTCTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACT 669

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAGGCCGGCTACCCTTACAATTATAATACTACCGCTAGTGACCAAATTTTGATTGAGAAT 729

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        730 GCGGCCGGCCACCGTGTCGCTATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACC 789

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502
              |||||||||      ||||||||||||      ||||||||||||||||||||||||||||
Db        790 TCGATCTCTGCGGTCGGCGTACTGGCTCCACACTCTGCCCTTGCCGTTCTTGAGGATACT 849

Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522
                  |||||||||   ||||||||||||||||||||||||||||||||||||||   |||
Db        850 ATTGATTACCCCGCCCGTGCCCATACTTTTGATGATTTTTGCCCGGAGTGCCGTACCCTA 909

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLys 542
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||   |||
Db        910 GGTTTGCAGGGTTGTGCATTCCAGTCTACTATTGCTGAGCTCCAGCGTTTAAAAATGAAG 969

Qy        543 ValGlyLysThrArgGlu 548
              ||||||||||||||||||
Db        970 GTAGGTAAAACCCGGGAG 987

RESULT 41
AX181913
LOCUS       AX181913               1026 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 195 from Patent WO0146696.
ACCESSION   AX181913
VERSION     AX181913.1  GI:15133219
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 195 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .1026
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="plorf2.2-6.seq"

Alignment Scores:
Pred. No.:                19.7          Length:          1026
Score:                    300.00        Matches:         300
Percent Similarity:       92.02%        Conservative:    0
Best Local Similarity:    92.02%        Mismatches:      26
Query Match:              54.64%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x AX181913 (1-1026)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCCACACGTTTCATGAAGGACCTG 69

Qy        243 HisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeu 262
              ||||||   |||  ||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CACTTCGCTGGCACGAATGGCGTTGGTGAGGTGGGTCGTGGTATCGCCCTGACACTGTTC 129

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 AATCTCGCTGATACGCTTCTCGGCGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGC 189

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CAACTGTTTTACTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATAT 249

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ACATCTGTTGAGAATGCGCAGCAAGACAAGGGCATCACCATTCCACATGATATAGACCTG 309

Qy        323 GlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCATGAGCAAGACCGACCTACT 369

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CCGTCACCTGCCCCCTCTCGCCCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTT 429

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
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Db        430 TCCCTCACTGCCGCTGAGTATGACCAGACTACGTATGGGTCGTCCACCAACCCTATGTAT 489

Qy        383 IleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402

Db        490 GTCTCTGACACAGTTACGCTTGTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCC 549

Qy        403 LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer 422

Db        550 CTTGATTGGTCTAAAGTTACTCTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCT 609

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442

Db        610 AAGACATTTTATGTTCTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACT 669

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462

Db        670 AAGGCCGGCTACCCTTACAATTATAATACTACCGCTAGTGACCAAATTTTGATTGAGAAT 729

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482

Db        730 GCGGCCGGCCACCGTGTCGCTATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACC 789

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502

Db        790 TCGATCTCTGCGGTCGGCGTACTGGCTCCACACTCTGCCCTTGCCGTTCTTGAGGATACT 849

Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522

Db        850 ATTGATTACCCCGCCCGTGCCCATACTTTTGATGATTTTTGCCCGGAGTGCCGTACCCTA 909

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLys 542

Db        910 GGTTTGCAGGGTTGTGCATTCCAGTCTACTATTGCTGAGCTCCAGCGTTTAAAAATGAAG 969

Qy        543 ValGlyLysThrArgGlu 548

Db        970 GTAGGTAAAACCCGGGAG 987

RESULT 42
BD077295
LOCUS       BD077295               1026 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077295
VERSION     BD077295.1  GI:22622898
KEYWORDS    JP 2001520384-A/174.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 174 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/174
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   cksorf2m-2.seq
            FH   Key             Location/Qualifiers
            FT   source          1. .1026
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                        virus)'.
FEATURES             Location/Qualifiers
     source          1. .1026
                     /organism="unidentified"
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                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              19.7          Length:         1026
Score:                  300.00        Matches:        300
Percent Similarity:     92.02%        Conservative:   0
Best Local Similarity:  92.02%        Mismatches:     26
Query Match:            54.64%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x BD077295 (1-1026)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242

Db         10 GGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCCACACGTTTCATGAAGGACCTG 69

Qy        243 HisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeu 262

Db         70 CACTTCGCTGGCACGAATGGCGTTGGTGAGGTGGGTCGTGGTATCGCCCTGACACTGTTC 129

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282

Db        130 AATCTCGCTGATACGCTTCTCGGCGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGC 189

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302

Db        190 CAACTGTTTTACTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATAT 249

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu 322

Db        250 ACATCTGTTGAGAATGCGCAGCAAGACAAGGGCATCACCATTCCACATGATATAGACCTG 309

Qy        323 GlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342

Db        310 GGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCATGAGCAAGACCGACCTACT 369

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362

Db        370 CCGTCACCTGCCCCCTCTCGCCCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTT 429

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382

Db        430 TCCCTCACTGCCGCTGAGTATGACCAGACTACGTATGGGTCGTCCACCAACCCTATGTAT 489

Qy        383 IleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402

Db        490 GTCTCTGACACAGTTACGCTTGTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCC 549

Qy        403 LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer 422

Db        550 CTTGATTGGTCTAAAGTTACTCTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCT 609

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442

Db        610 AAGACATTTTATGTTCTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACT 669

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462

Db        670 AAGGCCGGCTACCCTTACAATTATAATACTACCGCTAGTGACCAAATTTTGATTGAGAAT 729

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482

Db        730 GCGGCCGGCCACCGTGTCGCTATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACC 789

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502

Db        790 TCGATCTCTGCGGTCGGCGTACTGGCTCCACACTCTGCCCTTGCCGTTCTTGAGGATACT 849

Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522

Db        850 ATTGATTACCCCGCCCGTGCCCATACTTTTGATGATTTTTGCCCGGAGTGCCGTACCCTA 909
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Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLys 542
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||  |||
Db        910 GGTTTGCAGGGTTGTGCATTCCAGTCTACTATTGCTGAGCTCCAGCGTTTAAAAATGAAG 969

Qy        543 ValGlyLysThrArgGlu 548
              ||||||||||||||||||
Db        970 GTAGGTAAAACCCGGGAG 987

RESULT 43
BD077298
LOCUS       BD077298                1026 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077298
VERSION     BD077298.1  GI:22622901
KEYWORDS    JP 2001520384-A/177.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 177 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/177
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   plorf2.2-6.seq
            FH   Key             Location/Qualifiers
            FT   source          1. .1026
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                        virus)'.
FEATURES              Location/Qualifiers
     source           1. .1026
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              19.7          Length:         1026
Score:                  300.00        Matches:        300
Percent Similarity:     92.02%        Conservative:   0
Best Local Similarity:  92.02%        Mismatches:     26
Query Match:            54.64%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x BD077298 (1-1026)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCCACACGTTTCATGAAGGACCTG 69

Qy        243 HisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeu 262
              ||||||   |||   ||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CACTTCGCTGGCACGAATGGCGTTGGTGAGGTGGGTCGTGGTATCGCCCTGACACTGTTC 129

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 AATCTCGCTGATACGCTTCTCGGCGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGC 189

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CAACTGTTTTACTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATAT 249

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ACATCTGTTGAGAATGCGCAGCAAGACAAGGGCATCACCATTCCACATGATATAGACCTG 309

Qy        323 GlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCATGAGCAAGACCGACCTACT 369

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CCGTCACCTGCCCCCTCTCGCCCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTT 429

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||||||||  ||||||||||||||||  |||  |||
Db        430 TCCCTCACTGCCGCTGAGTATGACCAGACTACGTATGGGTCGTCCACCAACCCTATGTAT 489

Qy        383 IleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              |||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GTCTCTGACACAGTTACGCTTGTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCC 549

Qy        403 LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer 422
              ||||||||||||||||||||||||||||||||||||  |||      |||||||||
Db        550 CTTGATTGGTCTAAAGTTACTCTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCT 609

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 AAGACATTTTATGTTCTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACT 669

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAGGCCGGCTACCCTTACAATTATAATACTACCGCTAGTGACCAAATTTTGATTGAGAAT 729

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        730 GCGGCCGGCCACCGTGTCGCTATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACC 789

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502
              |||||||||      ||||||||||||   ||||||||||||   ||||||||||||
Db        790 TCGATCTCTGCGGTCGGCGTACTGGCTCCACACTCTGCCCTTGCCGTTCTTGAGGATACT 849

Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522
              |||||||||   ||||||||||||||||||||||||||||||||||||   |||
Db        850 ATTGATTACCCCGCCCGTGCCCATACTTTTGATGATTTTTGCCCGGAGTGCCGTACCCTA 909

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLys 542
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||  |||
Db        910 GGTTTGCAGGGTTGTGCATTCCAGTCTACTATTGCTGAGCTCCAGCGTTTAAAAATGAAG 969

Qy        543 ValGlyLysThrArgGlu 548
              ||||||||||||||||||
Db        970 GTAGGTAAAACCCGGGAG 987

RESULT 44
AX181742
LOCUS       AX181742                899 bp.   DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 24 from Patent WO0146696.
ACCESSION   AX181742
VERSION     AX181742.1  GI:15133065
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 24 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES              Location/Qualifiers
     source           1. .899
                      /organism="Hepatitis E virus"
                      /mol_type="unassigned DNA"
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                     /db_xref="taxon:12461"
                     /note="Clone: df-orf2/3"

Alignment Scores:
Pred. No.:                24.3          Length:         899
Score:                    285.00        Matches:        285
Percent Similarity:       95.96%        Conservative:   0
Best Local Similarity:    95.96%        Mismatches:     12
Query Match:              51.91%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-16 (1-549) x AX181742 (1-899)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              |||      ||||||   ||||||   ||||||||||||||||||||||||||||||||||||
Db          8 GCCATATCACCAGCCCCTGATACAGCTCCTGTACCTGATGTTGACTCACGTGGTGCTATT 67

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 TTGCGCCGGCAGTACAATTTGTCTACGTCCCCGCTTACATCATCTGTTGCTTCTGGTACT 127

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        128 AATCTGGTTCTCTATGCTGCCCCGCTGAACCCTCTCTTGCCTCTTCAGGATGGCACCAAC 187

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||
Db        188 ACTCATATTATGGCTACTGAGGCATCTAATTACGCCCAGTATCGGGTTGTTCGGGCTACG 247

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 ATTCGTTATCGCCCGTTGGTGCCAAATGCTGTTGGTGGTTATGCTATCTCTATTTCTTTC 307

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 TGGCCTCAAACTACAACTACCCCTACTTCTGTTGACATGAATTCTATCACTTCTACTGAT 367

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 GTCAGGATCTTGGTCCAGCCCGGTATAGCCTCCGAGTTAGTCATCCCTAGTGAACGCCTT 427

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        428 CACTACCGCAACCAAGGCTGGCGCTCTGTTGAGACCACGGGTGTGGCCGAAGAGGAGGCT 487

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 ACCTCCGGTCTGGTAATGCTTTGTATTCATGGCTCCCCTGTTAACTCCTACACTAATACA 547

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 CCTTACACCGGTGCATTGGGGCTTCTTGATTTTGCATTAGAACTTGAATTTAGAAATTTG 607

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||      ||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        608 ACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACTAGCACAGCCCGCCACCGGCTG 667

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CGCCGCGGTGCTGATGGGACCGCTGAGCTCACCACCACAGCAGCCACACGCTTCATGAAG 727

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        728 GATTTGCATTTTACTGGTACGAACGGCGTTGGTGAGGTGGGTCGTGGTATTGCCCTGACT 787

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CTGTTTAATCTTGCTGATACGCTTCTTGGTGGTTTACCGACAGAATTGATTTCGTCGGCT 847

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 GGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCAGCCAATGGCGAGCCA 898
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RESULT 45
BD077145
LOCUS       BD077145                 899 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077145
VERSION     BD077145.1  GI:22622748
KEYWORDS    JP 2001520384-A/24.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 899)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 24 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/24
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   Clone: df-orf2/3
            FH   Key             Location/Qualifiers
            FT   source          1. .899
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                              virus)'.
FEATURES             Location/Qualifiers
     source          1. .899
                     /organism="unidentified"
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Alignment Scores:
Pred. No.:                24.3          Length:         899
Score:                    285.00        Matches:        285
Percent Similarity:       95.96%        Conservative:   0
Best Local Similarity:    95.96%        Mismatches:     12
Query Match:              51.91%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-16 (1-549) x BD077145 (1-899)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              |||      ||||||   ||||||   ||||||||||||||||||||||||||||||||||||
Db          8 GCCATATCACCAGCCCCTGATACAGCTCCTGTACCTGATGTTGACTCACGTGGTGCTATT 67

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 TTGCGCCGGCAGTACAATTTGTCTACGTCCCCGCTTACATCATCTGTTGCTTCTGGTACT 127

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        128 AATCTGGTTCTCTATGCTGCCCCGCTGAACCCTCTCTTGCCTCTTCAGGATGGCACCAAC 187

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||
Db        188 ACTCATATTATGGCTACTGAGGCATCTAATTACGCCCAGTATCGGGTTGTTCGGGCTACG 247

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 ATTCGTTATCGCCCGTTGGTGCCAAATGCTGTTGGTGGTTATGCTATCTCTATTTCTTTC 307

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 TGGCCTCAAACTACAACTACCCCTACTTCTGTTGACATGAATTCTATCACTTCTACTGAT 367

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
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Db        368 GTCAGGATCTTGGTCCAGCCCGGTATAGCCTCCGAGTTAGTCATCCCTAGTGAACGCCTT 427

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160

Db        428 CACTACCGCAACCAAGGCTGGCGCTCTGTTGAGACCACGGGTGTGGCCGAAGAGGAGGCT 487

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180

Db        488 ACCTCCGGTCTGGTAATGCTTTGTATTCATGGCTCCCCTGTTAACTCCTACACTAATACA 547

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200

Db        548 CCTTACACCGGTGCATTGGGGCTTCTTGATTTTGCATTAGAACTTGAATTTAGAAATTTG 607

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db        608 ACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACTAGCACAGCCCGCCACCGGCTG 667

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db        668 CGCCGCGGTGCTGATGGGACCGCTGAGCTCACCACCACAGCAGCCACACGCTTCATGAAG 727

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260

Db        728 GATTTGCATTTTACTGGTACGAACGGCGTTGGTGAGGTGGGTCGTGGTATTGCCCTGACT 787

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db        788 CTGTTTAATCTTGCTGATACGCTTCTTGGTGGTTTACCGACAGAATTGATTTCGTCGGCT 847

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297

Db        848 GGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCAGCCAATGGCGAGCCA 898
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RESULT 46
AF516178
LOCUS AF516178 860 bp RNA linear VRL 07-AUG-2003
DEFINITION Swine hepatitis E virus isolate KOR1 capsid protein gene, partial cds.
ACCESSION AF516178
VERSION AF516178.1 GI:21541734
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 860)
AUTHORS Choi,I.S., Kwon,H.J., Shin,N.R. and Yoo,H.S.
TITLE Identification of Swine Hepatitis E Virus (HEV) and Prevalence of Anti-HEV Antibodies in Swine and Human Populations in Korea
JOURNAL J. Clin. Microbiol. 41 (8), 3602-3608 (2003)
PUBMED 12904362
REFERENCE 2 (bases 1 to 860)
AUTHORS Choi,I.-S. and Yoo,H.S.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2002) Infectious Diseases, College of Veterinary Medicine, Seoul National University, 103 Seodun-dong, Suwon 441-744, Republic of Korea
FEATURES Location/Qualifiers
source 1. .860
/organism="Swine hepatitis E virus"
/mol_type="genomic RNA"
/isolate="KOR1"
/db_xref="taxon:63421"
CDS <1. .>860
/note="ORF2; structural protein"
/codon_start=2
/product="capsid protein"
/protein_id="AAM61949.1"
/db_xref="GI:21541735"
/translation="VPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPPLP
LQDGTNTHIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVD
MNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETTGVAEEEATSGLVMLCIH
GSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTARHRLRRGADGTA
ELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPTELISSAGGQLFY
SRPVVSANGE"

Alignment Scores:

Pred. No.:	26.5	Length:	860
Score:	279.00	Matches:	279
Percent Similarity:	97.55%	Conservative:	0
Best Local Similarity:	97.55%	Mismatches:	7
Query Match:	50.82%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AF516178 (1-860)

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Qy         11 ValProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThrSer 30

Db          2 GTACCTGATGTTGACTCACGTGGTGCCATCTTGCGTCGGCAGTACAATTTGTCCACGTCC 61

Qy         31 ProLeuThrSerSerValAlaSerGlyThrAsnLeuValLeuTyrAlaAlaProLeuAsn 50

Db         62 CCGCTCACGTCTTCTGTCGCTTCTGGTACTAATTTAGTTCTCTATGCCGCCCCGCTGAAC 121

Qy         51 ProProLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSerAsn 70

Db        122 CCTCCCTTGCCCCTTCAGGATGGCACCAATACTCATATCATGGCTACTGAGGCATCCAAT 181

Qy         71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90

Db        182 TATGCTCAGTATCGGGTTGTTCGAGCTACGATCCGCTATCGCCCGCTGGTGCCAAATGCT 241

Qy         91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110

Db        242 GTTGGTGGTTATGCTATCTCTATTTCTTTCTGGCCTCAAACCACAACTACCCCTACTTCT 301

Qy        111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130

Db        302 GTTGACATGAATTCTATTACTTCCACTGATGTTAGGATTTTGGTCCAGCCCGGTATTGCC 361

Qy        131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150

Db        362 TCCGAGCTGGTCATCCCTAGCGAGCGTCTTCATTATCGTAATCAAGGCTGGCGCTCTGTT 421

Qy        151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170

Db        422 GAGACCACGGGTGTGGCCGAGGAGGAGGCCACTTCCGGTCTAGTAATGCTTTGCATCCAT 481

Qy        171 GlySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190

Db        482 GGCTCCCCTGTTAATTCTTACACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGAT 541

Qy        191 PheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSer 210

Db        542 TTTGCATTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCC 601

Qy        211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230

Db        602 CGGTACACCAGCACAGCCCGCCACCGGCTGCGTCGCGGTGCAGATGGGACCGCTGAGCTT 661

Qy        231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyVal 250

Db        662 ACTACCACAGCAGCCACACGTTTTATGAAAGATTTGCATTTTACTGGCACGAATGGCGTT 721

Qy        251 GlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGly 270

Db        722 GGTGAGGTGGGTCGTGGTATTGCCCTGACACTGTTCAATCTTGCTGATACGCTTCTCGGT 781

Qy        271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProVal 290

Db        782 GGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAGTTGTTCTACTCCCGCCCTGTT 841

Qy        291 ValSerAlaAsnGlyGlu 296

Db        842 GTCTCAGCCAATGGCGAGCCA 898
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Db        842 GTCTCGGCCAATGGCGAG 859

RESULT 47
AF516179
LOCUS       AF516179                 860 bp    RNA     linear   VRL 07-AUG-2003
DEFINITION  Swine hepatitis E virus isolate KOR2 capsid protein gene, partial
            cds.
ACCESSION   AF516179
VERSION     AF516179.1  GI:21541736
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 860)
  AUTHORS   Choi,I.S., Kwon,H.J., Shin,N.R. and Yoo,H.S.
  TITLE     Identification of Swine Hepatitis E Virus (HEV) and Prevalence of
            Anti-HEV Antibodies in Swine and Human Populations in Korea
  JOURNAL   J. Clin. Microbiol. 41 (8), 3602-3608 (2003)
   PUBMED   12904362
REFERENCE   2  (bases 1 to 860)
  AUTHORS   Choi,I.-S. and Yoo,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAY-2002) Infectious Diseases, College of Veterinary
            Medicine, Seoul National University, 103 Seodun-dong, Suwon
            441-744, Republic of Korea
FEATURES             Location/Qualifiers
     source          1. .860
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="KOR2"
                     /db_xref="taxon:63421"
     CDS             <1. .>860
                     /note="ORF2; structural protein"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM61950.1"
                     /db_xref="GI:21541737"
                     /translation="VPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPLLP
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                     MNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETTGVAEEEATSGLVMLCIH
                     GSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTARHRLRRGADGTA
                     ELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPTELISSAGGQLFY
                     SRPVVSANGE"

Alignment Scores:
Pred. No.:              26.8          Length:         860
Score:                  278.00        Matches:        278
Percent Similarity:     97.20%        Conservative:   0
Best Local Similarity:  97.20%        Mismatches:     8
Query Match:            50.64%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF516179 (1-860)

Qy         11 ValProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThrSer 30
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Db          2 GTACCTGATGTTGACTCACGTGGTGCCATCTTGCGTCGGCAGTACAATTTGTCCACGTCC 61

Qy         31 ProLeuThrSerSerValAlaSerGlyThrAsnLeuValLeuTyrAlaAlaProLeuAsn 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCGCTCACGTCTTCTGTCGCTTCTGGTACTAATTTAGTTCTCTATGCCGCCCCGCTGAAC 121

Qy         51 ProProLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSerAsn 70
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CCTCTCTTGCCCCTTCAGGATGGCACCAATACTCATATCATGGCTACTGAGGCATCCAAT 181

Qy         71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        182 TATGCTCAGTATCGGGTTGTTCGAGCTACGATCCGCTATCGCCCGCTGGTGCCAAATGCT 241

Qy         91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        242 GTTGGTGGTTATGCTATCTCTATTTCTTTCTGGCCTCAAACCACAACTACCCCTACTTCT 301

Qy        111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GTTGACATGAATTCTATTACTTCCACTGATGTTAGGATTTTGGTCCAGCCCGGTATTGCC 361

Qy        131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TCCGAGCTGGTCATCCCTAGCGAGCGTCTTCATTATCGTAATCAAGGCTGGCGCTCTGTT 421

Qy        151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GAGACCACGGGTGTGGCCGAGGAGGAGGCCACTTCCGGTCTAGTAATGCTTTGCATCCAT 481

Qy        171 GlySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 GGCTCCCCTGTTAATTCTTACACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGAT 541

Qy        191 PheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSer 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 TTTGCATTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCC 601

Qy        211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 CGGTACACCAGCACAGCCCGCCACCGGCTGCGTCGCGGTGCAGATGGGACCGCTGAGCTT 661

Qy        231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyVal 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 ACTACCACAGCAGCCACACGTTTTATGAAAGATTTGCATTTTACTGGCACGAATGGCGTT 721

Qy        251 GlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGly 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GGTGAGGTGGGTCGTGGTATTGCCCTGACACTGTTTAATCTTGCTGATACGCTTCTCGGT 781

Qy        271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProVal 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAGTTGTTCTACTCCCGCCCTGTT 841

Qy        291 ValSerAlaAsnGlyGlu 296
              ||||||||||||||||||
Db        842 GTCTCGGCCAATGGCGAG 859

RESULT 48
AF527942
LOCUS       AF527942                 860 bp    RNA     linear   VRL 07-AUG-2003
DEFINITION  Swine hepatitis E virus isolate KOR3 capsid protein gene, partial
            cds.
ACCESSION   AF527942
VERSION     AF527942.1  GI:22023950
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 860)
  AUTHORS   Choi,I.S., Kwon,H.J., Shin,N.R. and Yoo,H.S.
  TITLE     Identification of Swine Hepatitis E Virus (HEV) and Prevalence of
            Anti-HEV Antibodies in Swine and Human Populations in Korea
  JOURNAL   J. Clin. Microbiol. 41 (8), 3602-3608 (2003)
   PUBMED   12904362
REFERENCE   2  (bases 1 to 860)
  AUTHORS   Choi,I.-S. and Yoo,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUL-2002) Infectious Diseases, College of Veterinary
            Medicine, Seoul National University, 103 Seodun-dong, Suwon
            441-744, Republic of Korea
FEATURES             Location/Qualifiers
     source          1. .860
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="KOR3"
                     /db_xref="taxon:63421"
     CDS             <1. .>860
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                /note="structural protein; ORF2"
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                /db_xref="GI:22023951"
                /translation="VPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLNPLLP
                LQDGTNTHIMATEASNYAQYRVVRATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVD
                MNSITSTDVRTLVQPGIASELVIPSERLHYRNQGWRSVETTGVAEEEATSGLVMLCIH
                GSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTARHRLRRGADGTA
                ELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPTELISSAGGQLFY
                SRPVVSANGE"

Alignment Scores:
Pred. No.:                27.2          Length:          860
Score:                    277.00        Matches:         277
Percent Similarity:       96.85%        Conservative:    0
Best Local Similarity:    96.85%        Mismatches:      9
Query Match:              50.46%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x AF527942 (1-860)

Qy         11 ValProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThrSer 30
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GTACCTGATGTTGACTCACGTGGTGCTATCTTGCGCCGGCAATACAATCTTTCCACGTCC 61

Qy         31 ProLeuThrSerSerValAlaSerGlyThrAsnLeuValLeuTyrAlaAlaProLeuAsn 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCGCTTACATCTTCTGTCGCCTCTGGTACTAATTTGGTCCTCTACGCCGCTCCGTTAAAT 121

Qy         51 ProProLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSerAsn 70
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CCCCTCCTGCCTCTTCAGGATGGCACCAACACTCATATTATGGCTACTGAAGCATCCAAT 181

Qy         71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
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Db        182 TATGCCCAGTATCGGGTTGTTCGAGCTACGATCCGTTACCGCCCGCTAGTGCCAAATGCT 241

Qy         91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GTTGGTGGTTATGCTATTTCTATCTCTTTTTGGCCTCAAACCACAACTACCCCCACCTCT 301

Qy        111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
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Db        302 GTTGACATGAATTCTATTACTTCCACTGATGTTAGGACTTTGGTCCAGCCCGGTATTGCC 361

Qy        131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TCCGAGCTAGTCATCCCTAGCGAGCGCCTGCATTACCGTAATCAAGGCTGGCGCTCTGTT 421

Qy        151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GAGACCACGGGTGTCGCTGAGGAGGAGGCTACATCTGGTCTGGTAATGCTTTGCATCCAT 481

Qy        171 GlySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 GGCTCTCCTGTTAATTCTTATACTAACACACCTTACACTGGTGCACTGGGGCTTCTTGAT 541

Qy        191 PheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSer 210
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        542 TTCGCATTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACCAATACCCGTGTCTCC 601

Qy        211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 CGGTATACCAGCACAGCTCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAACTT 661

Qy        231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyVal 250
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Db        662 ACTACCACAGCAGCCACACGCTTTATGAAAGATCTGCATTTTACTGGCACTAATGGCGTT 721

Qy        251 GlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGly 270
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        722 GGTGAGGTGGGCCGTGGTATTGCTCTGACACTGTTTAATCTCGCTGATACGCTTCTCGGT 781

Qy        271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProVal 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTT 841

Qy        291 ValSerAlaAsnGlyGlu 296
              |||||||||||||||||
Db        842 GTCTCGGCCAATGGCGAG 859

RESULT 49
HEU40045/c
LOCUS       HEU40045                 849 bp    DNA     linear   VRL 26-JAN-1999
DEFINITION  Hepatitis E virus structural protein 2 (orf2) mRNA, partial cds.
ACCESSION   U40045
VERSION     U40045.1  GI:4096793
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 849)
  AUTHORS   Van Cuyck-Gandre,H., Clements,N.J., Zhang,H.Y., Caudill,J.C.,
            Cohen,S.G., Coursaget,P., Buisson,Y., Warren,R.L. and Longer,C.F.
  TITLE     Partial Sequence of HEV Isolates from North Africa and Pakistan:
            Comparison with Known HEV Sequences
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 849)
  AUTHORS   Van Cuyck-Gandre,H., Clements,N.J., Zhang,H.Y., Caudill,J.C.,
            Cohen,S.G., Coursaget,P., Buisson,Y., Warren,R.L. and Longer,C.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-NOV-1995) Helene Van Cuyck-Gandre, Virus Disease,
            Walter Reed Army Institute of Research, BLD 40, Washington, DC
            20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .849
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                     /mol_type="genomic DNA"
                     /strain="2B NIH Abbottabad, Pakistan"
                     /db_xref="taxon:12461"
                     /note="HEV mRNA from patient feces"
     CDS             complement(<1. .>849)
                     /note="orf2; capsid protein"
                     /codon_start=1
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                     /protein_id="AAD09446.1"
                     /db_xref="GI:4096794"
                     /translation="GLYNGSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMAT
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                     VQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTPY
                     TGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMK
                     DLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPT
                     VKLYRSV"

Alignment Scores:
Pred. No.:                30.6          Length:          849
Score:                    269.00        Matches:         269
Percent Similarity:       95.73%        Conservative:    0
Best Local Similarity:    95.73%        Mismatches:      12
Query Match:              49.00%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x HEU40045 (1-849)

Qy         25 TyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThrAsnLeuValLeu 44
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Db        843 TATAACGGATCCACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACCAACCTGGTTCTT 784

Qy         45 TyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsnThrHisIleMet 64
              ||||||||||||||  |||  ||||||||||||||||||||||||||||||||||||||||
Db        783 TATGCTGCTCCCCTTAGCCCACTTCTACCCCTTCAGGACGGCACTAATACTCATATAATG 724

Qy         65 AlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArg 84
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Db        723 GCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACAATCCGTTACCGC 664

Qy         85 ProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThr 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        663 CCGCTTGTTCCCAACGCTGTCGGCGGTTACGCCATTTCCATCTCATTTTGGCCACAGACC 604

Qy        105 ThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAspValArgIleLeu 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 ACCACCACCCCGACGTCCGTTGATATGAATTCAATAACTTCGACGGATGTTCGTATTTTA 544

Qy        125 ValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeuHisTyrArgAsn 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 GTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACACTATCGTAAC 484

Qy        145 GlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeu 164
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Db        483 CAAGGTTGGCGCTCCGTCGAGACCTCCGGGGTGGCTGAGGAGGAGGCTACCTCTGGTCTT 424

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTACACTAATACACCTTATACCGGT 364

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAATTTCGCAACCTCACCCCCGGTAAC 304

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 ACTAACACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCG 244

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
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Db        243 GACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGTTTTATGAAGGACCTCTATTTC 184

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              |||     ||||||||||||||   ||||||||||||||||||||||||   ||||||
Db        183 ACTAGTACCAATGGTGTCGGTGAGATCGGCCGCGGGATAGCTCTCACCCTGTTCAACCTT 124

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeu 284
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GCTGACACTCTGCTTGGTGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTG 64

Qy        285 PheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSer 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
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Qy        305 Val 305
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Db          3 GTA 1
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RESULT 50
AX181806
LOCUS       AX181806                960 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 88 from Patent WO0146696.
ACCESSION   AX181806
VERSION     AX181806.1  GI:15133129
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 88 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .960
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Alignment Scores:
Pred. No.:                37.1          Length:          960
Score:                    256.00        Matches:         256
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Best Local Similarity:    91.10%        Mismatches:      25
Query Match:              46.63%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x AX181806 (1-960)

Qy        268 LeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSer 287
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Db          3 CTTCTTGGTGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCC 62

Qy        288 ArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsn 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGCCCTGTTGTCTCGGCCAATGGCGAGCCAACAGTAAAGTTATACACATCTGTTGAGAAT 122

Qy        308 AlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeuGlyAspSerArgVal 327
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        123 GCGCAGCAAGACAAGGGCATCACCATTCCACACGACATAGATTTAGGTGACTCCCGTGTG 182

Qy        328 ValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaPro 347
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GTTATCCAGGATTATGATAACCAGCACGAACAAGATCGACCTACCCCGTCACCTGCCCCC 242

Qy        348 SerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAla 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 TCCCGCCCTTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTCTCTCTCACTGCCGCT 302

Qy        368 GluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrIleSerAspSerVal 387
              ||||||  |||  ||||||||||||||||  |||  |||  ||||||  |||
Db        303 GAGTACGRCCAGACCACGTATGGGTCGTCCACCAACCCTATGTATGTCTCTGATACAGTC 362

Qy        388 ThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLys 407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 ACGCTTGTTAATGTAGCCACTGGTGCTCAGGCTGTTGCCCGCTCTCTTGACTGGTCTAAA 422

Qy        408 ValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheVal 427
              ||||||||||||||||||||  |||  ||||||||||||  |||  |||
Db        423 GTTACTCTGGATGGTCGCCCTCTTACTACCATTCAGCAGTATTCTAAGAAATTTTATGTT 482

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 CTCCCGCTTCGSGGGAAGCTGTCCTTTTGGGAGGCTGGTACGACCAAGGCCGGCTACCCG 542

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 TATAATTATAATACCACTGCTAGTGACCAAATTTTGATTGAGAACGCGGCCGGTCACCGT 602

Qy        468 ValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAla 487
              ||||||||||||||||||||  ||||||||||||  ||||||||||  |||||||||
Db        603 GTCGCCATTTCTACTTATACCACTAGTTTGGGTGCCGGCCCTACCTCGATYTCTGCGGTC 662

Qy        488 AlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGly 507
              ||||||||||||  ||||||||||||  ||||||||||||  |||||||||
Db        663 GGTGTACTAGCTCCACATTCGGCCCTTGCTGTTCTCGAGGATACTGTTGATTATCCTGCT 722

Qy        508 ArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCys 527
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        723 CGTGCCCATACTTTTGATGATTTCTGCCCGGAGTGTCGCACCCTTGGTCTGCAGGGTTGT 782

Qy        528 AlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLysValGlyLysThrArg 547
              ||||||||||||||  ||||||||||||||||||||  ||||||||||||||||||
Db        783 GCATTCCAATCTACTATTGCTGAACTTCAGCGTCTTAAAATGAAGGTAGGTAAAACCCGG 842

Qy        548 Glu 548
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Db        843 GAG 845
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RESULT 51
BD077209
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LOCUS       BD077209                960 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077209
VERSION     BD077209.1  GI:22622812
KEYWORDS    JP 2001520384-A/88.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 960)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 88 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/88
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   Clone: HEV 3p RACE
            FH   Key             Location/Qualifiers
            FT   source          1. .960
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                        virus)'.
FEATURES             Location/Qualifiers
     source          1. .960
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              37.1          Length:         960
Score:                  256.00        Matches:        256
Percent Similarity:     91.10%        Conservative:   0
Best Local Similarity:  91.10%        Mismatches:     25
Query Match:            46.63%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x BD077209 (1-960)

Qy        268 LeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSer 287
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CTTCTTGGTGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCC 62

Qy        288 ArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsn 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGCCCTGTTGTCTCGGCCAATGGCGAGCCAACAGTAAAGTTATACACATCTGTTGAGAAT 122

Qy        308 AlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeuGlyAspSerArgVal 327
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        123 GCGCAGCAAGACAAGGGCATCACCATTCCACACGACATAGATTTAGGTGACTCCCGTGTG 182

Qy        328 ValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaPro 347
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GTTATCCAGGATTATGATAACCAGCACGAACAAGATCGACCTACCCCGTCACCTGCCCCC 242

Qy        348 SerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAla 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 TCCCGCCCTTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTCTCTCTCACTGCCGCT 302

Qy        368 GluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrIleSerAspSerVal 387
              ||||||   |||   ||||||||||||||||||   |||   |||   ||||||   |||
Db        303 GAGTACGRCCAGACCACGTATGGGTCGTCCACCAACCCTATGTATGTCTCTGATACAGTC 362

Qy        388 ThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLys 407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 ACGCTTGTTAATGTAGCCACTGGTGCTCAGGCTGTTGCCCGCTCTCTTGACTGGTCTAAA 422

Qy        408 ValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheVal 427
              ||||||||||||||||||||||   |||   ||||||||||||   |||   |||
Db        423 GTTACTCTGGATGGTCGCCCTCTTACTACCATTCAGCAGTATTCTAAGAAATTTTATGTT 482

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 CTCCCGCTTCGSGGGAAGCTGTCCTTTTGGGAGGCTGGTACGACCAAGGCCGGCTACCCG 542

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 TATAATTATAATACCACTGCTAGTGACCAAATTTTGATTGAGAACGCGGCCGGTCACCGT 602

Qy        468 ValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAla 487
              ||||||||||||||||||||||  ||||||||||||||||      |||||||||
Db        603 GTCGCCATTTCTACTTATACCACTAGTTTGGGTGCCGGCCCTACCTCGATYTCTGCGGTC 662

Qy        488 AlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGly 507
              ||||||||||||  ||||||||||||  ||||||||||||  |||||||||
Db        663 GGTGTACTAGCTCCACATTCGGCCCTTGCTGTTCTCGAGGATACTGTTGATTATCCTGCT 722

Qy        508 ArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCys 527
              ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        723 CGTGCCCATACTTTTGATGATTTCTGCCCGGAGTGTCGCACCCTTGGTCTGCAGGGTTGT 782

Qy        528 AlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLysValGlyLysThrArg 547
              ||||||||||||||  ||||||||||||||||||  ||||||||||||||||||
Db        783 GCATTCCAATCTACTATTGCTGAACTTCAGCGTCTTAAAATGAAGGTAGGTAAAACCCGG 842

Qy        548 Glu 548
              |||
Db        843 GAG 845

RESULT 52
AR278919
LOCUS       AR278919                803 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 17 from patent US 6514690.
ACCESSION   AR278919
VERSION     AR278919.1  GI:29713553
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 803)
  AUTHORS   Li,F., Hui,Z., Anderson,D.A., Logarnini,S.A. and Torresi,J.
  TITLE     Immunoreactive antigens of Hepatitis E Virus
  JOURNAL   Patent: US 6514690-A 17 04-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .803
                     /organism="unknown"
                     /mol_type="genomic DNA"

Alignment Scores:
Pred. No.:              40.1          Length:         803
Score:                  250.00        Matches:        250
Percent Similarity:     93.63%        Conservative:   0
Best Local Similarity:  93.63%        Mismatches:     17
Query Match:            45.54%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AR278919 (1-803)

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAGCTTTAT 60

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATCGACCTC 120

Qy        323 GlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGACCGACA 180
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Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTTTGGCTT 240

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCAGTCTAT 300

Qy        383 IleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCA 360

Qy        403 LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer 422
              |||||||||   ||||||||||||||||||||||||||   |||       |||||||||
Db        361 CTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAGTATTCA 420

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGTACTACT 480

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTTGAGAAT 540

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTC 600

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502
              |||||||||   ||||||||||||||||   |||||||||||||||||||||||||||||
Db        601 TCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCCGCGCTAGCATTGCTTGAGGATACC 660

Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||   |||
Db        661 ATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGCCCCCTT 720

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        721 GGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAG 780

Qy        543 ValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||
Db        781 GTGGGTAAAACTCGGGAGTTA 801

RESULT 53
AX181904
LOCUS       AX181904                 919 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 186 from Patent WO0146696.
ACCESSION   AX181904
VERSION     AX181904.1  GI:15133214
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 186 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .919
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="z12-3p.con"

Alignment Scores:
Pred. No.:              40.4          Length:        919
Score:                  250.00        Matches:       250
Percent Similarity:     90.91%        Conservative:  0
Best Local Similarity:  90.91%        Mismatches:    25
Query Match:            45.54%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AX181904 (1-919)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTAATTTCGTCGGCTGGGGGTCAACTGTTCTACTCCCGCCCTGTCGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTCAAGTTATACACATCTGTTGAGAATGCACAGCAGGATAAGGGG 121

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        122 ATAGCTATTCCACATGACATAGATTTGGGCGACTCTCGTTTGGTAATCCAGGATTACGAT 181

Qy        334 AsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgProPheSerVal 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AATCAGCACGAGCAGGACCGGCCCACCCCTTCGCCCGCCCCGTCTCGTCCTTTCTCGGTC 241

Qy        354 LeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThr 373
              ||||||||||||||   ||||||||||||||||||||||||||||||||||   |||||||
Db        242 CTCCGCGCTAATGATGCTTTGTGGCTTTCTCTTACCGCTGCTGAGTATGACCAGACTACA 301

Qy        374 TyrGlySerSerThrGlyProValTyrIleSerAspSerValThrLeuValAsnValAla 393
              ||||||||||||||   |||   |||   ||||||   ||||||   ||||||||||||
Db        302 TATGGGTCGTCCACCAACCCGATGTATGTCTCAGACACTGTTACATTTGTCAATGTGGCC 361

Qy        394 ThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArg 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 ACAGGGGCTCAGGCTGTCGCCCGTTCTCTTGATTGGTCTAAAGTTACCCTGGACGGCCGC 421

Qy        414 ProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLys 433
              ||||||   |||       ||||||||||||||||||   ||||||||||||||||||||
Db        422 CCTCTTACTACCATCCAGCAGTACTCTAAGACATTTTATGTTCTCCCACTTCGCGGGAAG 481

Qy        434 LeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThr 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 TTATCTTTTTGGGAGGCTGGCACAACTAAAGCCGGTTACCCTTATAATTATAACACAACT 541

Qy        454 AlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyr 473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 GCTAGTGACCAGATTCTGATTGAAAACGCGGCTGGCCATCGTGTCGCTATATCTACTTAT 601

Qy        474 ThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArg 493
              ||||||   ||||||||||||||||||       ||||||       ||||||||||||
Db        602 ACTACTAGCCTGGGCGCCGGCCCTGTGTCAGTTTCTGCGGTTGGTGTGTTAGCCCCACAC 661

Qy        494 SerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAsp 513
              |||   ||||||   ||||||||||||   |||||||||   ||||||||||||||||||
Db        662 TCGAGCCTTGCTATTCTTGAAGACACTGTTGACTATCCGGCCCGTGCTCACACTTTTGAT 721

Qy        514 AspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrVal 533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GACTTCTGTCCGGAATGCCGTGCCCTGGGTCTGCAGGGGTGTGCTTTTCAATCTACTATC 781

Qy        534 AlaGluLeuGlnArgLeuLysValLysValGlyLysThrArgGlu 548
              ||||||||||||||||||||   ||||||||||||||||||||||
Db        782 GCTGAGCTCCAGCGTCTTAAAATGAAGGTAGGCAAAACCCGGGAG 826

RESULT 54
BD077293
LOCUS       BD077293                 919 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077293
VERSION     BD077293.1  GI:22622896
KEYWORDS    JP 2001520384-A/172.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 919)
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  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 172 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/172
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   z12-3p.con
            FH   Key             Location/Qualifiers
            FT   source          1. .919
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                           virus)'.
FEATURES             Location/Qualifiers
     source          1. .919
                     /organism="unidentified"
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Alignment Scores:
Pred. No.:                40.4          Length:          919
Score:                    250.00        Matches:         250
Percent Similarity:       90.91%        Conservative:    0
Best Local Similarity:    90.91%        Mismatches:      25
Query Match:              45.54%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x BD077293 (1-919)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTAATTTCGTCGGCTGGGGGTCAACTGTTCTACTCCCGCCCTGTCGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTCAAGTTATACACATCTGTTGAGAATGCACAGCAGGATAAGGGG 121

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
                 ||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        122 ATAGCTATTCCACATGACATAGATTTGGGCGACTCTCGTTTGGTAATCCAGGATTACGAT 181

Qy        334 AsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgProPheSerVal 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AATCAGCACGAGCAGGACCGGCCCACCCCTTCGCCCGCCCCGTCTCGTCCTTTCTCGGTC 241

Qy        354 LeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThr 373
              ||||||||||||||   |||||||||||||||||||||||||||||||||||   |||
Db        242 CTCCGCGCTAATGATGCTTTGTGGCTTTCTCTTACCGCTGCTGAGTATGACCAGACTACA 301

Qy        374 TyrGlySerSerThrGlyProValTyrIleSerAspSerValThrLeuValAsnValAla 393
              ||||||||||||||   |||  |||  ||||||  ||||||  ||||||||||||
Db        302 TATGGGTCGTCCACCAACCCGATGTATGTCTCAGACACTGTTACATTTGTCAATGTGGCC 361

Qy        394 ThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArg 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 ACAGGGGCTCAGGCTGTCGCCCGTTCTCTTGATTGGTCTAAAGTTACCCTGGACGGCCGC 421

Qy        414 ProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLys 433
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Db        422 CCTCTTACTACCATCCAGCAGTACTCTAAGACATTTTATGTTCTCCCACTTCGCGGGAAG 481

Qy        434 LeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThr 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 TTATCTTTTTGGGAGGCTGGCACAACTAAAGCCGGTTACCCTTATAATTATAACACAACT 541

Qy        454 AlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyr 473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 GCTAGTGACCAGATTCTGATTGAAAACGCGGCTGGCCATCGTGTCGCTATATCTACTTAT 601

Qy        474 ThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArg 493
              ||||||  ||||||||||||||||||      ||||||      ||||||||||||
Db        602 ACTACTAGCCTGGGCGCCGGCCCTGTGTCAGTTTCTGCGGTTGGTGTGTTAGCCCCACAC 661

Qy        494 SerAlaLeuAlaLeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAsp 513
              |||   ||||||   ||||||||||||   |||||||||   ||||||||||||||||||
Db        662 TCGAGCCTTGCTATTCTTGAAGACACTGTTGACTATCCGGCCCGTGCTCACACTTTTGAT 721

Qy        514 AspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrVal 533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GACTTCTGTCCGGAATGCCGTGCCCTGGGTCTGCAGGGGTGTGCTTTTCAATCTACTATC 781

Qy        534 AlaGluLeuGlnArgLeuLysValLysValGlyLysThrArgGlu 548
              ||||||||||||||||||||   ||||||||||||||||||||
Db        782 GCTGAGCTCCAGCGTCTTAAAATGAAGGTAGGCAAAACCCGGGAG 826

RESULT 55
HPECCAP
LOCUS       HPECCAP                  775 bp    RNA     linear   VRL 02-FEB-1999
DEFINITION  Hepatitis E virus RNA, capsid region.
ACCESSION   D10332
VERSION     D10332.1  GI:221700
KEYWORDS    structural protein.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (sites)
  AUTHORS   Tam,A.W., Smith,M.M., Guerra,M.E., Huang,C.C., Bradley,D.W.,
            Fry,K.E. and Reyes,G.R.
  TITLE     Hepatitis E virus (HEV): molecular cloning and sequencing of the
            full-length viral genome
  JOURNAL   Virology 185 (1), 120-131 (1991)
  MEDLINE   92024067
   PUBMED   1926770
REFERENCE   2  (bases 1 to 775)
  AUTHORS   Aye,T.T., Uchida,T., Ma,X., Iida,F., Shikata,T., Zhuang,H. and
            Win,K.M.
  TITLE     Sequence comparison of the capsid region of hepatitis E viruses
            isolated from Myanmar and China
  JOURNAL   Microbiol. Immunol. 36 (6), 615-621 (1992)
  MEDLINE   92396046
   PUBMED   1387921
REFERENCE   3  (bases 1 to 775)
  AUTHORS   Uchida,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JAN-1992) Toshikazu Uchida, Nihon University School
            of Medicine, 1st Department of Pathology; 30-1 Oyaguchi-Kamimachi,
            Itabashi-ku, Tokyo 173, Japan (Tel:03-3972-8111, Fax:03-3972-8830)
COMMENT     Submitted (23-Jan-1992) to DDBJ by:
            Toshikazu Uchida
            Ist Department of Pathology
            Nihon University School of Medicine
            30-1 Oyaguchi Kamimachi
            Itabashi-ku, Tokyo 173
            Japan
            Phone:  03-3972-8111
            Fax:    03-3972-8830.
FEATURES             Location/Qualifiers
     source          1. .775
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="ChinaEpi-1-3"
                     /db_xref="taxon:12461"
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                     /db_xref="GI:391712"
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                ATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNY
                NTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLEDTMDYPAR
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Alignment Scores:
Pred. No.:                46.9          Length:         775
Score:                    239.00        Matches:        239
Percent Similarity:       93.00%        Conservative:   0
Best Local Similarity:    93.00%        Mismatches:     18
Query Match:              43.53%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-16 (1-549) x HPECCAP (1-775)

Qy        291 ValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGln 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GTCTCAGCCAATGGCGAGCCGACTGTTAAGCTTTATACATCTGTAGAGAATGCTCAGCAG 61

Qy        311 AspLysGlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGln 330
              |||||||||   |||||||||||||||||||||||||||   |||||||||||||||||||
Db         62 GATAAGGGTATTGCAATCCCGCATGACATCGACCTCGGGGAGTCTCGTGTAGTTATTCAG 121

Qy        331 AspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgPro 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GATTATGACAACCAACATGAGCAGGACCGACCGACACCTTCCCCAGCCCCATCGCGCCCT 181

Qy        351 PheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAsp 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 TTTTCTGTCCTCCGAGCTAATGATGTGCTTTGGCTTTCTCTCACCGCTGCCGAGTATGAC 241

Qy        371 GlnSerThrTyrGlySerSerThrGlyProValTyrIleSerAspSerValThrLeuVal 390
              ||||||||||||||||||||||||   |||||||||   |||||||||||||||||||||
Db        242 CAGTCCACTTACGGCTCTTCGACGGCCCCAGTCTATGTCTCTGACTCTGTGACCTTGGTT 301

Qy        391 AsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeu 410
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||||
Db        302 AATGTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCACTCGACTGGACCAAGGTCACACTT 361

Qy        411 AspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuProLeu 430
              ||||||||||||||||   |||       |||||||||||||||||||||||||||||||
Db        362 GATGGTCGCCCCCTTTCCACCATCCAGCAGTATTCAAAGACCTTCTTTGTCCTGCCGCTC 421

Qy        431 ArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyr 450
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 CGCGGTAAGCTCTCCTTTTGGGAGGCAGGTACTACTAAAGCCGGGTACCCTTATAATTAT 481

Qy        451 AsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIle 470
              ||||||||||||||||||||||   |||   |||||||||||||||||||||||||||||||
Db        482 AACACCACTGCTAGTGACCAACTGCTCGTTGAGAATGCCGCTGGGCATCGGGTTGCTATT 541

Qy        471 SerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeu 490
              ||||||||||||||||   ||||||||||||||||||   |||||||||   |||||||||
Db        542 TCCACTTACACCACTAGCCTGGGTGCTGGCCCCGTCTCTATTTCCGCGGTTGCTGTTTTA 601

Qy        491 AlaProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHis 510
              ||||||   |||||||||||||||||||||||||||   |||||||||   |||||||||
Db        602 GCCCCCCACTCCGCGCTAGCATTGCTTGAGGATACCATGGACTACCCTGCCCGCGCCCAT 661

Qy        511 ThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGln 530
              ||||||||||||||||||||||||||||   |||||||||||||||||||||||||||||||
Db        662 ACTTTCGATGACTTCTGCCCGGAGTGCCGCCCCCTTGGCCTCCAGGGCTGTGCTTTTCAG 721

Qy        531 SerThrValAlaGluLeuGlnArgLeuLysValLysValGlyLysThrArg 547
              ||||||||||||||||||||||||||||||   |||||||||||||||||
Db        722 TCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGG 772

RESULT 56
AX181871
LOCUS       AX181871                 901 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 153 from Patent WO0146696.
ACCESSION   AX181871
VERSION     AX181871.1  GI:15133192
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 153 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .901
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="us2-3p"

Alignment Scores:
Pred. No.:                49.4          Length:         901
Score:                    236.00        Matches:        236
Percent Similarity:       91.12%        Conservative:   0
Best Local Similarity:    91.12%        Mismatches:     23
Query Match:              42.99%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-16 (1-549) x AX181871 (1-901)

Qy        290 ValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGln 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATATACATCTGTTGAGAATGCGCAG 60

Qy        310 GlnAspLysGlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIle 329
              ||||||||||||      ||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAGACAAGGGCATCACCATTCCACATGATATAGACCTGGGTGACTCCCGTGTGGTTATC 120

Qy        330 GlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArg 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGGATTATGATAACCAGCAYGAGCAAGACCGACCTACTCCGTCACCTGCCCCCTCTCGC 180

Qy        350 ProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyr 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTTTCCCTCACTGCCGCTGAGTAT 240

Qy        370 AspGlnSerThrTyrGlySerSerThrGlyProValTyrIleSerAspSerValThrLeu 389
              ||||||   |||||||||||||||||||   |||   ||||||   |||||||||||||||
Db        241 GACCAGACTACGTATGGGTCGTCCACCAACCCTATGTATGTCTCTGACACAGTTACGCTT 300

Qy        390 ValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThr 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCCCTTGATTGGTCTAAAGTTACT 360

Qy        410 LeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuPro 429
              ||||||||||||||||   |||       ||||||||||||||||||   |||||||||
Db        361 CTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCTAAGACATTTTATGTTCTCCCG 420

Qy        430 LeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsn 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACTAAGGCCGGCTACCCTTACAAT 480

Qy        450 TyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAla 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TATAATACTACCGCTAGTGACCAAATTTTGATTGAGAATGCGGCCGGCCACCGTGTCGCT 540

Qy        470 IleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaVal 489
              ||||||||||||||||   ||||||||||||||      |||||||||      |||
Db        541 ATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACCTCGATCTCTGCGGTCGGCGTA 600

Qy        490 LeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAla 509
              |||||||||   |||||||||||   |||||||||||   |||||||||   ||||||
Db        601 CTGGCTCCACACTCTGCCCTTGCCGTTCTTGAGGATACTATTGATTACCCCGCCCGTGCC 660
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Qy        510 HisThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPhe 529
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        661 CATACTTTTGATGATTTTTGCCCGGAGTGCCGTACCCTAGGTTTGCAGGGTTGTGCATTC 720

Qy        530 GlnSerThrValAlaGluLeuGlnArgLeuLysValLysValGlyLysThrArgGlu 548
              |||||||||  ||||||||||||||||||||  ||||||||||||||||||||
Db        721 CAGTCTACTATTGCTGAGCTCCAGCGTTTAAAAATGAAGGTAGGTAAAACCCGGGAG 777

RESULT 57
BD077271
LOCUS       BD077271                901 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077271
VERSION     BD077271.1  GI:22622874
KEYWORDS    JP 2001520384-A/150.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 901)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 150 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/150
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   us2-3p
            FH   Key             Location/Qualifiers
            FT   source          1. .901
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                        virus)'.
FEATURES              Location/Qualifiers
     source           1. .901
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                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              49.4          Length:         901
Score:                  236.00        Matches:        236
Percent Similarity:     91.12%        Conservative:   0
Best Local Similarity:  91.12%        Mismatches:     23
Query Match:            42.99%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x BD077271 (1-901)

Qy        290 ValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGln 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATATACATCTGTTGAGAATGCGCAG 60

Qy        310 GlnAspLysGlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIle 329
              ||||||||||||      ||||||||||||||||||||||||||||||||||||||||
Db         61 CAAGACAAGGGCATCACCATTCCACATGATATAGACCTGGGTGACTCCCGTGTGGTTATC 120

Qy        330 GlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArg 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGGATTATGATAACCAGCAYGAGCAAGACCGACCTACTCCGTCACCTGCCCCCTCTCGC 180

Qy        350 ProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyr 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTTTCCCTCACTGCCGCTGAGTAT 240

Qy        370 AspGlnSerThrTyrGlySerSerThrGlyProValTyrIleSerAspSerValThrLeu 389
              ||||||  ||||||||||||||||||  |||  |||  ||||||  |||||||||
Db        241 GACCAGACTACGTATGGGTCGTCCACCAACCCTATGTATGTCTCTGACACAGTTACGCTT 300

Qy        390 ValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThr 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCCCTTGATTGGTCTAAAGTTACT 360

Qy        410 LeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuPro 429
              ||||||||||||||||  |||       ||||||||||||||||||  |||||||||
Db        361 CTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCTAAGACATTTTATGTTCTCCCG 420

Qy        430 LeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsn 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACTAAGGCCGGCTACCCTTACAAT 480

Qy        450 TyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAla 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TATAATACTACCGCTAGTGACCAAATTTTGATTGAGAATGCGGCCGGCCACCGTGTCGCT 540

Qy        470 IleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaVal 489
              ||||||||||||||||  ||||||||||||||  |||||||||  |||
Db        541 ATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACCTCGATCTCTGCGGTCGGCGTA 600

Qy        490 LeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAla 509
              |||||||||  ||||||||||||  ||||||||||||  |||||||||  ||||||
Db        601 CTGGCTCCACACTCTGCCCTTGCCGTTCTTGAGGATACTATTGATTACCCCGCCCGTGCC 660

Qy        510 HisThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPhe 529
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        661 CATACTTTTGATGATTTTTGCCCGGAGTGCCGTACCCTAGGTTTGCAGGGTTGTGCATTC 720

Qy        530 GlnSerThrValAlaGluLeuGlnArgLeuLysValLysValGlyLysThrArgGlu 548
              |||||||||  ||||||||||||||||||||  ||||||||||||||||||||
Db        721 CAGTCTACTATTGCTGAGCTCCAGCGTTTAAAAATGAAGGTAGGTAAAACCCGGGAG 777

RESULT 58
AX181903
LOCUS       AX181903                890 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 185 from Patent WO0146696.
ACCESSION   AX181903
VERSION     AX181903.1  GI:15133213
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 185 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES              Location/Qualifiers
     source           1. .890
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                      /note="z12-3p.race"

Alignment Scores:
Pred. No.:              50.8          Length:         890
Score:                  234.00        Matches:        234
Percent Similarity:     90.35%        Conservative:   0
Best Local Similarity:  90.35%        Mismatches:     25
Query Match:            42.62%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AX181903 (1-890)

Qy        290 ValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGln 309
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Qy        310 GlnAspLysGlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIle 329
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Db         61 CAGGATAAGGGGATAGCTATTCCACATGACATAGATTTGGGCGACTCTCGTTTGGTAATC 120

Qy        330 GlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArg 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGGATTACGATAATCAGCACGAGCAGGACCGGCCCACCCCTTCGCCCGCCCCGTCTCGT 180

Qy        350 ProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyr 369
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Db        181 CCTTTCTCGGTCCTCCGCGCTAATGATGCTTTGTGGCTTTCTCTTACCGCTGCTGAGTAT 240

Qy        370 AspGlnSerThrTyrGlySerSerThrGlyProValTyrIleSerAspSerValThrLeu 389
              ||||||  ||||||||||||||||||  |||  |||  ||||||  ||||||
Db        241 GACCAGACTACATATGGGTCGTCCACCAACCCGATGTATGTCTCAGACACTGTTACATTT 300

Qy        390 ValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThr 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTCAATGTGGCCACAGGGGCTCAGGCTGTCGCCCGTTCTCTTGATTGGTCTAAAGTTACC 360

Qy        410 LeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuPro 429
              ||||||||||||||||||  |||      ||||||||||||||||||  |||||||||
Db        361 CTGGACGGCCGCCCTCTTACTACCATCCAGCAGTACTCTAAGACATTTTATGTTCTCCCA 420

Qy        430 LeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsn 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTTCGCGGGAAGTTATCTTTTTGGGAGGCTGGCACAACTAAAGCCGGTTACCCTTATAAT 480

Qy        450 TyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAla 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TATAACACAACTGCTAGTGACCAGATTCTGATTGAAAACGCGGCTGGCCATCGTGTCGCT 540

Qy        470 IleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaVal 489
              ||||||||||||||||||  ||||||||||||||||||      ||||||      |||
Db        541 ATATCTACTTATACTACTAGCCTGGGCGCCGGCCCTGTGTCAGTTTCTGCGGTTGGTGTG 600

Qy        490 LeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAla 509
              |||||||||  |||  ||||||  ||||||||||||  |||||||||  ||||||
Db        601 TTAGCCCCACACTCGAGCCTTGCTATTCTTGAAGACACTGTTGACTATCCGGCCCGTGCT 660

Qy        510 HisThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPhe 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACACTTTTGATGACTTCTGTCCGGAATGCCGTGCCCTGGGTCTGCAGGGGTGTGCTTTT 720

Qy        530 GlnSerThrValAlaGluLeuGlnArgLeuLysValLysValGlyLysThrArgGlu 548
              |||||||||  ||||||||||||||||||||  ||||||||||||||||||||
Db        721 CAATCTACTATCGCTGAGCTCCAGCGTCTTAAAATGAAGGTAGGCAAAACCCGGGAG 777

RESULT 59
BD077292
LOCUS       BD077292                 890 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077292
VERSION     BD077292.1  GI:22622895
KEYWORDS    JP 2001520384-A/171.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 890)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 171 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/171
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   z12-3p.race
            FH   Key             Location/Qualifiers
            FT   source          1. .890
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                              virus)'.
FEATURES             Location/Qualifiers
     source          1. .890
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              50.8          Length:          890
Score:                  234.00        Matches:         234
Percent Similarity:     90.35%        Conservative:    0
Best Local Similarity:  90.35%        Mismatches:      25
Query Match:            42.62%        Indels:          0
DB:                     1             Gaps:            0

US-09-769-066-16 (1-549) x BD077292 (1-890)

Qy        290 ValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGln 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCGTCTCGGCCAATGGCGAGCCGACTGTCAAGTTATACACATCTGTTGAGAATGCACAG 60

Qy        310 GlnAspLysGlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIle 329
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGATAAGGGGATAGCTATTCCACATGACATAGATTTGGGCGACTCTCGTTTGGTAATC 120

Qy        330 GlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArg 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGGATTACGATAATCAGCACGAGCAGGACCGGCCCACCCCTTCGCCCGCCCCGTCTCGT 180

Qy        350 ProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyr 369
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        181 CCTTTCTCGGTCCTCCGCGCTAATGATGCTTTGTGGCTTTCTCTTACCGCTGCTGAGTAT 240

Qy        370 AspGlnSerThrTyrGlySerSerThrGlyProValTyrIleSerAspSerValThrLeu 389
              ||||||  ||||||||||||||||||  |||  |||  ||||||  ||||||
Db        241 GACCAGACTACATATGGGTCGTCCACCAACCCGATGTATGTCTCAGACACTGTTACATTT 300

Qy        390 ValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThr 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTCAATGTGGCCACAGGGGCTCAGGCTGTCGCCCGTTCTCTTGATTGGTCTAAAGTTACC 360

Qy        410 LeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuPro 429
              ||||||||||||||||||  |||      ||||||||||||||||||  |||||||||
Db        361 CTGGACGGCCGCCCTCTTACTACCATCCAGCAGTACTCTAAGACATTTTATGTTCTCCCA 420

Qy        430 LeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsn 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTTCGCGGGAAGTTATCTTTTTGGGAGGCTGGCACAACTAAAGCCGGTTACCCTTATAAT 480

Qy        450 TyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAla 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TATAACACAACTGCTAGTGACCAGATTCTGATTGAAAACGCGGCTGGCCATCGTGTCGCT 540

Qy        470 IleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaVal 489
              ||||||||||||||||||  ||||||||||||||||||      ||||||      |||
Db        541 ATATCTACTTATACTACTAGCCTGGGCGCCGGCCCTGTGTCAGTTTCTGCGGTTGGTGTG 600

Qy        490 LeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAla 509
              |||||||||  |||  ||||||  ||||||||||||  |||||||||  ||||||
Db        601 TTAGCCCCACACTCGAGCCTTGCTATTCTTGAAGACACTGTTGACTATCCGGCCCGTGCT 660

Qy        510 HisThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPhe 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACACTTTTGATGACTTCTGTCCGGAATGCCGTGCCCTGGGTCTGCAGGGGTGTGCTTTT 720

Qy        530 GlnSerThrValAlaGluLeuGlnArgLeuLysValLysValGlyLysThrArgGlu 548
              |||||||||  ||||||||||||||||||||  ||||||||||||||||||||
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Db        721 CAATCTACTATCGCTGAGCTCCAGCGTCTTAAAATGAAGGTAGGCAAAACCCGGGAG 777

RESULT 60
AY641398
LOCUS       AY641398                720 bp    RNA     linear   VRL 03-JUL-2004
DEFINITION  Hepatitis E virus isolate hKOR capsid protein gene, partial cds.
ACCESSION   AY641398
VERSION     AY641398.1  GI:49339406
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Identification of human Hepatitis E virus (HEV) and prevalence of
            anti-HEV antibodies in human populations in Korea
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-MAY-2004) Department of Infectious Diseases, College
            of Veterinary Medicine and School of Agricultural Biotechnology,
            Seoul National University, Shinlim-dong, san56-1, Seoul, Kwanak-Gu
            151-742, South Korea
FEATURES             Location/Qualifiers
     source          1. .720
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="hKOR"
                     /db_xref="taxon:12461"
                     /country="South Korea"
     CDS             <1. .>720
                     /note="ORF2; structural protein"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT64889.1"
                     /db_xref="GI:49339407"
                     /translation="NPLLPLQDGTNTHIMATEASNYAQYRVVRATIRYRPLVPNAVGG
                     YAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVE
                     TTGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRV
                     SRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLANT
                     LLGGLPTELISSAGGQLFYSRP"

Alignment Scores:
Pred. No.:              52.5          Length:         720
Score:                  231.00        Matches:        231
Percent Similarity:     96.25%        Conservative:   0
Best Local Similarity:  96.25%        Mismatches:     9
Query Match:            42.08%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AY641398 (1-720)

Qy         50 AsnProProLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSer 69
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AACCCTCTCTTGCCTCTTCAGGATGGCACCAATACTCATATCATGGCTACTGAGGCATCC 60

Qy         70 AsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsn 89
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db         61 AATTATGCTCAGTATCGGGTTGTTCGAGCTACGATCCGCTATCGCCCGCTGGTGCCAAAT 120

Qy         90 AlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThr 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTGTTGGTGGTTATGCTATCTCTATTTCTTTCTGGCCTCAAACCACAACCACCCCTACT 180

Qy        110 SerValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIle 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCTGTTGACATGAATTCTATTACTTCCACTGATGTTAGGATTTTGGTCCAGCCCGGTATT 240

Qy        130 AlaSerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSer 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCTCCGAGCTGGTCATCCCTAGTGAGCGTCTTCATTATCGTAATCAAGGCTGGCGCTCT 300

Qy        150 ValGluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIle 169
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTTGAGACCACGGGTGTGGCCGAGGAGGAGGCCACTTCCGGTCTAGTAATGCTTTGCATC 360

Qy        170 HisGlySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeu 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CATGGCTCCCCTGTTAATTCTTACACTAATACACCTTATACTGGTGCACTGGGGCTTCTT 420

Qy        190 AspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgVal 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GATTTTGCATTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTT 480

Qy        210 SerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGlu 229
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCCGGTACACCAGCACAGCCCGCCACCGGCTGCGTCGCGGTGCAGATGGGACCGCTGAG 540

Qy        230 LeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGly 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTTACTACCACAGCAGCCACACGTTTTATGAAAGATTTGCATTTTACTGGCACGAATGGC 600

Qy        250 ValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeu 269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTTGGCGAGGTGGGTCGTGGTATTGCCCTGACACTGTTTAATCTTGCTAATACGCTTCTC 660

Qy        270 GlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgPro 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGTGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCT 720

RESULT 61
AY714267
LOCUS       AY714267                720 bp    RNA     linear   VRL 15-SEP-2004
DEFINITION  Hepatitis E virus isolate hKOR-JMA capsid protein gene, partial
            cds.
ACCESSION   AY714267
VERSION     AY714267.1  GI:51980112
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Identification of human Hepatitis E virus (HEV) and prevalence of
            anti-HEV antibodies in human populations in Korea
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2004) Infectious Diseases, College of Veterinary
            Medicine and School of Agricultural Biotechnology, Seoul National
            University, Shinlim-Dong, San56-1, Seoul, Kwanak-Gu 151-742, South
            Korea
FEATURES             Location/Qualifiers
     source          1. .720
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="hKOR-JMA"
                     /db_xref="taxon:12461"
                     /country="South Korea"
     CDS             <1. .>720
                     /note="ORF2; structural protein"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAU20758.1"
                     /db_xref="GI:51980113"
                     /translation="NPLLPLQDGTNTHIMATEASNYAQYRVVRATIRYRPLVPNAVGG
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                     SRYTSTARHRLRRGADGTAELTTTAATRFMKDLYFTGTNGVGEVGRGIALTLFNLADT
                     LLGGLPTELISSAGGQLFYSRP"

Alignment Scores:
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Pred. No.:              53.2          Length:         720
Score:                  230.00        Matches:        230
Percent Similarity:     95.83%        Conservative:   0
Best Local Similarity:  95.83%        Mismatches:     10
Query Match:            41.89%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AY714267 (1-720)

Qy         50 AsnProProLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSer 69
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AACCCTCTCTTGCCTCTTCAGGATGGCACCAACACTCATATTATGGCTACTGAAGCATCC 60

Qy         70 AsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsn 89
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db         61 AATTATGCCCAGTATCGGGTTGTTCGAGCTACGATCCGTTACCGCCCGCTAGTGCCAAAT 120

Qy         90 AlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThr 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTGTTGGTGGTTATGCTATTTCTATCTCTTTTTGGCCTCAAACCACAACTACCCCCACC 180

Qy        110 SerValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIle 129
              |||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        181 TCTGTTGACATGAATTCTATTACTTCCACTGATGTTAGGACTTTGGTCCAGCCCGGTATT 240

Qy        130 AlaSerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSer 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCTCCGAGCTAGTCATCCCTAGCGAGCGCCTGCATTACCGTAATCAAGGCTGGCGCTCT 300

Qy        150 ValGluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIle 169
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTTGAGACCACGGGTGTCGCTGAGGAGGAGGCTACATCTGGTCTGGTAATGCTTTGCATC 360

Qy        170 HisGlySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeu 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CATGGCTCTCCTGTTAATTCTTATACTAACACACCTTACACTGGTGCACTAGGGCTTCTT 420

Qy        190 AspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgVal 209
              |||||||||||||||||||||||||||||||||||      |||||||||||||||||||
Db        421 GATTTCGCATTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACCAATACCCGTGTC 480

Qy        210 SerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGlu 229
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCCGGTATACCAGCACAGCTCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAA 540

Qy        230 LeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGly 249
              ||||||||||||||||||||||||||||||||||||||||||||   |||||||||   ||||||
Db        541 CTTACTACCACAGCAGCCACACGCTTTATGAAAGATCTGTATTTTACTGGCACTAATGGC 600

Qy        250 ValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeu 269
              |||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        601 GTTGGTGAGGTGGGCCGTGGTATTGCTCTGACACTGTTTAATCTCGCTGATACGCTTCTC 660

Qy        270 GlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgPro 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGTGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCT 720

RESULT 62
AY714269
LOCUS       AY714269                720 bp    RNA     linear   VRL 15-SEP-2004
DEFINITION  Hepatitis E virus isolate hKOR-SGK capsid protein gene, partial
            cds.
ACCESSION   AY714269
VERSION     AY714269.1  GI:51980116
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Identification of human Hepatitis E virus (HEV) and prevalence of
            anti-HEV antibodies in human populations in Korea
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2004) Infectious Diseases, College of Veterinary
            Medicine and School of Agricultural Biotechnology, Seoul National
            University, Shinlim-Dong, San56-1, Seoul, Kwanak-Gu 151-742, South
            Korea
FEATURES             Location/Qualifiers
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                     /isolate="hKOR-SGK"
                     /db_xref="taxon:12461"
                     /country="South Korea"
     CDS             <1. .>720
                     /note="ORF2; structural protein"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAU20760.1"
                     /db_xref="GI:51980117"
                     /translation="NPLLPLQDGTNTHIMATEASNYAQYRVVRATIRYRPLVPNAVGG
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                     LLGGLPTELISSAGGQLFYSRP"

Alignment Scores:
Pred. No.:              53.2          Length:         720
Score:                  230.00        Matches:        230
Percent Similarity:     95.83%        Conservative:   0
Best Local Similarity:  95.83%        Mismatches:     10
Query Match:            41.89%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AY714269 (1-720)

Qy         50 AsnProProLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSer 69
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AACCCTCTCTTGCCTCTTCAGGATGGCACCAACACTCATATTATGGCTACTGAAGCATCC 60

Qy         70 AsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsn 89
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db         61 AATTATGCCCAGTATCGGGTTGTTCGAGCTACGATCCGTTACCGCCCGCTAGTGCCAAAT 120

Qy         90 AlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThr 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTGTTGGTGGTTATGCTATTTCTATCTCTTTTTGGCCTCAAACCACAACTACCCCCACC 180

Qy        110 SerValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIle 129
              |||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        181 TCTGTTGACATGAATTCTATTACTTCCACTGATGTCAGGACTTTGGTCCAGCCCGGTATT 240

Qy        130 AlaSerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSer 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCTCCGAGCTAGTCATCCCTAGCGAGCGCCTGCATTACCGTAATCAAGGCTGGCGCTCT 300

Qy        150 ValGluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIle 169
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTTGAGACCACGGGTGTCGCTGAGGAGGAGGCTACATCTGGTCTGGTAATGCTTTGCATC 360

Qy        170 HisGlySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeu 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CATGGCTCTCCTGTTAATTCTTATACTAACACACCTTACACTGGTGCACTAGGGCTTCTT 420

Qy        190 AspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgVal 209
              |||||||||||||||||||||||||||||||||||      |||||||||||||||||||
Db        421 GATTTCGCATTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACCAATACCCGTGTC 480

Qy        210 SerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGlu 229
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCCGGTATACCAGCACAGCTCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAA 540
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Qy        230 LeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGly 249
              ||||||||||||||||||||||||||||||||||||||||  |||||||||  ||||||
Db        541 CTTACTACCACAGCAGCCACACGCTTTATGAAAGATCTGTATTTTACTGGCACTAATGGC 600

Qy        250 ValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeu 269
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        601 GTTGGTGAGGTGGGCCGTGGTATTGCTCTGACACTGTTTAATCTCGCTGATACGCTTCTC 660

Qy        270 GlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgPro 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGTGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCT 720

RESULT 63
AY714270
LOCUS       AY714270                720 bp    RNA     linear   VRL 15-SEP-2004
DEFINITION  Hepatitis E virus isolate hKOR-DYL capsid protein gene, partial
            cds.
ACCESSION   AY714270
VERSION     AY714270.1  GI:51980118
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Identification of human Hepatitis E virus (HEV) and prevalence of
            anti-HEV antibodies in human populations in Korea
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2004) Infectious Diseases, College of Veterinary
            Medicine and School of Agricultural Biotechnology, Seoul National
            University, Shinlim-Dong, San56-1, Seoul, Kwanak-Gu 151-742, South
            Korea
FEATURES             Location/Qualifiers
     source          1. .720
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="hKOR-DYL"
                     /db_xref="taxon:12461"
                     /country="South Korea"
     CDS             <1. .>720
                     /note="ORF2; structural protein"
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                     /db_xref="GI:51980119"
                     /translation="NPLLPLQDGTNTHIMATEASNYAQYRVVRATIRYRPLVPNAVGG
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                     LLGGLPTELISSAGGQLFYSRP"

Alignment Scores:
Pred. No.:              53.2          Length:         720
Score:                  230.00        Matches:        230
Percent Similarity:     95.83%        Conservative:   0
Best Local Similarity:  95.83%        Mismatches:     10
Query Match:            41.89%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AY714270 (1-720)

Qy         50 AsnProProLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSer 69
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AACCCTCTCTTGCCTCTTCAGGATGGCACCAACACTCATATTATGGCTACTGAAGCATCC 60

Qy         70 AsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsn 89
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db         61 AATTATGCCCAGTATCGGGTTGTTCGAGCTACGATCCGTTACCGCCCGCTAGTGCCAAAT 120

Qy         90 AlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrProThr 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTGTTGGTGGTTATGCTATTTCTATCTCTTTTTGGCCTCAAACCACAACTACCCCCACC 180

Qy        110 SerValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIle 129
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db        181 TCTGTTGACATGAATTCTATTACTTCCACTGATGTTAGGACTTTGGTCCAGCCCGGTATT 240

Qy        130 AlaSerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSer 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCTCCGAGCTAGTCATCCCTAGCGAGCGCCTGCATTACCGTAATCAAGGCTGGCGCTCT 300

Qy        150 ValGluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIle 169
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Db        301 GTTGAGACCACGGGTGTCGCTGAGGAGGAGGCTACATCTGGTCTGGTAATGCTTTGCATC 360

Qy        170 HisGlySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeu 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CATGGCTCTCCTGTTAATTCTTATACTAACACACCTTACACTGGTGCACTAGGGCTTCTT 420

Qy        190 AspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgVal 209
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Db        421 GATTTCGCATTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACCAATACCCGTGTC 480

Qy        210 SerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGlu 229
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCCGGTATACCAGCACAGCTCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAA 540

Qy        230 LeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGly 249
              ||||||||||||||||||||||||||||||||||||||||  |||||||||  ||||||
Db        541 CTTACTACCACAGCAGCCACACGCTTTATGAAAGATCTGTATTTTACTGGCACTAATGGC 600

Qy        250 ValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeu 269
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        601 GTTGGCGAGGTGGGCCGTGGTATTGCTCTGACACTGTTTAATCTCGCTGATACGCTTCTC 660

Qy        270 GlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgPro 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGTGGTTTACCGACAGAATTGATTTCGTCAGCTGGGGGTCAACTGTTTTACTCCCGCCCT 720

RESULT 64
AY714272
LOCUS       AY714272                720 bp    RNA     linear   VRL 15-SEP-2004
DEFINITION  Hepatitis E virus isolate hKOR-HJY capsid protein gene, partial
            cds.
ACCESSION   AY714272
VERSION     AY714272.1  GI:51980122
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Identification of human Hepatitis E virus (HEV) and prevalence of
            anti-HEV antibodies in human populations in Korea
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2004) Infectious Diseases, College of Veterinary
            Medicine and School of Agricultural Biotechnology, Seoul National
            University, Shinlim-Dong, San56-1, Seoul, Kwanak-Gu 151-742, South
            Korea
FEATURES             Location/Qualifiers
     source          1. .720
                     /organism="Hepatitis E virus"
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                     /isolate="hKOR-HJY"
                     /db_xref="taxon:12461"
                     /country="South Korea"
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                  YAISISFWPQTTTTPTSVDMNSITSTDVRTLVQPGIASELVIPSERLHYRNQGWRSVE
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                  LLGGLPTELISSAGGQLFYSRP"

Alignment Scores:
Pred. No.:              53.2          Length:         720
Score:                  230.00        Matches:        230
Percent Similarity:     95.83%        Conservative:   0
Best Local Similarity:  95.83%        Mismatches:     10
Query Match:            41.89%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AY714272 (1-720)

Qy         50 AsnProProLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSer 69
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AACCCTCTCTTGCCTCTTCAGGATGGCACCAACACTCATATTATGGCTACTGAAGCATCC 60

Qy         70 AsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsn 89
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db         61 AATTATGCCCAGTATCGGGTTGTTCGAGCTACGATCCGTTACCGCCCGCTAGTGCCAAAT 120

Qy         90 AlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThr 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTGTTGGTGGTTATGCTATTTCTATCTCTTTTTGGCCTCAAACCACAACTACCCCCACC 180

Qy        110 SerValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIle 129
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        181 TCTGTTGACATGAATTCTATTACTTCCACTGATGTTAGGACTTTGGTCCAGCCCGGTATT 240

Qy        130 AlaSerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSer 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCTCCGAGCTAGTCATCCCTAGCGAGCGCCTGCATTACCGTAATCAAGGCTGGCGCTCT 300

Qy        150 ValGluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIle 169
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTTGAGACCACGGGTGTCGCTGAGGAGGAGGCTACATCTGGTCTGGTAATGCTTTGCATC 360

Qy        170 HisGlySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeu 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CATGGCTCTCCTGTTAATTCCTATACTAACACACCTTACACTGGTGCACTAGGGCTTCTC 420

Qy        190 AspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgVal 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GATTTCGCATTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACCAATACCCGTGTC 480

Qy        210 SerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGlu 229
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCCGGTATACCAGCACAGCTCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAA 540

Qy        230 LeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGly 249
              ||||||||||||||||||||||||||||||||||||   |||||||||   ||||||||||
Db        541 CTTACTACCACAGCAGCCACACGCTTTATGAAAGATCTGTATTTTACTGGCACTAATGGC 600

Qy        250 ValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeu 269
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        601 GTTGGTGAGGTGGGCCGTGGTATTGCTCTGACACTGTTTAATCTCGCTGATACGCTTCTC 660

Qy        270 GlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgPro 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGTGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCT 720

RESULT 65
HPEBCAP
LOCUS       HPEBCAP                  745 bp    RNA     linear   VRL 02-FEB-1999
DEFINITION  Hepatitis E virus RNA, capsid region.
ACCESSION   D10333
VERSION     D10333.1  GI:221699
KEYWORDS    structural protein.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (sites)
  AUTHORS   Tam,A.W., Smith,M.M., Guerra,M.E., Huang,C.C., Bradley,D.W.,
            Fry,K.E. and Reyes,G.R.
  TITLE     Hepatitis E virus (HEV): molecular cloning and sequencing of the
            full-length viral genome
  JOURNAL   Virology 185 (1), 120-131 (1991)
  MEDLINE   92024067
   PUBMED   1926770
REFERENCE   2  (bases 1 to 745)
  AUTHORS   Aye,T.T., Uchida,T., Ma,X., Iida,F., Shikata,T., Zhuang,H. and
            Win,K.M.
  TITLE     Sequence comparison of the capsid region of hepatitis E viruses
            isolated from Myanmar and China
  JOURNAL   Microbiol. Immunol. 36 (6), 615-621 (1992)
  MEDLINE   92396046
   PUBMED   1387921
REFERENCE   3  (bases 1 to 745)
  AUTHORS   Uchida,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JAN-1992) Toshikazu Uchida, Nihon University School
            of Medicine, 1st Department of Pathology; 30-1 Oyaguchi-Kamimachi,
            Itabashi-ku, Tokyo 173, Japan (Tel:03-3972-8111, Fax:03-3972-8830)
COMMENT     Submitted (23-Jan-1992) to DDBJ by:
            Toshikazu Uchida
            1st Department of Pathology
            Nihon University School of Medicine
            30-1 Oyaguchi Kamimachi
            Itabashi-ku, Tokyo 173
            Japan
            Phone:  03-3972-8111
            Fax:    03-3972-8830.
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
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Alignment Scores:
Pred. No.:              53.3          Length:         745
Score:                  230.00        Matches:        230
Percent Similarity:     92.74%        Conservative:   0
Best Local Similarity:  92.74%        Mismatches:     18
Query Match:            41.89%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x HPEBCAP (1-745)

Qy        296 GluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAla 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db          1 GAGCCGACTGTTAAGCTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCA 60

Qy        316 IleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGln 335
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         61 ATCCCGCATGATATTGACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAA 120

Qy        336 HisGluGlnAspArgProThrProSerProAlaProSerArgProPheSerValLeuArg 355
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Db        121 CATGAACAAGACCGGCCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTTCTTCGA 180

Qy        356 AlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGly 375

Db        181 GCTAATGATGTGCTCTGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACCTATGGC 240

Qy        376 SerSerThrGlyProValTyrIleSerAspSerValThrLeuValAsnValAlaThrGly 395

Db        241 TCTTCGACTGGCCCAGTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGC 300

Qy        396 AlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeu 415

Db        301 GCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTC 360

Qy        416 ProThrValGluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSer 435

Db        361 TCTACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCT 420

Qy        436 PheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSer 455

Db        421 TTCTGGGAGGCAGGCACAACTAAGGCCGGGTACCCTTATAATTACAACACCACTGCTAGC 480

Qy        456 AspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThr 475

Db        481 GACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTTGCTATTTCTACTTACACTACT 540

Qy        476 ArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAla 495

Db        541 AGCCTGGGCGCTGGCCCCGTCTCCATTTCTGCGGTTGCCGTCTTAGCCCCCCACTCTGCG 600

Qy        496 LeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPhe 515

Db        601 CTAGCATTGCTTGAGGATACTTTGGACTACCCTGCCTGCGCCCATACTTTTGATGATTTC 660

Qy        516 CysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGlu 535

Db        661 TGCCCAGAGTGCCGCCCCCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAG 720

Qy        536 LeuGlnArgLeuLysValLysVal 543

Db        721 CTTCAGCGCCTTAAGATGAAGGTG 744

RESULT 66
AY714268
LOCUS       AY714268                720 bp    RNA     linear   VRL 15-SEP-2004
DEFINITION  Hepatitis E virus isolate hKOR-HSY capsid protein gene, partial
            cds.
ACCESSION   AY714268
VERSION     AY714268.1  GI:51980114
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Identification of human Hepatitis E virus (HEV) and prevalence of
            anti-HEV antibodies in human populations in Korea
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2004) Infectious Diseases, College of Veterinary
            Medicine and School of Agricultural Biotechnology, Seoul National
            University, Shinlim-Dong, San56-1, Seoul, Kwanak-Gu 151-742, South
            Korea
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:12461"
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     CDS             <1. .>720
                     /note="ORF2; structural protein"
                     /codon_start=1
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                     /protein_id="AAU20759.1"
                     /db_xref="GI:51980115"
                     /translation="NPLLPLQDGTNTHIMATEASNYAQYRVVRATIRYRPLVPNAVGG
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Alignment Scores:
Pred. No.:                  54              Length:          720
Score:                      229.00          Matches:         229
Percent Similarity:         95.42%          Conservative:    0
Best Local Similarity:      95.42%          Mismatches:      11
Query Match:                41.71%          Indels:          0
DB:                         1               Gaps:            0

US-09-769-066-16 (1-549) x AY714268 (1-720)

Qy         50 AsnProProLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSer 69

Db          1 AACCCTCTCTTGCCTCTTCAGGATGGCACCAACACTCATATTATGGCTACTGAAGCATCC 60

Qy         70 AsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsn 89

Db         61 AATTATGCCCAGTATCGGGTTGTTCGAGCTACGATCCGTTACCGCCCGCTAGTGCCAAAT 120

Qy         90 AlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThr 109

Db        121 GCTGTTGGTGGTTATGCTATTTCTATCTCTTTTTGGCCTCAAACCACAACTACCCCCACC 180

Qy        110 SerValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIle 129

Db        181 TCTGTTGACATGAATTCTATTACTTCCACTGATGTTAGGACTTTGGTCCAGCCCGGTATT 240

Qy        130 AlaSerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSer 149

Db        241 GCCTCCGAGCTAGTCATCCCTAGCGAGCGCCTGCATTACCGTAATCAAGGCTGGCGCTCT 300

Qy        150 ValGluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIle 169

Db        301 GTTGAGACCACGGGTGTCGCTGAGGAGGAGGCTACATCTGGTCTGGTAATGCTTTGCATC 360

Qy        170 HisGlySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeu 189

Db        361 CATGGCTCTCCTGTTAATCCTTATACTAACACACCTTACACTGGTGCACTAGGGCTTCTT 420

Qy        190 AspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgVal 209

Db        421 GATTTCGCATTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACCAATACCCGTGTC 480

Qy        210 SerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGlu 229

Db        481 TCCCGGTATACCAGCACAGCTCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAA 540

Qy        230 LeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGly 249

Db        541 CTTACTACCACAGCAGCCACACGCTTTATGAAAGATCTGTATTTTACTGGCACTAATGGC 600

Qy        250 ValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeu 269

Db        601 GTTGGTGAGGTGGGCCGTGGTATTGCCCTGACACTGTTTAATCTCGCTGATACGCTTCTC 660

Qy        270 GlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgPro 289

Db        661 GGTGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCT 720

RESULT 67
AY714271
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LOCUS       AY714271               720 bp    RNA     linear   VRL 15-SEP-2004
DEFINITION  Hepatitis E virus isolate hKOR-NAB capsid protein gene, partial
            cds.
ACCESSION   AY714271
VERSION     AY714271.1  GI:51980120
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Identification of human Hepatitis E virus (HEV) and prevalence of
            anti-HEV antibodies in human populations in Korea
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Ahn,J.M. and Yoo,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2004) Infectious Diseases, College of Veterinary
            Medicine and School of Agricultural Biotechnology, Seoul National
            University, Shinlim-Dong, San56-1, Seoul, Kwanak-Gu 151-742, South
            Korea
FEATURES             Location/Qualifiers
     source          1. .720
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="hKOR-NAB"
                     /db_xref="taxon:12461"
                     /country="South Korea"
     CDS             <1. .>720
                     /note="ORF2; structural protein"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAU20762.1"
                     /db_xref="GI:51980121"
                     /translation="NPLLPLQDGTNTHIMATEASNYAQYRVVRATIRYRPLVPNAVGG
                     YAISISFWPQTTTTPTSVDMNSITSTDVRTLVQPGIASELVIPSERLHYRNQGWRSVE
                     TTGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRV
                     SRYTSTARHWLRRGADGTAELTTTAATRFMKDLYFTGTNGVGEVGRGIALTLFNLADT
                     LLGGLPTELISAAGGQLFYSRP"

Alignment Scores:
Pred. No.:              54.8          Length:         720
Score:                  228.00        Matches:        228
Percent Similarity:     95.00%        Conservative:   0
Best Local Similarity:  95.00%        Mismatches:     12
Query Match:            41.53%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AY714271 (1-720)

Qy         50 AsnProProLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSer 69
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AACCCTCTCTTGCCTCTTCAGGATGGCACCAACACTCATATTATGGCTACTGAAGCATCC 60

Qy         70 AsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsn 89
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db         61 AATTATGCCCAGTATCGGGTTGTTCGAGCTACGATCCGTTACCGCCCGCTAGTGCCAAAT 120

Qy         90 AlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThr 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTGTTGGTGGTTATGCTATTTCTATCTCTTTTTGGCCTCAAACCACAACTACCCCCACC 180

Qy        110 SerValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIle 129
              |||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        181 TCTGTTGACATGAATTCTATTACTTCCACTGATGTTAGGACTTTGGTCCAGCCCGGTATT 240

Qy        130 AlaSerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSer 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCTCCGAGCTAGTCATCCCTAGCGAGCGCCTGCATTACCGTAATCAAGGCTGGCGCTCT 300

Qy        150 ValGluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIle 169
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTTGAGACCACGGGTGTCGCTGAGGAGGAGGCTACATCTGGTCTGGTAATGCTTTGCATC 360

Qy        170 HisGlySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeu 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CATGGCTCTCCTGTTAATTCTTATACTAACACACCTTACACTGGTGCACTAGGGCTTCTT 420

Qy        190 AspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgVal 209
              ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        421 GATTTCGCATTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACCAATACCCGTGTC 480

Qy        210 SerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGlu 229
              |||||||||  ||||||||||||||||  ||||||||||||||||||||||||||||||
Db        481 TCCCGGTATACCAGCACAGCTCGCCACTGGCTGCGCCGCGGTGCTGATGGGACCGCTGAA 540

Qy        230 LeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGly 249
              ||||||||||||||||||||||||||||||||||||||||  |||||||||  ||||||
Db        541 CTTACTACCACAGCAGCCACACGCTTTATGAAAGATCTGTATTTTACTGGCACTAATGGC 600

Qy        250 ValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeu 269
              ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        601 GTTGGTGAGGTGGGCCGTGGTATTGCTCTGACACTGTTTAATCTCGCTGATACGCTTCTC 660

Qy        270 GlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgPro 289
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        661 GGTGGTTTACCGACAGAATTGATTTCGGCGGCTGGGGGTCAACTGTTTTACTCCCGCCCT 720

RESULT 68
AF020603
LOCUS       AF020603               680 bp    RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus TK104/91/Nepal capsid protein gene, partial cds.
ACCESSION   AF020603
VERSION     AF020603.1  GI:2731803
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 680)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 680)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th & Dahlia St, Washington, DC 20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .680
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TK104/91/Nepal"
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     CDS             <1. .>680
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                     /protein_id="AAB93554.1"
                     /db_xref="GI:2731804"
                     /translation="YAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMN
                     SITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGS
                     PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAEL
                     TTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSR
                     PVVSANGEP"

Alignment Scores:
Pred. No.:              62.1          Length:         680
Score:                  219.00        Matches:        219
Percent Similarity:     96.90%        Conservative:   0
Best Local Similarity:  96.90%        Mismatches:     7
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Query Match:            39.89%      Indels:        0
DB:                     1           Gaps:          0

US-09-769-066-16 (1-549) x AF020603 (1-680)

Qy         71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TATGCCCAGTACCGGGTTGCCCGTGCCACGATCCGTTACCGCCCGTTGGTTCCCAACGCT 60

Qy         91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTCGGCGGTTACGCCATCTCCATCTCATTCTGGCCACAGACCACCACCACCCCGACGTCC 120

Qy        111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTTGATATGAATTCAATAACCTCGACGGATGTTCGTATCTTAGTCCAGCCCGGCATAGCC 180

Qy        131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCTGAGCTTGTGATCCCAAGCGAGCGCCTACACTACCGTAACCAAGGTTGGCGCTCCGTC 240

Qy        151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
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Db        241 GAGACCTCCGGGGTGGCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACAT 300

Qy        171 GlySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCTCACCCGTAAATTCCTATACTAATACACCTTATACCGGTGCCCTCGGGCTGCTGGAC 360

Qy        191 PheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSer 210
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Db        361 TTTGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCC 420

Qy        211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTC 480

Qy        231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyVal 250
              ||||||||||||||||||||||||||||||||||||  ||||||     |||||||||
Db        481 ACCACCACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTT 540

Qy        251 GlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGly 270
              ||||||   ||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        541 GGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGC 600

Qy        271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProVal 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTT 660

Qy        291 ValSerAlaAsnGlyGlu 296
              |||||||||||||||||
Db        661 GTCTCAGCCAATGGCGAG 678

RESULT 69
AF020606
LOCUS       AF020606                680 bp    RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus TK4/95/Nepal capsid protein gene, partial cds.
ACCESSION   AF020606
VERSION     AF020606.1  GI:2731809
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 680)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 680)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th & Dahlia St, Washington, DC 20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .680
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TK4/95/Nepal"
                     /db_xref="taxon:12461"
     CDS             <1. .>680
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                     /codon_start=1
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                     /protein_id="AAB93557.1"
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                     TTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSR
                     PVVSANGEP"

Alignment Scores:
Pred. No.:              62.1        Length:        680
Score:                  219.00      Matches:       219
Percent Similarity:     96.90%      Conservative:  0
Best Local Similarity:  96.90%      Mismatches:    7
Query Match:            39.89%      Indels:        0
DB:                     1           Gaps:          0

US-09-769-066-16 (1-549) x AF020606 (1-680)

Qy         71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
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Db          1 TATGCCCAGTACCGGGTTGCCCGTGCCACGATCCGTTACCGCCCGTTGGTTCCCAACGCT 60

Qy         91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTCGGCGGTTACGCCATCTCCATCTCATTCTGGCCACAGACCACCACCACCCCGACGTCC 120

Qy        111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTTGATATGAATTCAATAACCTCGACGGATGTTCGTATTCTAGTCCAGCCCGGCATAGCC 180

Qy        131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCTGAGCTTGTGATCCCAAGCGAGCGCCTACACTACCGTAACCAAGGTTGGCGCTCCGTC 240

Qy        151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGACCTCCGGGGTGGCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACAT 300

Qy        171 GlySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
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Db        301 GGCTCACCCGTAAATTCCTATACTAATACACCTTATACCGGTGCCCTCGGGCTGCTGGAC 360

Qy        191 PheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSer 210
              ||||||||||||||||||||||||||||||||||||      ||||||||||||||||||||
Db        361 TTTGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCC 420

Qy        211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
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Db        421 CGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTC 480

Qy        231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyVal 250
              ||||||||||||||||||||||||||||||||||||  ||||||     |||||||||
Db        481 ACCACCACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTT 540

Qy        251 GlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGly 270
              ||||||   ||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        541 GGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGC 600

Qy        271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProVal 290
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Db        601 GGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTT 660

Qy        291 ValSerAlaAsnGlyGlu 296
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Db        661 GTCTCAGCCAATGGCGAG 678

RESULT 70
AF020607
LOCUS       AF020607                680 bp    RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus Nep4/94/Nepal capsid protein gene, partial cds.
ACCESSION   AF020607
VERSION     AF020607.1  GI:2731811
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 680)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 680)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th & Dahlia St, Washington, DC 20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .680
                     /organism="Hepatitis E virus"
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                     /strain="Nep4/94/Nepal"
                     /db_xref="taxon:12461"
     CDS             <1. .>680
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                     /product="capsid protein"
                     /protein_id="AAB93558.1"
                     /db_xref="GI:2731812"
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                     TTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSR
                     PVVSANGEP"

Alignment Scores:
Pred. No.:              62.1          Length:         680
Score:                  219.00        Matches:        219
Percent Similarity:     96.90%        Conservative:   0
Best Local Similarity:  96.90%        Mismatches:     7
Query Match:            39.89%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF020607 (1-680)

Qy         71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
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Db          1 TATGCCCAGTACCGGGTTGCCCGTGCCACGATCCGTTACCGCCCGTTGGTTCCCAACGCT 60

Qy         91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTCGGCGGTTACGCCATTTCCATATCATTCTGGCCACAGACCACCACCACCCCGACGTCC 120

Qy        111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTTGATATGAATTCAATAACCTCGACGGATGTTCGTATTCTAGTCCAGCCCGGCATAGCC 180

Qy        131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
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Db        181 TCTGAGCTTGTGATCCCAAGCGAGCGCCTACACTACCGTAACCAAGGTTGGCGCTCCGTC 240

Qy        151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
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Db        241 GAGACCTCCGGGGTGGCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACAT 300

Qy        171 GlySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCTCACCCGTAAATTCCTATACTAATACACCTTATACCGGTGCCCTCGGGCTGCTGGAC 360

Qy        191 PheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSer 210
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Db        361 TTTGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCC 420

Qy        211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
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Db        421 CGTTACTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTC 480

Qy        231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyVal 250
              ||||||||||||||||||||||||||||||||||||    ||||||      |||||||||
Db        481 ACCACCACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTT 540

Qy        251 GlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGly 270
              ||||||    ||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        541 GGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGC 600

Qy        271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProVal 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTT 660

Qy        291 ValSerAlaAsnGlyGlu 296
                ||||||||||||||||||
Db        661 GTCTCAGCCAATGGCGAG 678

RESULT 71
AF020608
LOCUS       AF020608                680 bp    RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus TK78/87/Nepal capsid protein gene, partial cds.
ACCESSION   AF020608
VERSION     AF020608.1  GI:2731813
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 680)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 680)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th & Dahlia St, Washington, DC 20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .680
                     /organism="Hepatitis E virus"
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TTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSR
PVVSANGEP"

Alignment Scores:

Pred. No.:	62.1	Length:	680
Score:	219.00	Matches:	219
Percent Similarity:	96.90%	Conservative:	0
Best Local Similarity:	96.90%	Mismatches:	7
Query Match:	39.89%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AF020608 (1-680)

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Qy         71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
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Db          1 TATGCCCAGTACCGGGTTGCCCGTGCCACAATCCGTTACCGCCCGCTGGTCCCAAACGCT 60

Qy         91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTCGGCGGTTACGCCATCTCCATCTCATTCTGGCCACAGACCACCACCACCCCGACGTCC 120

Qy        111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
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Db        121 GTTGATATGAATTCAATAACCTCGACGGATGTTCGTATCTTAGTCCAGCCTGGCATAGCC 180

Qy        131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
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Db        181 TCTGAGCTTGTGATCCCAAGCGAGCGCCTACACTATCGTAACCAGGGTTGGCGCTCCGTC 240

Qy        151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
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Db        241 GAGACCTCCGGGGTGGCTGAGGAGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATACAT 300

Qy        171 GlySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
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Db        301 GGCTCACCCGTAAATTCCTATACTAATACACCCTACACCGGTGCCCTCGGGCTGCTGGAC 360

Qy        191 PheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSer 210
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Db        361 TTTGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCC 420

Qy        211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTC 480

Qy        231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyVal 250
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Db        481 ACCACCACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTC 540

Qy        251 GlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGly 270
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Db        541 GGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGC 600

Qy        271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProVal 290
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Db        601 GGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTT 660

Qy        291 ValSerAlaAsnGlyGlu 296
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Db        661 GTCTCAGCCAATGGCGAG 678
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RESULT 72
AF020604
LOCUS AF020604 680 bp RNA linear VRL 04-SEP-2001
DEFINITION Hepatitis E virus TK15/92/Nepal capsid protein gene, partial cds.
ACCESSION AF020604
VERSION AF020604.1 GI:2731805
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 680)
AUTHORS Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S., Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
TITLE Hepatitis E virus in Nepal: similarities with the Burmese and Indian variants
JOURNAL Virus Res. 52 (1), 87-96 (1997)
MEDLINE 98115237
PUBMED 9453147
REFERENCE 2 (bases 1 to 680)
AUTHORS Gouvea,V.
TITLE Direct Submission
JOURNAL Submitted (25-AUG-1997) Virus Diseases, Walter Reed Army Institute of Research, 14th & Dahlia St, Washington, DC 20307-5100, USA
FEATURES Location/Qualifiers
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/organism="Hepatitis E virus"
/mol_type="genomic RNA"
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/db_xref="taxon:12461"
CDS <1. .>680
/note="ORF2"
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/product="capsid protein"
/protein_id="AAB93555.1"
/db_xref="GI:2731806"
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PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAEL
TTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSR
PVVSANGEP"

Alignment Scores:

Pred. No.:	63	Length:	680
Score:	218.00	Matches:	218
Percent Similarity:	96.46%	Conservative:	0
Best Local Similarity:	96.46%	Mismatches:	8
Query Match:	39.71%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AF020604 (1-680)

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Qy         71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
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Db          1 TATGCCCAGTACCGGGTTGCCCGTGCCGCGATCCGTTACCGCCCGTTGGTTCCCAACGCT 60

Qy         91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTCGGCGGTTACGCCATCTCCATCTCATTCTGGCCACAGACCACCACCACCCCGACGTCC 120

Qy        111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTTGATATGAATTCAATAACCTCGACGGATGTTCGTATTCTAGTCCAGCCCGGCATAGCC 180

Qy        131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
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Db        181 TCTGAGCTTGTGATCCCAAGCGAGCGCCTACACTACCGTAACCAAGGTTGGCGCTCCGTC 240

Qy        151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
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Db        241 GAGACCTCCGGGGTGGCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACAT 300

Qy        171 GlySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
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Db        301 GGCTCACCCGTAAATTCCTATACTAATACACCTTATACCGGTGCCCTCGGGCTGCTGGAC 360

Qy        191 PheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSer 210
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Db        361 TTTGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCC 420

Qy        211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
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Db        421 CGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTC 480

Qy        231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyVal 250
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Db        481 ACCACCACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTT 540

Qy        251 GlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGly 270
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Db        541 GGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGC 600

Qy        271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProVal 290
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Db        601 GGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTT 660

Qy        291 ValSerAlaAsnGlyGlu 296
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Db        661 GTCTCAGCCAATGGCGAG 678

RESULT 73
AF020605
LOCUS       AF020605                680 bp    RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus TK5/95/Nepal capsid protein gene, partial cds.
ACCESSION   AF020605
VERSION     AF020605.1  GI:2731807
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 680)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 680)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th & Dahlia St, Washington, DC 20307-5100, USA
FEATURES             Location/Qualifiers
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                     /mol_type="genomic RNA"
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                     /db_xref="taxon:12461"
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                     /codon_start=1
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                     PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAEL
                     TTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSR
                     PVVSANGEP"

Alignment Scores:
Pred. No.:              63              Length:         680
Score:                  218.00          Matches:        218
Percent Similarity:     96.46%          Conservative:   0
Best Local Similarity:  96.46%          Mismatches:     8
Query Match:            39.71%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF020605 (1-680)

Qy         71 TyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAla 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TATGCCCAGTACCGGGTTGCCCGTGCCACGATCCGTTACCGCCCGTTGGTTCCCAACGCT 60

Qy         91 ValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSer 110
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Db         61 GTCGGCGGTTACGCCATCTCCATCTCATTCTGGCCACAGACCACCACCACCCCGACGTCC 120

Qy        111 ValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIleAla 130
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        121 GTTGATATGAATTCAATAACCTCGATGGATGTTCGTATTCTAGTCCAGCCCGGCATAGCC 180

Qy        131 SerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerVal 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCTGAGCTTGTGATCCCAAGCGAGCGCCTACACTACCGTAACCAAGGTTGGCGCTCCGTC 240

Qy        151 GluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHis 170
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Db        241 GAGACCTCCGGGGTGGCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACAT 300

Qy        171 GlySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAsp 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCTCACCCGTAAATTCCTATACTAATACACCTTATACCGGTGCCCTCGGGCTGCTGGAC 360

Qy        191 PheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSer 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCC 420

Qy        211 ArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeu 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTC 480

Qy        231 ThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyVal 250
              ||||||||||||||||||||||||||||||||||   ||||||      |||||||||
Db        481 ACCACCACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTT 540

Qy        251 GlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGly 270
              ||||||   ||||||||||||||||||||||||   ||||||||||||||||||||||
Db        541 GGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGC 600

Qy        271 GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProVal 290
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Db        601 GGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTT 660

Qy        291 ValSerAlaAsnGlyGlu 296
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Db        661 GTCTCAGCCAATGGCGAG 678

RESULT 74
AX181828
LOCUS       AX181828                678 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 110 from Patent WO0146696.
ACCESSION   AX181828
VERSION     AX181828.1  GI:15133148
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 110 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .678
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
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                     /note="us2-667"

Alignment Scores:
Pred. No.:              71.7            Length:         678
Score:                  209.00          Matches:        209
Percent Similarity:     92.89%          Conservative:   0
Best Local Similarity:  92.89%          Mismatches:     16
Query Match:            38.07%          Indels:         0
DB:                     1               Gaps:           0
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US-09-769-066-16 (1-549) x AX181828 (1-678)

Qy        268 LeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSer 287
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Db          3 CTTCTTGGTGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGCCAACTGTTTTACTCC 62

Qy        288 ArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsn 307
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Db         63 CGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATATACATCTGTTGAGAAT 122

Qy        308 AlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeuGlyAspSerArgVal 327
              |||||||||||||||||      ||||||||||||||||||||||||||||||||||||||
Db        123 GCGCAGCAAGACAAGGGCATCACCATTCCACATGATATAGACCTGGGTGACTCCCGTGTG 182

Qy        328 ValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaPro 347
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Db        183 GTTATCCAGGATTATGATAACCAGCAYGAGCAAGACCGACCTACTCCGTCACCTGCCCCC 242

Qy        348 SerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAla 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 TCTCGCCCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTTTCCCTCACTGCCGCT 302

Qy        368 GluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrIleSerAspSerVal 387
              ||||||||||||    ||||||||||||||||||    |||   |||   ||||||   |||
Db        303 GAGTATGACCAGACTACGTATGGGTCGTCCACCAACCCTATGTATGTCTCTGACACAGTT 362

Qy        388 ThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLys 407
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Db        363 ACGCTTGTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCCCTTGATTGGTCTAAA 422

Qy        408 ValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheVal 427
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Db        423 GTTACTCTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCTAAGACATTTTATGTT 482

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
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Db        483 CTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACTAAGGCCGGCTACCCT 542

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArg 467
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Db        543 TACAATTATAATACTACCGCTAGTGACCAAATTTTGATTGAGAATGCGGCCGGCCACCGT 602

Qy        468 ValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAla 487
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Db        603 GTCGCTATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACCTCGATCTCTGCGGTC 662

Qy        488 AlaValLeuAlaPro 492
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Db        663 GGTGTACTAGCTCCA 677

RESULT 75
BD077228
LOCUS       BD077228                678 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077228
VERSION     BD077228.1  GI:22622831
KEYWORDS    JP 2001520384-A/107.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 678)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 107 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/107
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
                 DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   us2-667
            FH   Key             Location/Qualifiers
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            FT                   /organism='Hepatitis virus (hepatitis E  FT
                              virus)'.
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:                71.7          Length:          678
Score:                    209.00        Matches:         209
Percent Similarity:       92.89%        Conservative:    0
Best Local Similarity:    92.89%        Mismatches:      16
Query Match:              38.07%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x BD077228 (1-678)

Qy        268 LeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSer 287
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Db          3 CTTCTTGGTGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGCCAACTGTTTTACTCC 62

Qy        288 ArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsn 307
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Db         63 CGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATATACATCTGTTGAGAAT 122

Qy        308 AlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeuGlyAspSerArgVal 327
              |||||||||||||||||      ||||||||||||||||||||||||||||||||||||||
Db        123 GCGCAGCAAGACAAGGGCATCACCATTCCACATGATATAGACCTGGGTGACTCCCGTGTG 182

Qy        328 ValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaPro 347
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GTTATCCAGGATTATGATAACCAGCAYGAGCAAGACCGACCTACTCCGTCACCTGCCCCC 242

Qy        348 SerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAla 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 TCTCGCCCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTTTCCCTCACTGCCGCT 302

Qy        368 GluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrIleSerAspSerVal 387
              ||||||||||||    ||||||||||||||||||    |||   |||   ||||||   |||
Db        303 GAGTATGACCAGACTACGTATGGGTCGTCCACCAACCCTATGTATGTCTCTGACACAGTT 362

Qy        388 ThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLys 407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 ACGCTTGTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCCCTTGATTGGTCTAAA 422

Qy        408 ValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheVal 427
              ||||||||||||||||||||||    |||       ||||||||||||||||||    |||
Db        423 GTTACTCTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCTAAGACATTTTATGTT 482

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 CTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACTAAGGCCGGCTACCCT 542

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 TACAATTATAATACTACCGCTAGTGACCAAATTTTGATTGAGAATGCGGCCGGCCACCGT 602

Qy        468 ValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAla 487
              ||||||||||||||||||||||    ||||||||||||||    |||||||||
Db        603 GTCGCTATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACCTCGATCTCTGCGGTC 662

Qy        488 AlaValLeuAlaPro 492
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Db        663 GGTGTACTAGCTCCA 677
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RESULT 76
AF170450
LOCUS       AF170450                617 bp    RNA     linear   VRL 09-AUG-1999
DEFINITION  Hepatitis E virus structural protein 2 gene, partial cds.
ACCESSION   AF170450
VERSION     AF170450.1  GI:5713199
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 617)
  AUTHORS   Nguyen,T.N., Nguyen,T.V., Hoang,T.N., Meng,J.H., Purdy,M.A.,
            Khudyakov,Y. and Fields,H.W.
  TITLE     Partial sequence and phylogenetic analysis HEV isolated from Viet
            Nam
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 617)
  AUTHORS   Nguyen,T.N., Nguyen,T.V., Hoang,T.N., Meng,J.H., Purdy,M.A.,
            Khudyakov,Y. and Fields,H.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-1999) Hepatitis Laboratory, National Institute of
            Hygiene and Epidemiology, 1 Yersin, Hanoi 10000, Viet Nam
FEATURES             Location/Qualifiers
     source          1. .617
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:12461"
                     /map="ORF2"
                     /country="Viet Nam"
     CDS             <1. .>617
                     /note="ORF2"
                     /codon_start=1
                     /product="structural protein 2"
                     /protein_id="AAD47842.1"
                     /db_xref="GI:5713200"
                     /translation="GLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTN
                     TRVSRYSSTARHRLRRSADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNL
                     ADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDL
                     GESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAA"

Alignment Scores:
Pred. No.:              87              Length:         617
Score:                  195.00          Matches:        195
Percent Similarity:     95.12%          Conservative:   0
Best Local Similarity:  95.12%          Mismatches:     10
Query Match:            35.52%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF170450 (1-617)

Qy        163 GlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyr 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAATACACCCTAT 60

Qy        183 ThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThr 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGTAACCTTACCCCT 120

Qy        203 CysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArg 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTAACACTAATACGCGGGTCTCCCGCTATTCCAGCACTGCTCGCCACCGCCTTCGCCGC 180

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGTGCGGACGGGACTGCTGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTC 240

Qy        243 HisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeu 262
              ||||||      ||||||||||||||||   ||||||||||||||||||||||||
Db        241 TATTTTACTAGTACTAATGGTGTCGGTGAAATCGGCCGCGGGATAGCCCTCACCCTGTTC 300

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAATTGATTTCGTCGGCTGGCGGC 360

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGCTGTTCTACTCTCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGCTGTAT 420

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        421 ACATCTGTAGAGAATGCTCAGCAAGATAAGGGTATTGCAATCCCGCATGACATTGACCTC 480

Qy        323 GlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGGGAATCTCGTGTGGTTATCCAGGATTATGATAACCAACATGAACAAGACCGGCCGACA 540

Qy        343 ProSerProAlaProSerArgProProSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCTTCTCCAGCCCCATCGCGCCCTTTTTCTGTCCTTCGGGCTAATGATGTGCTCTGGCTC 600

Qy        363 SerLeuThrAlaAla 367
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Db        601 TCTCTCACCGCCGCC 615

RESULT 77
HEU62654
LOCUS       HEU62654                506 bp    mRNA    linear   VRL 26-JAN-1999
DEFINITION  Hepatitis E virus structural protein 2 mRNA, partial cds.
ACCESSION   U62654
VERSION     U62654.1  GI:4097490
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 506)
  AUTHORS   Van Cuyck-Gandre,H., Zhang,H., Clements,N., Caudill,J., Cohen,S.,
            Coursaget,P., Buisson,Y. and Longer,C.
  TITLE     Partial sequences of HEV from Algerian and Chad isolates
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 506)
  AUTHORS   Van Cuyck-Gandre,H., Zhang,H., Clements,N., Caudill,J., Cohen,S.,
            Coursaget,P., Buisson,Y. and Longer,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-1996) Virus Diseases, WRAIR, Bld. 40, Washington,
            D.C. 20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .506
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Chad T5"
                     /db_xref="taxon:12461"
                     /note="isolated from the stools of infected patients from
                     Chad, 1981 outbreak"
     CDS             <1. .>506
                     /note="ORF2; capsid protein; polyprotein"
                     /codon_start=1
                     /product="structural protein 2"
                     /protein_id="AAD09495.1"
                     /db_xref="GI:4097491"
                     /translation="NTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNG
                     VGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVEN
                     AQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLT
                     AAEYDQST"

Alignment Scores:
Pred. No.:              139             Length:         506
Score:                  161.00          Matches:        161
Percent Similarity:     95.83%          Conservative:   0
Best Local Similarity:  95.83%          Mismatches:     7
Query Match:            29.33%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x HEU62654 (1-506)
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Qy        206 AsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAsp 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATACGCGGGTCTCGCGTTACTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGAC 60

Qy        226 GlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThr 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db         61 GGGACTGCCGAGCTCACCACCACGGCTGCTACCCGTTTTATGAAGGACCTCTATTTCACT 120

Qy        246 GlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAla 265
              ||||||||||||||||  ||||||||||||||||||||||||  |||||||||
Db        121 AGTACCAATGGTGTCGGTGAGATCGGCCGCGGGATAGCTCTCACCCTGTTCAACCTTGCT 180

Qy        266 AspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPhe 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACACTCTGCTTGGTGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTC 240

Qy        286 TyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerVal 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAGCTGTATACATCTGTA 300

Qy        306 GluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeuGlyAspSer 325
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||   |||
Db        301 GAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGGGAATCT 360

Qy        326 ArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerPro 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGTGGTTATTCAGGACTATGATAACCAACATGAACAGGACCGGCCGACGCCTTCGCCA 420

Qy        346 AlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThr 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCTCCATCGCGCCCTTTTTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTCTCTCTCACC 480

Qy        366 AlaAlaGluTyrAspGlnSerThr 373
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Db        481 GCTGCCGAGTATGACCAGTCCACC 504

RESULT 78
AF332620
LOCUS       AF332620                476 bp ss-RNA     linear   VRL 02-FEB-2002
DEFINITION  Swine hepatitis E virus NLSW15 structural protein gene, partial
            cds.
ACCESSION   AF332620
VERSION     AF332620.1  GI:18478362
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine in the Netherlands are closely
            related to human hepatitis E virus sequences
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-DEC-2000) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
     source          1. .476
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="NLSW15"
                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAL73138.1"
                     /db_xref="GI:18478363"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPT
                     ELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGDSRVVIQ"

Alignment Scores:
Pred. No.:              157          Length:          476
Score:                  152.00       Matches:         152
Percent Similarity:     96.20%       Conservative:    0
Best Local Similarity:  96.20%       Mismatches:      6
Query Match:            27.69%       Indels:          0
DB:                     1            Gaps:            0

US-09-769-066-16 (1-549) x AF332620 (1-476)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTTAACTCCTACACCAATACACCCTATACCGGGGCATTGGGGCTCCTCGACTTTGCA 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db         63 CTCGAGCTTGAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGCTAC 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACTAGCACAGCCCGGCACCGTCTGCGTCGTGGTGCCGATGGGACGGCTGAGCTTACGACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        183 ACTGCAGCCACACGTTTTATGAAGGACTTGCATTTCACCGGGACAAACGGCGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db        243 GTGGGCCGTGGTATAGCCCTAACGTTGTTTAATCTTGCTGACACACTTCTCGGCGGGCTA 302

Qy        273 ProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CCGACAGAATTRATTTCGTCGGCTGGAGGTCAGTTGTTTTACTCCCGCCCGGTCGTCTCA 362

Qy        293 AlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLys 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GCCAATGGCGAGCCGACTGTTAAGCTATACACCTCTGTCGAGAATGCACAGCAGGACAAG 422

Qy        313 GlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGln 330
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GGCATTGCTATACCGCATGATATAGACTTAGGGGACTCCCGTGTGGTCATACAA 476

RESULT 79
AF336290
LOCUS       AF336290                476 bp ss-RNA     linear   VRL 05-MAR-2002
DEFINITION  Swine hepatitis E virus isolate NLSW20 structural protein gene,
            partial cds.
ACCESSION   AF336290
VERSION     AF336290.1  GI:18478608
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I.,
            Vivo,A., Kooreman,M. and de Roda Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine related to sequences in
            humans, The Netherlands
  JOURNAL   Emerging Infect. Dis. 7 (6), 970-976 (2001)
  MEDLINE   21614760
   PUBMED   11747723
REFERENCE   2  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
     source          1. .476
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                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW20"
                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /note="ORF2"
                     /codon_start=3
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                     /protein_id="AAL73215.1"
                     /db_xref="GI:18478609"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPT
                     ELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGDSRVVIQ"

Alignment Scores:
Pred. No.:                157             Length:         476
Score:                    152.00          Matches:        152
Percent Similarity:       96.20%          Conservative:   0
Best Local Similarity:    96.20%          Mismatches:     6
Query Match:              27.69%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF336290 (1-476)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTTAATTCTTACACCAACACCCCCTACACTGGGGCGCTTGGGCTTCTTGATTTTGCT 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         63 TTAGAGCTTGAGTTTAGGAACTTGACACCCGGGAACACCAACACCCGTGTTTCACGGTAC 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACAAGTACAGCCCGTCACCGGCTGCGCCGCGGTGCTGATGGCACCGCCGAACTCACCACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||
Db        183 ACAGCGGCCACGCGTTTTATGAAGGACCTGCACTTCACCGGTACGAATGGGGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        243 GTGGGTCGTGGTATCGCCCTTACACTCTTTAATCTTGCTGACACGCTTCTCGGTGGTTTG 302

Qy        273 ProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CCGACAGAATTRATTTCGTCGGCTGGAGGCCAGCTATTTTACTCCCGTCCGGTTGTCTCA 362

Qy        293 AlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLys 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GCCAATGGCGAGCCGACTGTTAAGTTATACACCTCCGTCGAGAATGCACAGCAGGATAAG 422

Qy        313 GlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGln 330
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GGCATTGCTATACCGCATGATATAGATTTGGGAGATTCCCGTGTGGTTATTCAG 476

RESULT 80
AF336292
LOCUS       AF336292                476 bp ss-RNA     linear   VRL 05-MAR-2002
DEFINITION  Swine hepatitis E virus isolate NLSW28 structural protein gene,
            partial cds.
ACCESSION   AF336292
VERSION     AF336292.1  GI:18478614
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I.,
            Vivo,A., Kooreman,M. and de Roda Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine related to sequences in
            humans, The Netherlands
  JOURNAL   Emerging Infect. Dis. 7 (6), 970-976 (2001)
  MEDLINE   21614760
   PUBMED   11747723
REFERENCE   2  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
     source          1. .476
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW28"
                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAL73217.1"
                     /db_xref="GI:18478615"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPT
                     ELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGDSRVVIQ"

Alignment Scores:
Pred. No.:                157             Length:         476
Score:                    152.00          Matches:        152
Percent Similarity:       96.20%          Conservative:   0
Best Local Similarity:    96.20%          Mismatches:     6
Query Match:              27.69%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF336292 (1-476)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTCAACTCTTACACTAACACACCCTATACCGGGGCATTAGGGCTCCTCGATTTTGCA 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         63 CTCGAGCTTGAATTTAGGAACTTGACCCCCGGGAACACAAACACCCGTGTGTCCCGTTAC 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACTAGCACAGCTCGACATCGTTTGCGTCGTGGCGCCGATGGGACAGCCGAGCTCACGACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||
Db        183 ACTGCAGCCACACGTTTCATGAAGGACTTGCATTTCACCGGGACAAACGGCGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        243 GTGGGCCGTGGTATAGCCCTAACGTTATTTAATCTTGCTGATACACTTCTCGGTGGGCTA 302

Qy        273 ProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CCGACAGAATTRATTTCGTCGGCTGGAGGTCAGTTGTTCTACTCCCGCCCGGTCGTCTCA 362

Qy        293 AlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLys 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GCCAATGGCGAGCCGACTGTTAAGTTATACACCTCTGTCGAGAATGCACAGCAGGACAAG 422

Qy        313 GlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGln 330
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GGCATTGCTATACCACACGATATAGACTTAGGGGACTCCCGTGTGGTTATACAA 476

RESULT 81
AF336293
LOCUS       AF336293                476 bp ss-RNA     linear   VRL 05-MAR-2002
DEFINITION  Swine hepatitis E virus isolate NLSW36 structural protein gene,
            partial cds.
ACCESSION   AF336293
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VERSION     AF336293.1  GI:18478617
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I.,
            Vivo,A., Kooreman,M. and de Roda Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine related to sequences in
            humans, The Netherlands
  JOURNAL   Emerging Infect. Dis. 7 (6), 970-976 (2001)
  MEDLINE   21614760
   PUBMED   11747723
REFERENCE   2  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
     source          1. .476
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW36"
                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAL73218.1"
                     /db_xref="GI:18478618"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPT
                     ELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGDSRVVIQ"

Alignment Scores:
Pred. No.:              157          Length:         476
Score:                  152.00       Matches:        152
Percent Similarity:     96.20%       Conservative:   0
Best Local Similarity:  96.20%       Mismatches:     6
Query Match:            27.69%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AF336293 (1-476)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTTAATTCTTATACCAATACCCCCTATACCGGGGCGCTTGGGCTCCTTGATTTTGCT 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         63 TTAGAACTTGAGTTCAGGAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACAAGTACAGCCCGTCATCGGCTGCGTCGCGGTGCTGATGGCACCGCCGAACTTACTACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 ACAGCAGCTACACGTTTCATGAAGGACCTGCACTTCACCGGCACGAATGGGGTCGGCGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GTGGGCCGTGGTATCGCTCTCACACTCTTTAATCTTGCTGATACGCTCCTCGGTGGGTTA 302

Qy        273 ProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CCGACAGAATTRATTTCGTCGGCTGGGGGACAGTTGTTCTACTCCCGCCCCGTCGTCTCA 362

Qy        293 AlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLys 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GCCAATGGCGAACCGACTGTTAAGTTGTATACATCTGTGGAGAATGCACAGCAAGATAAA 422

Qy        313 GlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGln 330
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GGGATTGCCATTCCACATGACATAGATCTGGGCGACTCTCGTGTTGTCATTCAG 476

RESULT 82
AF336294
LOCUS       AF336294                476 bp ss-RNA     linear   VRL 05-MAR-2002
DEFINITION  Swine hepatitis E virus isolate NLSW82 structural protein gene,
            partial cds.
ACCESSION   AF336294
VERSION     AF336294.1  GI:18478620
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I.,
            Vivo,A., Kooreman,M. and de Roda Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine related to sequences in
            humans, The Netherlands
  JOURNAL   Emerging Infect. Dis. 7 (6), 970-976 (2001)
  MEDLINE   21614760
   PUBMED   11747723
REFERENCE   2  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
     source          1. .476
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW82"
                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAL73219.1"
                     /db_xref="GI:18478621"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPT
                     ELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGDSRVVIQ"

Alignment Scores:
Pred. No.:              157          Length:         476
Score:                  152.00       Matches:        152
Percent Similarity:     96.20%       Conservative:   0
Best Local Similarity:  96.20%       Mismatches:     6
Query Match:            27.69%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AF336294 (1-476)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTCAATTCCTATACCAACACGCCCTATACTGGGGCATTGGGGCTCCTCGACTTTGCA 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         63 CTCGAGCTTGAATTTAGAAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGTTAC 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACTAGCACAGCCCGACATCGTTTACGTCGTGGCGCCGATGGGACAGCCGAGCTCACAACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 ACTGCAGCCACACGTTTTATGAAGGACTTGCACTTCACCGGGACAAATGGCGTTGGTGAG 242
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Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        243 GTAGGCCGTGGCATAGCTCTAACTCTATTTAATCTTGCTGATACACTTCTCGGTGGGTTG 302

Qy        273 ProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CCGACAGAATTGATTTCGTCGGCTGGAGGTCAACTGTTCTACTCCCGCCCGGTTGTCTCA 362

Qy        293 AlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLys 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GCCAATGGCGAGCCGACTGTTAAGTTATACACCTCTGTCGAGAATGCACAGCAGGACAAG 422

Qy        313 GlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGln 330
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GGCATTGCTATACCACACGATATAGACCTAGGGGATTCCCGTGTGGTTATACAA 476
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RESULT 83
AF336295
LOCUS AF336295 476 bp ss-RNA linear VRL 05-MAR-2002
DEFINITION Swine hepatitis E virus isolate NLSW85 structural protein gene, partial cds.
ACCESSION AF336295
VERSION AF336295.1 GI:18478622
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 476)
AUTHORS van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I., Vivo,A., Kooreman,M. and de Roda Husman,A.M.
TITLE Hepatitis E virus sequences in swine related to sequences in humans, The Netherlands
JOURNAL Emerging Infect. Dis. 7 (6), 970-976 (2001)
MEDLINE 21614760
PUBMED 11747723
REFERENCE 2 (bases 1 to 476)
AUTHORS van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda Husman,A.M.
TITLE Direct Submission
JOURNAL Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9, Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES Location/Qualifiers
source 1. .476
/organism="Swine hepatitis E virus"
/mol_type="genomic RNA"
/isolate="NLSW85"
/db_xref="taxon:63421"
CDS <1. .>476
/note="ORF2"
/codon_start=3
/product="structural protein"
/protein_id="AAL73220.1"
/db_xref="GI:18478623"
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RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPT
ELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGDSRVVIQ"

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Alignment Scores:
Pred. No.:              157           Length:        476
Score:                  152.00        Matches:       152
Percent Similarity:     96.20%        Conservative:  0
Best Local Similarity:  96.20%        Mismatches:    6
Query Match:            27.69%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AF336295 (1-476)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTTAATTCCTATACCAACACGCCCTATACCGGGGCACTGGGGCTTCTCGACTTTGCA 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db         63 CTCGAGCTTGAATTTAGAAATTTGACCCCTGGGAACACCAACACCCGTGTGTCCCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACCAGCACAGCCCGACACCGTTTGCGTCGCGGTGCTGATGGTACAGCCGAGCTTACGACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||    ||||||||||||||||
Db        183 ACTGCAGCCACACGTTTATGAAGGACTTGCATTTCACCGGGACAAATGGTGTTGGCGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        243 GTAGGCCGTGGAATCGCCCTAACGCTATTTAATCTTGCTGATACACTTCTCGGCGGGCTG 302

Qy        273 ProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CCGACAGAATTRATTTCGTCGGCTGGAGGTCAACTGTTCTACTCCCGCCCGGTTGTCTCA 362

Qy        293 AlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLys 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GCCAATGGCGAGCCGACTGTTAAGTTATACACCTCTGTCGAGAATGCACAGCAGGACAAG 422

Qy        313 GlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGln 330
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GGCATTGCCATACCACACGATATAGACTTAGGGGATTCTCGTGTGGTTATACAA 476
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RESULT 84
AF336296
LOCUS AF336296 476 bp ss-RNA linear VRL 05-MAR-2002
DEFINITION Swine hepatitis E virus isolate NLSW97 structural protein gene, partial cds.
ACCESSION AF336296
VERSION AF336296.1 GI:18478625
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 476)
AUTHORS van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I., Vivo,A., Kooreman,M. and de Roda Husman,A.M.
TITLE Hepatitis E virus sequences in swine related to sequences in humans, The Netherlands
JOURNAL Emerging Infect. Dis. 7 (6), 970-976 (2001)
MEDLINE 21614760
PUBMED 11747723
REFERENCE 2 (bases 1 to 476)
AUTHORS van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda Husman,A.M.
TITLE Direct Submission
JOURNAL Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9, Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES Location/Qualifiers
source 1. .476
/organism="Swine hepatitis E virus"
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/isolate="NLSW97"
/db_xref="taxon:63421"
CDS <1. .>476
/note="ORF2"
/codon_start=3
/product="structural protein"
/protein_id="AAL73221.1"
/db_xref="GI:18478626"
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ELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGDSRVVIQ"

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Alignment Scores:
Pred. No.:              157           Length:        476
Score:                  152.00        Matches:       152
Percent Similarity:     96.20%        Conservative:  0
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Best Local Similarity:  96.20%        Mismatches:    6
Query Match:            27.69%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AF336296 (1-476)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTTAATTCCTATACTAATACACCCTATACCGGGGCTTTGGGGCTCCTCGACTTTGCG 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAATTTAGAAATTTGACCCCTGGGAACACTAACACCCGTGTTTCCCGTTAC 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACTAGTACAGCCCGGCACCGTTTGCGTCGTGGTGCCGATGGGACAGCTGAGCTTACAACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db        183 ACCGCAGCCACACGTTTTATGAAGGACTTACATTTCACCGGGACAAATGGTGTTGGCGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        243 GTGGGCCGTGGTATAGCCCTAACGCTATTCAATCTTGCTGATACACTTCTCGGTGGCCTG 302

Qy        273 ProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CCGACAGAATTRATTTCGTCGGCTGGAGGTCAATTGTTTTACTCCCGCCCGGTTGTCTCA 362

Qy        293 AlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLys 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GCCAATGGCGAGCCGACTGTTAAGTTGTACACCTCTGTCGAGAATGCACAGCAGGACAAG 422

Qy        313 GlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGln 330
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GGCATTGCTATACCACACGATATAGATCTAGGGGATTCTCGTGTGGTTATACAA 476

RESULT 85
AF336297
LOCUS       AF336297                476 bp ss-RNA     linear   VRL 05-MAR-2002
DEFINITION  Swine hepatitis E virus isolate NLSW99 structural protein gene,
            partial cds.
ACCESSION   AF336297
VERSION     AF336297.1  GI:18478628
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I.,
            Vivo,A., Kooreman,M. and de Roda Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine related to sequences in
            humans, The Netherlands
  JOURNAL   Emerging Infect. Dis. 7 (6), 970-976 (2001)
  MEDLINE   21614760
   PUBMED   11747723
REFERENCE   2  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
     source          1. .476
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                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAL73222.1"
                     /db_xref="GI:18478629"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGMNGVGEVGRGIALTLFNLADTLLGGLPT
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Alignment Scores:
Pred. No.:              157           Length:        476
Score:                  152.00        Matches:       152
Percent Similarity:     96.20%        Conservative:  0
Best Local Similarity:  96.20%        Mismatches:    6
Query Match:            27.69%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AF336297 (1-476)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTTAATTCTTATACCAATACCCCCTACACCGGGGCACTTGGACTCCTTGACTTTGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTAGGAACCTGACACCCGGGAACACTAACACCCGTGTCTCCCGGTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACGAGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGCACCGCCGAGCTTACCACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db        183 ACGGCGGCCACTCGCTTCATGAAGGACCTGCACTTCACCGGTATGAATGGGGTCGGTGAA 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        243 GTGGGTCGAGGTATTGCTCTCACACTCTTTAATCTCGCTGATACGCTTCTCGGTGGTCTG 302

Qy        273 ProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        303 CCGACAGAATTRATTTCGTCGGCTGGAGGTCAACTGTTTTACTCCCGCCCGGTTGTCTCA 362

Qy        293 AlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLys 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GCCAATGGCGAGCCGACTGTTAAGTTATACACCTCTGTCGAGAATGCACAGCAAGACAAG 422

Qy        313 GlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGln 330
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GGCATTGCCATACCACACGATATAGATTTAGGGGATTCCCGAGTGGTCATACAA 476

RESULT 86
AF336298
LOCUS       AF336298                476 bp ss-RNA     linear   VRL 05-MAR-2002
DEFINITION  Swine hepatitis E virus isolate NLSW105 structural protein gene,
            partial cds.
ACCESSION   AF336298
VERSION     AF336298.1  GI:18478631
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I.,
            Vivo,A., Kooreman,M. and de Roda Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine related to sequences in
            humans, The Netherlands
  JOURNAL   Emerging Infect. Dis. 7 (6), 970-976 (2001)
  MEDLINE   21614760
   PUBMED   11747723
REFERENCE   2  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
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  JOURNAL   Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
     source          1. .476
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW105"
                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAL73223.1"
                     /db_xref="GI:18478632"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPT
                     ELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGDSRVVIQ"

Alignment Scores:
Pred. No.:              157             Length:         476
Score:                  152.00          Matches:        152
Percent Similarity:     96.20%          Conservative:   0
Best Local Similarity:  96.20%          Mismatches:     6
Query Match:            27.69%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF336298 (1-476)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          3 CCTGTTAATTCTTATACCAATACTCCTTACACCGGGGCGCTTGGACTTCTCGACTTTGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              |||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         63 CTAGAGCTTGAGTTTAGGAACCTGACACCTGGGAACACTAACACCCGTGTTTCCCGGTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACAAGCACAGCCCGCCATCGGCTGCGCCGCGGTGCTGATGGCACCGCCGAGCTTACCACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||
Db        183 ACGGCGGCCACTCGCTTTATGAAGGACCTGCACTTCACCGGTACGAATGGGGTCGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              |||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        243 GTGGGTCGAGGTATTGCTCTCACACTCTTTAATCTTGCTGATACGCTTCTCGGTGGTTTG 302

Qy        273 ProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        303 CCGACAGAATTRATTTCGTCGGCTGGGGGACAGCTGTTCTACTCCCGCCCCGTCGTCTCA 362

Qy        293 AlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLys 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GCCAATGGCGAGCCGACCGTTAAGTTATATACATCTGTAGAGAATGCGCAGCAGGATAAA 422

Qy        313 GlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGln 330
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Db        423 GGGATTGCTATCCCACATGACATAGATCTGGGTGACTCTCGAGTGGTCATTCAA 476

RESULT 87
AF336299
LOCUS       AF336299                476 bp ss-RNA     linear   VRL 05-MAR-2002
DEFINITION  Swine hepatitis E virus isolate NLSW122 structural protein gene,
            partial cds.
ACCESSION   AF336299
VERSION     AF336299.1  GI:18478634
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I.,
            Vivo,A., Kooreman,M. and de Roda Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine related to sequences in
            humans, The Netherlands
  JOURNAL   Emerging Infect. Dis. 7 (6), 970-976 (2001)
  MEDLINE   21614760
   PUBMED   11747723
REFERENCE   2  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
     source          1. .476
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW122"
                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAL73224.1"
                     /db_xref="GI:18478635"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGMNGVGEVGRGIALTLFNLADTLLGGLPT
                     ELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGDSRVVIQ"

Alignment Scores:
Pred. No.:              157             Length:         476
Score:                  152.00          Matches:        152
Percent Similarity:     96.20%          Conservative:   0
Best Local Similarity:  96.20%          Mismatches:     6
Query Match:            27.69%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF336299 (1-476)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTTAATTCCTATACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGATTTTGCA 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              |||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         63 CTAGAGCTTGAATTTAGAAACCTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACCAGCACAGCCCGCCACCGGCTGCGCCGCGGCGCTGATGGTACTGCTGAGCTTACTACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||
Db        183 ACAGCAGCCACACGTTTCATGAAAGATTTGCACTTTACTGGCATGAATGGTGTCGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              |||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        243 GTGGGCCGTGGTATCGCTCTGACATTGTTTAATCTTGCTGATACGCTTCTCGGTGGTTTA 302

Qy        273 ProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CCGACAGAATTRATTTCGTCGGCTGGGGGTCAATTGTTTTACTCCCGCCCTGTTGTCTCG 362

Qy        293 AlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLys 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GCCAATGGCGAGCCAACAGTAAAGTTATACACATCTGTTGAGAATGCGCAGCAAGATAAG 422

Qy        313 GlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGln 330
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GGCATCGCCATCCCGCATGATATAGACCTCGGTGACTCCCGTGTGGTTATTCAG 476

RESULT 88
AF503511
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LOCUS       AF503511                473 bp ss-RNA     linear   VRL 01-DEC-2003
DEFINITION  Swine hepatitis E virus isolate P354/1/02 capsid gene, partial cds.
ACCESSION   AF503511
VERSION     AF503511.1  GI:33323622
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 473)
  AUTHORS   Banks,M., Heath,G., Grierson,S.S., King,D.P., Girones,R.,
            Harrison,T. and Emerson,S.
  TITLE     Hepatitis E virus in pigs in the UK, Sweden and Holland
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 473)
  AUTHORS   Grierson,S.S., King,D.P. and Banks,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-APR-2002) Virology, Veterinary Laboratories Agency,
            Woodham Lane, Addlestone, Surrey KT15 3NB, UK
FEATURES             Location/Qualifiers
     source          1. .473
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="P354/1/02"
                     /isolation_source="swine fecal material"
                     /db_xref="taxon:63421"
                     /country="United Kingdom"
     CDS             <1. .>473
                     /note="ORF2"
                     /codon_start=3
                     /product="capsid"
                     /protein_id="AAQ07590.1"
                     /db_xref="GI:33323623"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPT
                     ELISSAGGQLFYSRPVVSANGEPAVKLYTSVENAQQDKGIAIPHDIDLGDSRVVI"

Alignment Scores:
Pred. No.:              161             Length:         473
Score:                  150.00          Matches:        150
Percent Similarity:     95.54%          Conservative:   0
Best Local Similarity:  95.54%          Mismatches:     7
Query Match:            27.32%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF503511 (1-473)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTTAATTCCTACACTAATACGCCCTATACTGGGGCGTTGGGGCTTCTCGACTTTGCA 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTAGGAACTTGACCCCTGGGAATACCAACACCCGTGTGTCCCGGTAC 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACTAGCACGGCTCGCCACCGTTTACGCCGTGGTGCCGACGGGACTGCTGAGCTCACGACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 ACTGCTGCCACGCGTTTCATGAAGGACCTGCACTTCACCGGGACGAATGGCGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GTGGGCCGTGGCATAGCCTTAACTCTATTCAATCTTGCTGATACACTTCTCGGCGGTTTG 302

Qy        273 ProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CCGACAGAATTGATTTCGTCGGCCGGAGGTCAGCTCTTTTACTCCCGCCCAGTTGTCTCG 362

Qy        293 AlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLys 312
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        363 GCCAATGGCGAGCCGGCTGTTAAATTATATACATCCGTTGAGAATGCACAGCAGGATAAG 422

Qy        313 GlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIle 329
              |||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GGCATTGCCATACCGCATGATATAGATCTAGGGGATTCCCGTGTGGTTATC 473

RESULT 89
AF503512
LOCUS       AF503512                473 bp ss-RNA     linear   VRL 01-DEC-2003
DEFINITION  Swine hepatitis E virus isolate P143/11/02 capsid gene, partial
            cds.
ACCESSION   AF503512
VERSION     AF503512.1  GI:33323624
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 473)
  AUTHORS   Banks,M., Heath,G., Grierson,S.S., King,D.P., Girones,R.,
            Harrison,T. and Emerson,S.
  TITLE     Hepatitis E virus in pigs in the UK, Sweden and Holland
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 473)
  AUTHORS   Grierson,S.S., King,D.P. and Banks,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-APR-2002) Virology, Veterinary Laboratories Agency,
            Woodham Lane, Addlestone, Surrey KT15 3NB, UK
FEATURES             Location/Qualifiers
     source          1. .473
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="P143/11/02"
                     /isolation_source="swine fecal material"
                     /db_xref="taxon:63421"
                     /country="United Kingdom"
     CDS             <1. .>473
                     /note="ORF2"
                     /codon_start=3
                     /product="capsid"
                     /protein_id="AAQ07591.1"
                     /db_xref="GI:33323625"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPT
                     ELISSAGGQLFYSRPVVSANGEPAVKLYTSVENAQQDKGIAIPHDIDLGDSRVVI"

Alignment Scores:
Pred. No.:              161             Length:         473
Score:                  150.00          Matches:        150
Percent Similarity:     95.54%          Conservative:   0
Best Local Similarity:  95.54%          Mismatches:     7
Query Match:            27.32%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF503512 (1-473)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          3 CCTGTAAACTCTTATACCAATACGCCCTATACTGGGGCATTGGGCCTTCTTGACTTCGCA 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAAATTTAGAAACTTGACCCCTGGGAACACTAACACCCGTGTTTCCCGGTAC 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACTAGCACGGCTCGTCACCGCTTGCGCCGTGGTGCTGATGGAACTGCCGAGCTCACGACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 ACTGCGGCCACGCGCTTCATGAAGGACCTGCACTTTACTGGGACGAACGGCGTCGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
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Db        243 GTGGGCCGTGGCATAGCCCTAACATTATTCAACCTTGCTGACACACTTCTCGGCGGCTTG 302

Qy        273 ProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CCGACAGAATTGATTTCGTCGGCCGGAGGTCAGCTCTTTTACTCCCGCCCAGTCGTCTCG 362

Qy        293 AlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLys 312
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        363 GCCAATGGCGAGCCGGCTGTTAAATTATATACTTCCGTCGAGAATGCACAGCAGGATAAG 422

Qy        313 GlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIle 329
              |||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GGCATTGCCATACCTCACGATATAGACCTAGGGGATTCCCGCGTGGTTATC 473

RESULT 90
AF336291
LOCUS       AF336291                476 bp ss-RNA     linear   VRL 05-MAR-2002
DEFINITION  Swine hepatitis E virus isolate NLSW22 structural protein gene,
            partial cds.
ACCESSION   AF336291
VERSION     AF336291.1  GI:18478611
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   van der Poel,W.H., Verschoor,F., van der Heide,R., Herrera,M.I.,
            Vivo,A., Kooreman,M. and de Roda Husman,A.M.
  TITLE     Hepatitis E virus sequences in swine related to sequences in
            humans, The Netherlands
  JOURNAL   Emerging Infect. Dis. 7 (6), 970-976 (2001)
  MEDLINE   21614760
   PUBMED   11747723
REFERENCE   2  (bases 1 to 476)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van der Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2001) MGB, RIVM, Antonie van Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Netherlands
FEATURES             Location/Qualifiers
     source          1. .476
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW22"
                     /db_xref="taxon:63421"
     CDS             <1. .>476
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAL73216.1"
                     /db_xref="GI:18478612"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLDDTLLGGLPT
                     EXISSARGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGITIPHDIDLGDSRVVIQ"

Alignment Scores:
Pred. No.:              165           Length:        476
Score:                  148.00        Matches:       148
Percent Similarity:     93.67%        Conservative:  0
Best Local Similarity:  93.67%        Mismatches:    10
Query Match:            26.96%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AF336291 (1-476)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTTAACTCCTATACTAATACACCTTACACCGGTGCACTGGGGCTTCTTGATTTTGCA 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db         63 TTAGAGCTTGAATTTAGAAACCTGACACCCGGGAATACCAACACCCGTGTTTCCAGGTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACCAGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGTACCGCTGAGCTTACCACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db        183 ACAGCAGCCACACGTTTTATGAAAGACCTGCATTTTACTGGCACGAACGGTGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||||||
Db        243 GTGGGCCGCGGTATCGCCCTGACATTGTTTAATCTCGATGATACGCTTCTCGGTGGTTTA 302

Qy        273 ProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              |||||||||  ||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        303 CCGACAGAATTNATTTCGTCGGCTAGGGGTCAATTGTTTTACTCCCGCCCTGTTGTCTCG 362

Qy        293 AlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLys 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GCCAATGGCGAGCCAACAGTAAAGTTGTATACATCTGTTGAGAATGCGCAGCAAGATAAG 422

Qy        313 GlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGln 330
              |||      ||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GGCATCACCATTCCACATGATATAGATCTTGGTGACTCCCGTGTGGTTATTCAG 476

RESULT 91
AY370687
LOCUS       AY370687                451 bp    RNA     linear   VRL 15-JAN-2004
DEFINITION  Hepatitis E virus isolate Namibia7801 structural protein (ORF2)
            gene, partial cds.
ACCESSION   AY370687
VERSION     AY370687.1  GI:34484264
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 451)
  AUTHORS   Maila,H.T., Bowyer,S.M. and Swanepoel,R.
  TITLE     Identification of a new strain of hepatitis E virus from an
            outbreak in Namibia in 1995
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 89-95 (2004)
   PUBMED   14718623
REFERENCE   2  (bases 1 to 451)
  AUTHORS   Maila,H.T., Bowyer,S.M. and Swanepoel,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-AUG-2003) Molecular Virology, National Institute for
            Communicable Diseases, Private Bag X4, Sandringham, Johannesburg
            2131, South Africa
FEATURES             Location/Qualifiers
     source          1. .451
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="Namibia7801"
                     /db_xref="taxon:12461"
     gene            <1. .>451
                     /gene="ORF2"
     CDS             <1. .>451
                     /gene="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAQ72766.1"
                     /db_xref="GI:34484265"
                     /translation="RVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTGAEY
                     DQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTIEQYSKSFFV
                     LPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVSISTYTT"

Alignment Scores:
Pred. No.:              174           Length:        451
Score:                  144.00        Matches:       144
Percent Similarity:     96.64%        Conservative:  0
Best Local Similarity:  96.64%        Mismatches:    5
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Query Match:          26.23%      Indels:        0
DB:                   1           Gaps:          0

US-09-769-066-16 (1-549) x AY370687 (1-451)

Qy        326 ArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerPro 345
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Db          3 CGCGTGGTTATTCAGGATTATGACAATCAGCACGAGCAGGACCGCCCCACCCCCTCACCT 62

Qy        346 AlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThr 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 GCACCGTCCCGGCCCTTTTCTGTCCTCCGTGCAAATGATGTGCTTTGGCTGTCTCTTACT 122

Qy        366 AlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrIleSerAsp 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GGGGCCGAGTATGACCAATCTACGTACGGGTCGTCCACCGGCCCGGTTTATGTCTCGGAT 182

Qy        386 SerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrp 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AGTGTGACCTTGGTGAATGTAGCGACCGGCGCGCAGGCCGTAGCCCGGTCGCTCGACTGG 242

Qy        406 SerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhe 425
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Db        243 TCCAAGGTTACTCTTGACGGGCGGCCCTTACCTACTATTGAACAATATTCTAAGTCATTC 302

Qy        426 PheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGly 445
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Db        303 TTTGTGTTGCCCCTTCGTGGTAAGCTCTCTTTTTGGGAGGCCGGTACAACGAAAGCGGGT 362

Qy        446 TyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGly 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 TACCCCTATAATTACAACACCACTGCTAGTGACCAGATTCTGATCGAGAATGCGGCCGGC 422

Qy        466 HisArgValAlaIleSerThrTyrThr 474
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Db        423 CACCGAGTCTCCATTTCGACCTATACC 449

RESULT 92
AY370688
LOCUS       AY370688                451 bp    RNA     linear   VRL 15-JAN-2004
DEFINITION  Hepatitis E virus isolate Namibia7948 structural protein (ORF2)
            gene, partial cds.
ACCESSION   AY370688
VERSION     AY370688.1  GI:34484266
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 451)
  AUTHORS   Maila,H.T., Bowyer,S.M. and Swanepoel,R.
  TITLE     Identification of a new strain of hepatitis E virus from an
            outbreak in Namibia in 1995
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 89-95 (2004)
   PUBMED   14718623
REFERENCE   2  (bases 1 to 451)
  AUTHORS   Maila,H.T., Bowyer,S.M. and Swanepoel,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-AUG-2003) Molecular Virology, National Institute for
            Communicable Diseases, Private Bag X4, Sandringham, Johannesburg
            2131, South Africa
FEATURES             Location/Qualifiers
     source          1. .451
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="Namibia7948"
                     /db_xref="taxon:12461"
     gene            <1. .>451
                     /gene="ORF2"
     CDS             <1. .>451
                     /gene="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAQ72767.1"
                     /db_xref="GI:34484267"
                     /translation="RVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTGAEY
                     DQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTIEQYSKSFFV
                     LPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVSISTYTT"

Alignment Scores:
Pred. No.:            174           Length:        451
Score:                144.00        Matches:       144
Percent Similarity:   96.64%        Conservative:  0
Best Local Similarity: 96.64%       Mismatches:    5
Query Match:          26.23%        Indels:        0
DB:                   1             Gaps:          0

US-09-769-066-16 (1-549) x AY370688 (1-451)

Qy        326 ArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerPro 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CGCGTGGTTATTCAGGATTATGACAATCAGCACGAGCAGGACCGCCCCACCCCCTCACCT 62

Qy        346 AlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThr 365
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Db         63 GCACCGTCCCGGCCCTTTTCTGTCCTCCGTGCAAATGATGTGCTTTGGCTGTCTCTTACT 122

Qy        366 AlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrIleSerAsp 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GGGGCCGAGTATGACCAGTCTACGTACGGGTCGTCCACCGGCCCGGTTTATGTCTCGGAT 182

Qy        386 SerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrp 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AGTGTGACCTTGGTGAATGTAGCGACCGGCGCGCAGGCCGTAGCCCGGTCGCTCGACTGG 242

Qy        406 SerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhe 425
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Db        243 TCCAAGGTTACTCTTGACGGGCGGCCCTTACCTACTATTGAACAATATTCTAAGTCATTC 302

Qy        426 PheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGly 445
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Db        303 TTTGTGTTGCCCCTCCGTGGTAAGCTCTCTTTTTGGGAGGCCGGTACAACGAAAGCGGGT 362

Qy        446 TyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGly 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 TACCCCTATAATTACAACACCACTGCTAGTGACCAGATTCTGATCGAGAATGCGGCCGGC 422

Qy        466 HisArgValAlaIleSerThrTyrThr 474
              |||||||||   ||||||||||||||||
Db        423 CACCGAGTCTCCATTTCGACCTATACC 449

RESULT 93
AY370689
LOCUS       AY370689                451 bp    RNA     linear   VRL 15-JAN-2004
DEFINITION  Hepatitis E virus isolate Namibia8039 structural protein (ORF2)
            gene, partial cds.
ACCESSION   AY370689
VERSION     AY370689.1  GI:34484268
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 451)
  AUTHORS   Maila,H.T., Bowyer,S.M. and Swanepoel,R.
  TITLE     Identification of a new strain of hepatitis E virus from an
            outbreak in Namibia in 1995
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 89-95 (2004)
   PUBMED   14718623
REFERENCE   2  (bases 1 to 451)
  AUTHORS   Maila,H.T., Bowyer,S.M. and Swanepoel,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-AUG-2003) Molecular Virology, National Institute for
            Communicable Diseases, Private Bag X4, Sandringham, Johannesburg
            2131, South Africa
FEATURES             Location/Qualifiers
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     source          1. .451
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     gene            <1. .>451
                     /gene="ORF2"
     CDS             <1. .>451
                     /gene="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAQ72768.1"
                     /db_xref="GI:34484269"
                     /translation="RVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTGAEY
                     DQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTIEQYSKSFFV
                     LPLRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVSISTYTT"

Alignment Scores:
Pred. No.:              174             Length:         451
Score:                  144.00          Matches:        144
Percent Similarity:     96.64%          Conservative:   0
Best Local Similarity:  96.64%          Mismatches:     5
Query Match:            26.23%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AY370689 (1-451)

Qy        326 ArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerPro 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CGCGTGGTTATTCAGGATTATGACAATCAGCACGAGCAGGACCGCCCCCACCCCCTCACCT 62

Qy        346 AlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThr 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 GCACCGTCCCGGCCCTTTTCTGTCCTCCGTGCAAATGATGTGCTTTGGCTGTCTCTTACT 122

Qy        366 AlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrIleSerAsp 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GGGGCCGAGTATGACCAGTCTACGTACGGGTCGTCCACCGGCCCGGTTTATGTCTCGGAT 182

Qy        386 SerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrp 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AGTGTGACCTTGGTGAATGTAGCGACCGGCGCGCAGGCCGTAGCCCGGTCGCTCGACTGG 242

Qy        406 SerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhe 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 TCCAAGGTTACTCTTGACGGGCGGCCCTTACCTACTATTGAACAATATTCTAAGTCATTC 302

Qy        426 PheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGly 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TTTGTGTTGCCCCTTCGTGGTAAGCTCTCTTTTTGGGAGGCCGGTACAACGAAAGCGGGT 362

Qy        446 TyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGly 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 TACCCCTATAATTACAACACCACTGCTAGTGACCAGATTCTGATCGAGAATGCGGCCGGC 422

Qy        466 HisArgValAlaIleSerThrTyrThr 474
              |||||||||   ||||||||||||||
Db        423 CACCGAGTCTCCATTTCGACCTATACC 449

RESULT 94
AY370686
LOCUS       AY370686                451 bp    RNA     linear   VRL 15-JAN-2004
DEFINITION  Hepatitis E virus isolate Namibia7798 structural protein (ORF2)
            gene, partial cds.
ACCESSION   AY370686
VERSION     AY370686.1  GI:34484262
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 451)
  AUTHORS   Maila,H.T., Bowyer,S.M. and Swanepoel,R.
  TITLE     Identification of a new strain of hepatitis E virus from an
            outbreak in Namibia in 1995
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 89-95 (2004)
   PUBMED   14718623
REFERENCE   2  (bases 1 to 451)
  AUTHORS   Maila,H.T., Bowyer,S.M. and Swanepoel,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-AUG-2003) Molecular Virology, National Institute for
            Communicable Diseases, Private Bag X4, Sandringham, Johannesburg
            2131, South Africa
FEATURES             Location/Qualifiers
     source          1. .451
                     /organism="Hepatitis E virus"
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                     /isolate="Namibia7798"
                     /db_xref="taxon:12461"
     gene            <1. .>451
                     /gene="ORF2"
     CDS             <1. .>451
                     /gene="ORF2"
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                     /product="structural protein"
                     /protein_id="AAQ72765.1"
                     /db_xref="GI:34484263"
                     /translation="RVVIQDYDNQHEQDRPTPSPAPSRSFSVLRANDVLWLSLTGAEY
                     DQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTIEQYSKSFFV
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Alignment Scores:
Pred. No.:              179             Length:         451
Score:                  142.00          Matches:        142
Percent Similarity:     95.30%          Conservative:   0
Best Local Similarity:  95.30%          Mismatches:     7
Query Match:            25.87%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AY370686 (1-451)

Qy        326 ArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerPro 345
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Db          3 CGCGTGGTTATTCAGGATTATGACAATCAGCACGAGCAGGACCGCCCCACCCCCTCACCT 62

Qy        346 AlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThr 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 GCACCGTCCCGGTCCTTTTCTGTCCTCCGTGCAAATGATGTGCTTTGGCTGTCTCTCACT 122

Qy        366 AlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrIleSerAsp 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GGGGCCGAGTATGACCAATCTACGTACGGGTCGTCCACCGGCCCGGTTTATGTCTCGGAT 182

Qy        386 SerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrp 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AGTGTGACCTTGGTGAATGTAGCGACCGGCGCGCAGGCCGTAGCCCGGTCGCTCGACTGG 242

Qy        406 SerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhe 425
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Db        243 TCCAAGGTTACTCTTGACGGGCGGCCCTTACCTACTATTGAACAATATTCTAAGTCATTC 302

Qy        426 PheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGly 445
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Db        303 TTTGTGTTGCCCCTTCGTGGTAAGCTCTCTTTTTGGGAGGCCGGTACAACGAAAGCGGGT 362

Qy        446 TyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGly 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 TACCCCTATAATTACAATACCACTGCTAGTGACCAGATTCTGATCGAGAATGCGGGCGGG 422

Qy        466 HisArgValAlaIleSerThrTyrThr 474
              |||||||||   ||||||||||||||
Db        423 CACCGAGTCTCCATTTCGACCTATACC 449

RESULT 95
AB080579
LOCUS       AB080579                436 bp    RNA     linear   VRL 23-JUL-2002
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DEFINITION  Hepatitis E virus gene for ORF2 protein, partial cds,
            clone:HE-JI3C.
ACCESSION   AB080579
VERSION     AB080579.1  GI:21929140
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Yoshikawa,A., Sato,S., Isoda,N.,
            Ido,K., Sugano,K. and Okamoto,H.
  TITLE     Identification of two distinct genotypes of hepatitis E virus in a
            Japanese patient with acute hepatitis who had not travelled abroad
  JOURNAL   J. Gen. Virol. 83 (Pt 8), 1931-1940 (2002)
   PUBMED   12124457
REFERENCE   2  (bases 1 to 436)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-FEB-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology, Jichi
            Medical School; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun,
            Tochigi-Ken 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp,
            Tel:81-285-58-7404, Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /clone="HE-JI3C"
                     /tissue_type="serum"
                     /country="Japan"
     gene            2. .436
                     /gene="ORF2"
     CDS             <2. .>436
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                     /codon_start=1
                     /product="ORF2 protein"
                     /protein_id="BAC05704.1"
                     /db_xref="GI:21929141"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
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Alignment Scores:
Pred. No.:                184          Length:          436
Score:                    140.00       Matches:         140
Percent Similarity:       96.55%       Conservative:    0
Best Local Similarity:    96.55%       Mismatches:      5
Query Match:              25.50%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-16 (1-549) x AB080579 (1-436)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCCGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATTCACGGCTCCCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTACACTGGTGCACTGGGGCTCCTTGATTTTGCATTGGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||  ||||||
Db        122 GAATTTAGAAACTTGACACCCGGGAATACCAACACCCGTGTCTCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGTCGCGGTGCTGATGGGACAGCTGAGCTCACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        242 ACACGTTTCATGAAAGATCTGCATTTTACTGGCACGAACGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCCCTGACACTGTTTAATCTTGCTGACACGCTTCTTGGCGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGly 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCGGCCAATGGC 421

Qy        296 GluProThrValLys 300
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Db        422 GAGCCAACAGTAAAG 436

RESULT 96
AF020492
LOCUS       AF020492                448 bp ss-RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus strain TK5/95/Nepal capsid gene, partial cds.
ACCESSION   AF020492
VERSION     AF020492.1  GI:2731791
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 448)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 448)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th and Dahlia St. Bldg. 40, Washington, DC
            20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .448
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TK5/95/Nepal"
                     /db_xref="taxon:12461"
                     /note="from RT-PCR amplified virus in human serum"
     CDS             <1. .>448
                     /codon_start=1
                     /product="capsid"
                     /protein_id="AAB93548.1"
                     /db_xref="GI:2731792"
                     /translation="VATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFPVLPLRGKLS
                     FWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPH
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Alignment Scores:
Pred. No.:                194          Length:          448
Score:                    136.00       Matches:         136
Percent Similarity:       91.28%       Conservative:    0
Best Local Similarity:    91.28%       Mismatches:      13
Query Match:              24.77%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-16 (1-549) x AF020492 (1-448)

Qy        392 ValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeuAsp 411
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Db          1 GTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGAT 60

Qy        412 GlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuProLeuArg 431
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Db         61 GGTCGCCCTCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGC 120

Qy        432 GlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsn 451
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Db        121 GGCAAGCTCTCTTTCTGGGAGGCAGGCACAACTAAGGCCGGGTACCCTTATAATTACAAC 180

Qy        452 ThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSer 471
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Db        181 ACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTTGCTATCTCC 240

Qy        472 ThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAla 491
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Db        241 ACTTACACCACTAGCCTAGGTGCTGGCCCCGTCTCCATTTCTGCGGTTGCCGTCTTAGCC 300

Qy        492 ProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThr 511
              |||   ||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        301 CCACACTCTGCGCTAGCATTGCTTGAGGATACCTTGGATTACCCTGCCCGCGCCCATACT 360

Qy        512 PheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSer 531
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Db        361 TTTGATGATTTCTGCCCAGAGTGCCGCCCCCTTGGCCTCCAGGGCTGCGCTTTCCAATCT 420

Qy        532 ThrValAlaGluLeuGlnArgLeuLys 540
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Db        421 ACTGTCGCTGAGCTTCAGCGCCTTAAG 447

RESULT 97
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LOCUS       AF020493                448 bp ss-RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus strain TK104/91/Nepal capsid gene, partial cds.
ACCESSION   AF020493
VERSION     AF020493.1  GI:2731793
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 448)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 448)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th and Dahlia St. Bldg. 40, Washington, DC
            20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .448
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TK104/91/Nepal"
                     /db_xref="taxon:12461"
                     /note="from RT-PCR amplified virus in human feces"
     CDS             <1. .>448
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                     /product="capsid"
                     /protein_id="AAB93549.1"
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Alignment Scores:
Pred. No.:              194           Length:        448
Score:                  136.00        Matches:       136
Percent Similarity:     91.28%        Conservative:  0
Best Local Similarity:  91.28%        Mismatches:    13
Query Match:            24.77%        Indels:        0

DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AF020493 (1-448)

Qy        392 ValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeuAsp 411
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Db          1 GTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGAT 60

Qy        412 GlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuProLeuArg 431
              ||||||||||||   |||   ||||||||||||||||||||||||||||||||||||||
Db         61 GGTCGCCCTCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGC 120

Qy        432 GlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsn 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCAAGCTCTCTTTCTGGGAGGCAGGCACAACTAAGGCCGGGTACCCTTATAATTACAAC 180

Qy        452 ThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSer 471
              ||||||||||||||||||   |||   ||||||||||||||||||||||||||||||||
Db        181 ACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTTGCTATCTCC 240

Qy        472 ThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAla 491
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Qy        492 ProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThr 511
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Qy        512 PheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSer 531
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Db        361 TTTGATGATTTCTGCCCAGAGTGCCGCCCCCTTGGCCTCCAGGGCTGCGCTTTCCAATCT 420

Qy        532 ThrValAlaGluLeuGlnArgLeuLys 540
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Db        421 ACTGTCGCTGAGCTTCAGCGCCTTAAA 447

RESULT 98
AF020494
LOCUS       AF020494                448 bp ss-RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus strain TK4/95/Nepal capsid gene, partial cds.
ACCESSION   AF020494
VERSION     AF020494.1  GI:2731795
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 448)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 448)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th and Dahlia St. Bldg. 40, Washington, DC
            20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .448
                     /organism="Hepatitis E virus"
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Alignment Scores:
Pred. No.:                194             Length:         448
Score:                    136.00          Matches:        136
Percent Similarity:       91.28%          Conservative:   0
Best Local Similarity:    91.28%          Mismatches:     13
Query Match:              24.77%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF020494 (1-448)

Qy        392 ValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeuAsp 411
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Db          1 GTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGAC 60

Qy        412 GlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuProLeuArg 431
              |||||||||||||   |||   |||||||||||||||||||||||||||||||||||||||
Db         61 GGTCGCCCTCTTTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGC 120

Qy        432 GlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsn 451
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCAAGCTCTCTTTCTGGGAGGCAGGCACAACTAAGGCCGGGTACCCTTATAATTACAAC 180

Qy        452 ThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSer 471
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Db        181 ACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTTGCCATCTCC 240

Qy        472 ThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAla 491
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Db        241 ACTTACACCACTAGCCTGGGTGCTGGCCCCGTCTCCATTTCTGCGGTTGCCGTCTTAGCC 300

Qy        492 ProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThr 511
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Db        301 CCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGATTACCCTGCCCGCGCCCATACT 360

Qy        512 PheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSer 531
              |||||||||||||||||||||||||||||   |||||||||||||||||||||||||||||||
Db        361 TTTGATGATTTCTGCCCAGAGTGCCGCCCCCTTGGCCTCCAGGGCTGCGCTTTCCAGTCT 420

Qy        532 ThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||
Db        421 ACTGTCGCTGAGCTTCAGCGCCTTAAG 447

RESULT 99
AF020495
LOCUS       AF020495                448 bp ss-RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus strain TK78/87/Nepal capsid gene, partial cds.
ACCESSION   AF020495
VERSION     AF020495.1  GI:2731797
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 448)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 448)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th and Dahlia St. Bldg. 40, Washington, DC
            20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .448
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TK78/87/Nepal"
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                     /note="from RT-PCR amplified virus in human feces"
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Alignment Scores:
Pred. No.:                194             Length:         448
Score:                    136.00          Matches:        136
Percent Similarity:       91.28%          Conservative:   0
Best Local Similarity:    91.28%          Mismatches:     13
Query Match:              24.77%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF020495 (1-448)

Qy        392 ValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeuAsp 411
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Db          1 GTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGAC 60

Qy        412 GlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuProLeuArg 431
              |||||||||||   |||   |||||||||||||||||||||||||||||||||||||||
Db         61 GGTCGCCCTCTCTCCACCATCCAGCAGTATTCGAAGACCTTCTTTGTCCTGCCGCTCCGC 120

Qy        432 GlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsn 451
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTAAGCTCTCTTTCTGGGAGGCAGGCACAACTAAAGCCGGGTACCCCTATAATTACAAC 180

Qy        452 ThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSer 471
              |||||||||||||||||   |||   |||||||||||||||||||||||||||||||||||
Db        181 ACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTTGCTATTTCC 240

Qy        472 ThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAla 491
              |||||||||||   |||||||||||||||||   |||||||||   ||||||||||||||||
Db        241 ACTTACACCACCAGCCTGGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCC 300

Qy        492 ProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThr 511
              |||   |||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        301 CCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGCGCCCATACT 360

Qy        512 PheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSer 531
              |||||||||||||||||||||||||||||   |||||||||||||||||||||||||||||||
Db        361 TTTGATGATTTCTGCCCAGAGTGCCGCCCTCTCGGCCTCCAGGGCTGCGCTTTCCAGTCT 420

Qy        532 ThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||
Db        421 ACTGTCGCTGAGCTTCAGCGCCTTAAG 447

RESULT 100
AF020497
LOCUS       AF020497                448 bp ss-RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus strain Nep4/94/Nepal capsid gene, partial cds.
ACCESSION   AF020497
VERSION     AF020497.1  GI:2731801
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 448)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
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  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 448)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th and Dahlia St. Bldg. 40, Washington, DC
            20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .448
                     /organism="Hepatitis E virus"
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Alignment Scores:
Pred. No.:                194           Length:        448
Score:                    136.00        Matches:       136
Percent Similarity:       91.28%        Conservative:  0
Best Local Similarity:    91.28%        Mismatches:    13
Query Match:              24.77%        Indels:        0
DB:                       1             Gaps:          0

US-09-769-066-16 (1-549) x AF020497 (1-448)

Qy        392 ValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeuAsp 411
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Db          1 GTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGAT 60

Qy        412 GlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuProLeuArg 431
              |||||||||||||   |||      ||||||||||||||||||||||||||||||||||||
Db         61 GGCCGCCCTCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGC 120

Qy        432 GlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsn 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCAAGCTCTCTTTCTGGGAGGCAGGCACAACTAAGGCCGGGTACCCTTATAATTACAAC 180

Qy        452 ThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSer 471
              ||||||||||||||||||   |||   ||||||||||||||||||||||||||||||||
Db        181 ACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTTGCTATCTCC 240

Qy        472 ThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAla 491
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Db        241 ACTTACACCACTAGCCTAGGTGCTGGCCCCGTCTCCATTTCTGCGGTTGCCGTCTTGGCC 300

Qy        492 ProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThr 511
              |||   ||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        301 CCACACTCTGCGCTAGCATTGCTTGAGGATACCTTGGATTACCCTGCCCGCGCCCATACT 360

Qy        512 PheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSer 531
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        361 TTTGATGATTTCTGCCCAGAGTGCCGCCCCCTCGGCCTCCAGGGCTGCGCTTTCCAGTCT 420

Qy        532 ThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||
Db        421 ACTGTCGCTGAGCTTCAGCGCCTTAAG 447

RESULT 101
AB073911
LOCUS       AB073911                 421 bp    RNA     linear   VRL 15-DEC-2001
DEFINITION  Swine hepatitis E virus gene for capsid protein, partial cds,
            strain:swJ791.
ACCESSION   AB073911
VERSION     AB073911.1  GI:17826982
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Okamoto,H., Takahashi,M., Nishizawa,T., Fukai,K., Muramatsu,U. and
            Yoshikawa,A.
  TITLE     Analysis of the complete genome of indigenous swine hepatitis E
            virus isolated in Japan
  JOURNAL   Biochem. Biophys. Res. Commun. 289 (5), 929-936 (2001)
  MEDLINE   21616952
   PUBMED   11741279
REFERENCE   2  (bases 1 to 421)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-NOV-2001) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:                196           Length:        421
Score:                    135.00        Matches:       135
Percent Similarity:       96.43%        Conservative:  0
Best Local Similarity:    96.43%        Mismatches:    5
Query Match:              24.59%        Indels:        0
DB:                       1             Gaps:          0

US-09-769-066-16 (1-549) x AB073911 (1-421)

Qy        153 SerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySer 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TCGGGCGTGGCCGAGGAAGAGGCAACATCGGGTCTTGTCATGCTTTGTATACATGGTTCC 61

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCCGTTAATTCTTACACCAATACGCCCTACACTGGGGCGTTGGGGCTTCTTGACTTTGCA 121

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db        122 CTCGAGCTTGAATTCAGGAATTTGACCCCTGGGAACACCAATACTCGTGTGTCCCGGTAC 181

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 ACCAGTACGGCTCGCCACCGTTTACGCCGTGGCGCCGACGGAACCGCTGAGCTCACGACC 241

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||
Db        242 ACTGCCGCCACGCGCTTCATGAAGGACCTACATTTCACCGGGACGAATGGCGTTGGTGAG 301
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Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        302 GTGGGCCGTGGCATAGCCCTAACTCTATTTAATCTTGCTGATACACTTCTCGGCGGCTTG 361

Qy        273 ProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CCGACAGAATTGATTTCGTCGGCTGGAGGTCAGCTCTTTTATTCCCGCCCAGTTGTCTCG 421

RESULT 102
AF020496
LOCUS       AF020496                448 bp ss-RNA     linear   VRL 04-SEP-2001
DEFINITION  Hepatitis E virus strain TK15/92/Nepal capsid gene, partial cds.
ACCESSION   AF020496
VERSION     AF020496.1  GI:2731799
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 448)
  AUTHORS   Gouvea,V., Snellings,N., Cohen,S.J., Warren,R.L., Myint,K.S.,
            Shrestha,M.P., Vaughn,D.W., Hoke,C.H. Jr. and Innis,B.L.
  TITLE     Hepatitis E virus in Nepal: similarities with the Burmese and
            Indian variants
  JOURNAL   Virus Res. 52 (1), 87-96 (1997)
  MEDLINE   98115237
   PUBMED   9453147
REFERENCE   2  (bases 1 to 448)
  AUTHORS   Gouvea,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-AUG-1997) Virus Diseases, Walter Reed Army Institute
            of Research, 14th and Dahlia St. Bldg. 40, Washington, DC
            20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .448
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TK15/92/Nepal"
                     /db_xref="taxon:12461"
                     /note="from RT-PCR amplified virus in human feces"
     CDS             <1. .>448
                     /codon_start=1
                     /product="capsid"
                     /protein_id="AAB93552.1"
                     /db_xref="GI:2731800"
                     /translation="VATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLS
                     FWEAGTTKAGYPYNYNTTASGQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPH
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Alignment Scores:
Pred. No.:              197          Length:         448
Score:                  135.00       Matches:        135
Percent Similarity:     90.60%       Conservative:   0
Best Local Similarity:  90.60%       Mismatches:     14
Query Match:            24.59%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AF020496 (1-448)

Qy        392 ValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeuAsp 411
              ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db          1 GTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGAT 60

Qy        412 GlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuProLeuArg 431
              ||||||||||||  |||     ||||||||||||||||||||||||||||||||||||||
Db         61 GGCCGCCCTCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGC 120

Qy        432 GlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsn 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCAAGCTCTCTTTCTGGGAGGCAGGCACAACTAAGGCCGGGTACCCTTATAATTACAAC 180

Qy        452 ThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSer 471
              ||||||||||||  |||  |||  ||||||||||||||||||||||||||||||||||||
Db        181 ACCACTGCTAGCGGCCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTTGCTATCTCC 240

Qy        472 ThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAla 491
              ||||||||||||  ||||||||||||||||||  |||||||||  ||||||||||||||
Db        241 ACTTACACCACTAGCCTGGGCGCTGGCCCCGTCTCCATTTCTGCGGTTGCCGTCTTGGCC 300

Qy        492 ProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThr 511
              |||  ||||||||||||||||||||||||||||  |||||||||  ||||||||||||||
Db        301 CCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGATTACCCTGCCCGCGCCCATACT 360

Qy        512 PheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSer 531
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        361 TTTGATGATTTCTGCCCAGAGTGCCGCCCCCTTGGCCTCCAGGGCTGCGCTTTCCAGTCT 420

Qy        532 ThrValAlaGluLeuGlnArgLeuLys 540
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Db        421 ACTGTCGCTGAGCTCCAGCGCCTTAAG 447

RESULT 103
HEU40046
LOCUS       HEU40046                453 bp    DNA     linear   VRL 05-JAN-1998
DEFINITION  Hepatitis E virus structural protein 2 (orf2) mRNA, partial cds.
ACCESSION   U40046
VERSION     U40046.1  GI:2745952
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 453)
  AUTHORS   van Cuyck-Gandre,H., Zhang,H.Y., Tsarev,S.A., Clements,N.J.,
            Cohen,S.J., Caudill,J.D., Buisson,Y., Coursaget,P., Warren,R.L. and
            Longer,C.F.
  TITLE     Characterization of hepatitis E virus (HEV) from Algeria and Chad
            by partial genome sequence
  JOURNAL   J. Med. Virol. 53 (4), 340-347 (1997)
  MEDLINE   98071272
   PUBMED   9407381
REFERENCE   2  (bases 1 to 453)
  AUTHORS   Van Cuyck-Gandre,H., Clements,N.J., Zhang,H.Y., Caudill,J.C.,
            Cohen,S.G., Coursaget,P., Buisson,Y., Warren,R.L. and Longer,C.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-NOV-1995) Helene Van Cuyck-Gandre, Virus Disease,
            Walter Reed Army Institute of Research, BLD 40, Washington, DC
            20307-5100, USA
FEATURES             Location/Qualifiers
     source          1. .453
                     /organism="Hepatitis E virus"
                     /mol_type="genomic DNA"
                     /strain="M7 Mostaganem, Algeria"
                     /db_xref="taxon:12461"
                     /note="HEV from patient feces"
     CDS             <1. .453
                     /note="orf2; capsid protein"
                     /codon_start=1
                     /product="structural protein 2"
                     /protein_id="AAB94789.1"
                     /db_xref="GI:2745953"
                     /translation="DRSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTK
                     AGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLED
                     TLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTREL"

Alignment Scores:
Pred. No.:              197          Length:         453
Score:                  135.00       Matches:        135
Percent Similarity:     90.60%       Conservative:   0
Best Local Similarity:  90.60%       Mismatches:     14
Query Match:            24.59%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x HEU40046 (1-453)

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
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Db          4 CGGTCGCTTGACTGGACTAAGGTCACGCTTGACGGCCGCCCTCTCTCTACTATTCAGCAG 63

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db         64 TACTCGAAGACTTTCTTCGTCCTGCCGCTTCGTGGTAAACTCTCCTTCTGGGAGGCAGGT 123

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460

Db        124 ACTACTAAGGCCGGGTACCCTTATAATTATAATACTACTGCTAGTGACCAATTGCTCGTA 183

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480

Db        184 GAGAACGCCGCCGGGCACCGGGTGGCTATTTCCACTTACACCACCAGCTTGGGTGCTGGC 243

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500

Db        244 CCTGTTTCCATCTCTGCGGTCGCTGTCCTGGCCCCCCACTCCGCGCTAGCACTGCTTGAG 303

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db        304 GATACCCTGGACTACCCTGCTCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGTCGC 363

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db        364 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTCCAGCGACTTAAG 423

Qy        541 ValLysValGlyLysThrArgGluLeu 549

Db        424 ATGAAGGTGGGTAAAACTCGGGAGTTA 450

RESULT 104
AB073909
LOCUS       AB073909                421 bp    RNA     linear   VRL 15-DEC-2001
DEFINITION  Swine hepatitis E virus gene for capsid protein, partial cds,
            strain:swJ570.
ACCESSION   AB073909
VERSION     AB073909.1  GI:17826977
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Okamoto,H., Takahashi,M., Nishizawa,T., Fukai,K., Muramatsu,U. and
            Yoshikawa,A.
  TITLE     Analysis of the complete genome of indigenous swine hepatitis E
            virus isolated in Japan
  JOURNAL   Biochem. Biophys. Res. Commun. 289 (5), 929-936 (2001)
  MEDLINE   21616952
   PUBMED   11741279
REFERENCE   2  (bases 1 to 421)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-NOV-2001) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .421
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /strain="swJ570"
                     /isolate="No. 570"
                     /specific_host="pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     gene            1. .421
                     /gene="ORF2"
     CDS             <1. .>421
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAB79301.1"
                     /db_xref="GI:17826978"
                     /translation="TGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELE
                     FRNLTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVG
                     RGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199          Length:         421
Score:                  134.00       Matches:        134
Percent Similarity:     96.40%       Conservative:   0
Best Local Similarity:  96.40%       Mismatches:     5
Query Match:            24.41%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB073909 (1-421)

Qy        154 GlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerPro 173

Db          5 GGCGTGGCTGAAGAGGAGGCTACTTCCGGCCTAGTAATGCTCTGCATTCATGGCTCCCCT 64

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193

Db         65 GTCAATTCTTATACTAATACACCCTACACAGGAGCACTGGGGCTTCTTGATTTTGCATTG 124

Qy        194 GluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSer 213

Db        125 GAGCTTGAATTTAGGAATTTGACACCTGGGAATACTAACACCCGTGTATCCCGATATACC 184

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233

Db        185 AGCACAGCCCGCCATCGGCTGCGCCGCGGTGCCGACGGGACTGCCGAGCTTACTACTACG 244

Qy        234 AlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluVal 253

Db        245 GCGGCCACTCGATTTATGAAAGATCTGCACTTCACTGGTACGAATGGAGTTGGAGAGGTG 304

Qy        254 GlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273

Db        305 GGCCGTGGTATTGCTCTGACCTTGTTTAATCTTGCTGATACGCTTCTCGGTGGCCTGCCG 364

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292

Db        365 ACAGAATTGATTTCGTCGGCTGGGGGTCAGCTCTTCTACTCCCGCCCTGTCGTCTCG 421

RESULT 105
AB073910
LOCUS       AB073910                421 bp    RNA     linear   VRL 15-DEC-2001
DEFINITION  Swine hepatitis E virus gene for capsid protein, partial cds,
            strain:swJ681.
ACCESSION   AB073910
VERSION     AB073910.1  GI:17826980
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Okamoto,H., Takahashi,M., Nishizawa,T., Fukai,K., Muramatsu,U. and
            Yoshikawa,A.
  TITLE     Analysis of the complete genome of indigenous swine hepatitis E
            virus isolated in Japan
  JOURNAL   Biochem. Biophys. Res. Commun. 289 (5), 929-936 (2001)
  MEDLINE   21616952
   PUBMED   11741279
REFERENCE   2  (bases 1 to 421)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-NOV-2001) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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          Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .421
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /strain="swJ681"
                     /isolate="No. 681"
                     /specific_host="pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     gene            1. .421
                     /gene="ORF2"
     CDS             <1. .>421
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAB79302.1"
                     /db_xref="GI:17826981"
                     /translation="TGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELE
                     FRNLTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVG
                     RGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              199          Length:        421
Score:                  134.00       Matches:       134
Percent Similarity:     96.40%       Conservative:  0
Best Local Similarity:  96.40%       Mismatches:    5
Query Match:            24.41%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-16 (1-549) x AB073910 (1-421)

Qy        154 GlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerPro 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GGTGTCGCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTCTGTATTCATGGTTCCCCT 64

Qy        174 ValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GTCAATTCTTACACTAATACACCTTATACCGGTGCACTTGGGCTTCTTGATTTTGCACTA 124

Qy        194 GluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSer 213
              ||||||||||||||||||||||||      ||||||||||||||||||||||||||||||
Db        125 GAACTTGAATTCAGGAACCTGACACCCGGGAACACCAATACCCGTGTGTCCCGGTATACT 184

Qy        214 SerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThr 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 AGTACAGCCCGTCATAGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACTACTACG 244

Qy        234 AlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluVal 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GCGGCCACGCGTTTTATGAAGGATTTGCATTTCACTGGCACGAATGGAGTTGGTGAAGTG 304

Qy        254 GlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuPro 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 GGCCGAGGCATCGCTTTGACACTGTTCAACCTTGCTGACACGCTTCTCGGTGGTCTGCCG 364

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 ACAGAATTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 421

RESULT 106
AF047864
LOCUS       AF047864                 448 bp    DNA     linear   VRL 06-MAR-1998
DEFINITION  Hepatitis E virus capsid gene, partial cds.
ACCESSION   AF047864
VERSION     AF047864.1  GI:2935424
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 448)
  AUTHORS   Gouvea,V.S., Innis,B.L., Drabick,J.J., Gambel,J.M., Seriwatana,J.
            and Hoke,C.H. Jr.
  TITLE     Hepatitis E in Bangladeshi soldiers serving in the United Nations
            mission to Haiti (UNMIH)
  JOURNAL   (in) XTH INTERNATIONAL CONGRESS OF VIROLOGY, JERUSALEM ABSTRACTS:
            241-PW54-15;
            (1996)
REFERENCE   2  (bases 1 to 448)
  AUTHORS   Drabick,J.J., Gambel,J.M., Gouvea,V.S., Caudill,J.D., Sun,W.,
            Hoke,C.H. Jr. and Innis,B.L.
  TITLE     A cluster of acute hepatitis E infection in United Nations
            Bangladeshi peacekeepers in Haiti
  JOURNAL   Am. J. Trop. Med. Hyg. 57 (4), 449-454 (1997)
  MEDLINE   98006185
   PUBMED   9347962
REFERENCE   3  (bases 1 to 448)
  AUTHORS   Gouvea,V.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1998) Virus Diseases, Walter Reed Army Institute
            of Research, 14th & Dahlia St. Bldg 40, Washington, DC 20307-5100,
            USA
FEATURES             Location/Qualifiers
     source          1. .448
                     /organism="Hepatitis E virus"
                     /mol_type="genomic DNA"
                     /strain="HB-95"
                     /db_xref="taxon:12461"
                     /note="from Bangladeshi soldiers in Haiti"
     CDS             <1. .>448
                     /codon_start=1
                     /product="capsid"
                     /protein_id="AAC05118.1"
                     /db_xref="GI:2935425"
                     /translation="VATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLS
                     FWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPH
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Alignment Scores:
Pred. No.:              202          Length:        448
Score:                  133.00       Matches:       133
Percent Similarity:     89.26%       Conservative:  0
Best Local Similarity:  89.26%       Mismatches:    16
Query Match:            24.23%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-16 (1-549) x AF047864 (1-448)

Qy        392 ValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeuAsp 411
              ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db          1 GTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGAT 60

Qy        412 GlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuProLeuArg 431
              ||||||||||||  |||      ||||||||||||||||||||||||||||||||||||||
Db         61 GGTCGCCCCCCTCTCCACCATCCAGCAGTATTCGAAGACCTTCTTTGTCCTGCCGCTCCGC 120

Qy        432 GlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsn 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTAAGCTCTCTTTCTGGGAGGCAGGTACTACTAAAGCCGGGTACCCTTATAATTATAAC 180

Qy        452 ThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSer 471
              ||||||||||||||||||  |||  ||||||||||||||||||||||||||||||||||||
Db        181 ACCACTGCTAGCGACCAATTGCTCGTTGAGAATGCCGCTGGGCATCGGGTTGCTATTTCC 240

Qy        472 ThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAla 491
              ||||||||||  ||||||||||||||||||  |||||||||  ||||||||||||||||||
Db        241 ACTTACACCACTAGCCTGGGTGCTGGCCCCGTCTCCATTTCCGCGGTTGCCGTTTTAGCC 300

Qy        492 ProArgSerAlaLeuAlaLeuGluAspThrPheAspTyrProGlyArgAlaHisThr 511
              |||  ||||||||||||||||||||||||||  |||||||||  ||||||||||||||||
Db        301 CCCCACTCTGCGTTAGCATTGCTTGAGGATACTATGGACTACCCTGTCCGCGCCCATACT 360

Qy        512 PheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSer 531
              ||||||  ||||||||||||||||||  |||  ||||||||||||||||||||||||||||
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Db        361 TTTGATGAGTTCTGTCCAGAGTGCCGCCCCCTTGTCCTCCAGGGCTGCGCTTTCCAGTCT 420

Qy        532 ThrValAlaGluLeuGlnArgLeuLys 540
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Db        421 CCTGTCGCTGAGCTTCAGCGCCTTAAG 447

RESULT 107
AB079763
LOCUS       AB079763                412 bp    RNA     linear   VRL 06-NOV-2002
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JF2.
ACCESSION   AB079763
VERSION     AB079763.1  GI:24636299
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Suzuki,K., Aikawa,T. and Okamoto,H.
  TITLE     Fulminant hepatitis E in Japan
  JOURNAL   N. Engl. J. Med. 347 (18), 1456 (2002)
  MEDLINE   22297680
   PUBMED   12409557
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-FEB-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi, Tochigi 329-0498, Japan
            (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JF2"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Japan"
                     /note="HE-JF2 was isolated from a Japanese patient
                     (Patient 2) with fulminant hepatitis of unknown
                     etiology-genotype III"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC22750.1"
                     /db_xref="GI:24636300"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB079763 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGCCTGGTAATGCTTTGCATTCATGGCTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACAAATACACCTTATACTGGAGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||||
Db        122 GAATTCAGGAACTTGACACCTGGGAACACTAATACCCGTGTATCCCGATACACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGAGTTGGTGAGGTAGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCCCTGACACTGTTCAATCTTGCTGATACACTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGCTGTTCTACTCCCGCCCCGTCGTCTCA 412

RESULT 108
AB082560
LOCUS       AB082560                412 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA4.
ACCESSION   AB082560
VERSION     AB082560.1  GI:22759616
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JA4"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /clone="HE-JA4-2"
                     /country="Japan:Hokkaido, Sapporo"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /protein_id="BAC10959.1"
                     /db_xref="GI:22759617"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
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Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB082560 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTGGTAATGCTTTGTATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||     |||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGAAATCTGACACCCGGGAACACAAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCACCGGCTGCGCCGCGGTGCTGATGGGACTGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        242 ACACGTTTCATGAAGGATTTACATTTTACTGGCACGAACGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   |||||||||||||||||||||||||||||||||||||||
Db        302 GGCATCGCTCTGACATTGTTTAATCTCGCTGACACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 109
AB082561
LOCUS       AB082561                412 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA5.
ACCESSION   AB082561
VERSION     AB082561.1  GI:22759618
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /clone="HE-JA5-2"
                     /country="Japan:Iwate, Morioka"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /protein_id="BAC10960.1"
                     /db_xref="GI:22759619"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB082561 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTGATGCTCTGTATTCATGGCTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||     |||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATTTGACACCTGGGAATACCAACACTCGTGTATCTCGATACACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCCGAGCTCACTACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAGGACTTGCATTTCACTGGCACGAATGGAGTTGGTGAAGTRGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   |||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACACTGTTTAATCTTGCTGATACGCTTCTCGGTGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCCGTCGTCTCA 412

RESULT 110
AB082562
LOCUS       AB082562                412 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA6.
ACCESSION   AB082562
VERSION     AB082562.1  GI:22759620
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /organism="Hepatitis E virus"
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                     /db_xref="taxon:12461"
                     /clone="HE-JA6-2"
                     /country="Japan:Iwate, Morioka"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
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                     /codon_start=2
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                     /db_xref="GI:22759621"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB082562 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTAATGCTCTGTATTCACGGCTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTCGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAATACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGCCGCGGTGCCGACGGGACCGCTGAACTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACCTGCATTTTACTGGCACGAATGGGGTCGGCGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACATTGTTCAACCTTGCTGATACGCTTCTCGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTAATTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCG 412

RESULT 111
AB082563
LOCUS       AB082563                412 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA7.
ACCESSION   AB082563
VERSION     AB082563.1  GI:22759622
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /organism="Hepatitis E virus"
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                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /clone="HE-JA7-2"
                     /country="Japan:Iwate, Morioka"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /protein_id="BAC10962.1"
                     /db_xref="GI:22759623"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB082563 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTGGTAATGCTTTGTATCCACGGCTCCCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTATACTGGTGCTTTGGGGCTTCTTGATTTTGCATTAGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAACCTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGCCGCGGCGCTGATGGGACCGCTGAGCTCACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        242 ACACGTTTTATGAAGGATTTGCATTTTACTGGCACGAATGGCGTTGGAGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCCCTGACACTGTTTAATCTTGCTGATACGCTTCTTGGTGGCTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAATTGTTTTACTCCCGCCCTGTTGTCTCG 412
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RESULT 112
AB082564
LOCUS       AB082564                412 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA8.
ACCESSION   AB082564
VERSION     AB082564.1  GI:22759624
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /virion
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                     /isolation_source="serum"
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                     /db_xref="taxon:12461"
                     /clone="HE-JA8-2"
                     /country="Japan:Iwate, Morioka"
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                     /gene="ORF2"
     CDS             <1. .>412
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                     /db_xref="GI:22759625"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              204          Length:         412
Score:                  132.00       Matches:        132
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US-09-769-066-16 (1-549) x AB082564 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAACTA 121

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Db        302 GGCATCGCTCTGACATTGTTTAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

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DEFINITION  Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA9.
ACCESSION   AB082565
VERSION     AB082565.1  GI:22759626
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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     gene            1. .412
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     CDS             <1. .>412
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              204          Length:         412
Score:                  132.00       Matches:        132
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DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB082565 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 114
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LOCUS       AB082566                412 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA10.
ACCESSION   AB082566
VERSION     AB082566.1  GI:22759628
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              204          Length:          412
Score:                  132.00       Matches:         132
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DB:                     1            Gaps:            0

US-09-769-066-16 (1-549) x AB082566 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCCGAGGAGGAGGCTACCTCCGGCCTGGTAATGCTTTGTATCCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        302 GGCATCGCTCTGACATTGTTTAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 115
AB088418
LOCUS       AB088418                412 bp    RNA     linear   VRL 31-OCT-2002
DEFINITION  Hepatitis E virus gene for capsid, partial cds.
ACCESSION   AB088418
VERSION     AB088418.1  GI:24430384
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SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
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            Hepevirus.
REFERENCE   1
  AUTHORS   Aikawa,T., Kojima,M., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Identification of indigenous hepatitis E virus from a Japanese
            patient who contracted sporadic acute hepatitis in 1982
  JOURNAL   J. Infect. Dis. 186 (10), 1535-1536 (2002)
  MEDLINE   22292015
   PUBMED   12404177
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JUL-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
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US-09-769-066-16 (1-549) x AB088418 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACAAATACACCTTATACTGGAGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        302 GGTATTGCTCTGACACTGTTTAATCTTGCTGATACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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RESULT 116
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DEFINITION  Hepatitis E virus gene for capsid protein, partial cds.
ACCESSION   AB093535
VERSION     AB093535.1  GI:29824080
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yajima,Y., Takahashi,N., Yamagishi,H., Kodama,A., Miyazaki,A.,
            Sugiyama,K., Eda,Y. and Okamoto,H.
  TITLE     An acute hepatitis case domestically infected with a hepatitis E
            virus whose nucleotode sequence showed a high similarity to that
            from a domestic swine in Japan
  JOURNAL   Jpn. J. Gastroenterol. 100, 454-458 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    132.00          Matches:        132
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Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB093535 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCCGAGGAAGAGGCAACATCGGGTCTTGTCATGCTTTGTATACATGGCTCCCCCGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        242 ACGCGCTTCATGAAGGACCTACATTTCACCGGGACGAATGGCGTTGGTGAGGTGGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATAGCCCTAACTCTATTTAATCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTCTTTTATTCCCGCCCAGTTGTCTCG 412

RESULT 117
AB094203
LOCUS       AB094203                412 bp    RNA     linear   VRL 27-MAR-2003
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DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ1-1.
ACCESSION   AB094203
VERSION     AB094203.1  GI:29292661
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
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                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66226.1"
                     /db_xref="GI:29292662"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094203 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAGGAGGAGGCTACTTCCGGTCTCGTAATGCTTTGCATTCATGGTTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTAGAAATTTGACACCCGGGAACACCAACACCCGCGTTTCCAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        242 ACACGTTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTAGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCTCTTACACTGTTTAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 118
AB094205
LOCUS       AB094205                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ1-3.
ACCESSION   AB094205
VERSION     AB094205.1  GI:29292665
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ1-3"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66228.1"
                     /db_xref="GI:29292666"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094205 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAGGAGGAGGCTACTTCCGGTCTCGTAATGCTTTGCATTCATGGTTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215

Db        122 GAGTTTAGAAATTTGACACCCGGGAACACCAACACCCGCGTTTCCAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235

Db        182 GCCCGTCATCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255

Db        242 ACACGTTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTAGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275

Db        302 GGTATCGCTCTTACACTGTTTAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292

Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 119
AB094206
LOCUS       AB094206                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ1-4.
ACCESSION   AB094206
VERSION     AB094206.1  GI:29292667
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ1-4"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66229.1"
                     /db_xref="GI:29292668"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:          204          Length:        412
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Score:                  132.00      Matches:        132
Percent Similarity:     96.35%      Conservative:   0
Best Local Similarity:  96.35%      Mismatches:     5
Query Match:            24.04%      Indels:         0
DB:                     1           Gaps:           0

US-09-769-066-16 (1-549) x AB094206 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175

Db          2 GCGGAGGAGGAGGCTACTTCCGGTCTCGTAATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195

Db         62 TCCTATACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215

Db        122 GAGTTTAGAAATTTGACACCCGGGAACACCAACACCCGCGTTTCCAGGTACACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235

Db        182 GCCCGCCATCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255

Db        242 ACACGTTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTAGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275

Db        302 GGTATCGCTCTTACACTGTTTAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292

Db        362 TTGATATCGTCGGCTGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 120
AB094207
LOCUS       AB094207                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ2-1.
ACCESSION   AB094207
VERSION     AB094207.1  GI:29292669
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ2-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
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                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB094207 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTTGTAATGCTTTGCATTCATGGCTCGCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTGTCCAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        242 ACACGTTTCATGAAGGATCTGCATTTTACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCTCTTACACTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 121
AB094208
LOCUS       AB094208                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ2-2.
ACCESSION   AB094208
VERSION     AB094208.1  GI:29292671
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES              Location/Qualifiers
     source           1. .412
                      /organism="Swine hepatitis E virus"
                      /virion
                      /mol_type="genomic RNA"
                      /isolate="swJ2-2"
                      /isolation_source="swine serum"
                      /specific_host="farm pig"
                      /db_xref="taxon:63421"
                      /country="Japan"
     CDS              <1. .>412
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                      /codon_start=2
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                      /db_xref="GI:29292672"
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                      ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB094208 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTTGTAATGCTTTGCATTCATGGCTCGCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTGTCCAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        242 ACACGTTTCATGAAGGATCTGCATTTTACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCTCTTACACTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 122
AB094209
LOCUS       AB094209                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ2-3.
ACCESSION   AB094209
VERSION     AB094209.1  GI:29292673
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
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          Hepevirus.
REFERENCE 1
  AUTHORS Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
          Tsuda,F. and Okamoto,H.
  TITLE   Swine hepatitis E virus strains in Japan form four phylogenetic
          clusters comparable with those of Japanese isolates of human
          hepatitis E virus
  JOURNAL J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED 12655086
REFERENCE 2  (bases 1 to 412)
  AUTHORS Okamoto,H.
  TITLE   Direct Submission
  JOURNAL Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
          Immunology Division and Division of Molecular Virology; 3311-1
          Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
          Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
          Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ2-3"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094209 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTTGTAATGCTTTGCATTCATGGCTCGCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||    ||||||
Db        122 GAGTTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        242 ACACGTTTCATGAAGGATCTGCATTTTACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCTCTTACACTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 123
AB094210
LOCUS       AB094210                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ2-4.
ACCESSION   AB094210
VERSION     AB094210.1  GI:29292675
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ2-4"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66233.1"
                     /db_xref="GI:29292676"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094210 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTTGTAATGCTTTGCATTCATGGCTCGCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||    ||||||
Db        122 GAGTTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTGTCTAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255

Db        242 ACACGTTTCATGAAGGATCTGCATTTTACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275

Db        302 GGTATCGCTCTTACACTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292

Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 124
AB094211
LOCUS       AB094211                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ2-5.
ACCESSION   AB094211
VERSION     AB094211.1  GI:29292677
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
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                     /isolate="swJ2-5"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66234.1"
                     /db_xref="GI:29292678"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204          Length:        412
Score:                  132.00       Matches:       132
Percent Similarity:     96.35%       Conservative:  0
Best Local Similarity:  96.35%       Mismatches:    5
Query Match:            24.04%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-16 (1-549) x AB094211 (1-412)
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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175

Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTTGTAATGCTTTGTATTCATGGCTCGCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195

Db         62 TCTTACACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215

Db        122 GAGTTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTGTCCAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235

Db        182 GCCCGCCATCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255

Db        242 ACACGTTTCATGAAGGATCTGCATTTTACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275

Db        302 GGTATCGCTCTTACACTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292

Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 125
AB094212
LOCUS       AB094212                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ3-1.
ACCESSION   AB094212
VERSION     AB094212.1  GI:29292679
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ3-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66235.1"
                     /db_xref="GI:29292680"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                    LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                    ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094212 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAAGAGGCTACTTCCGGTCTCGTAATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAACACACCTTACACTGGGGCATTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAACTTGACGCCCGGGAACACTAACACCCGTGTTTCCAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        242 ACACGTTTCATGAAGGATTTGCATTTTACCGGCACGAACGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCTCTGACACTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 126
AB094213
LOCUS       AB094213                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ3-2.
ACCESSION   AB094213
VERSION     AB094213.1  GI:29292681
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ3-2"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094213 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAAGAGGCTACTTCCGGTCTCGTAATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAACACACCTTACACTGGGGCATTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAACTTGACGCCCGGGAACACTAACACCCGTGTTTCCAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        242 ACACGTTTCATGAAGGATTTGCATTTTACCGGCACGAACGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCTCTGACACTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 127
AB094214
LOCUS       AB094214                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ3-3.
ACCESSION   AB094214
VERSION     AB094214.1  GI:29292683
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
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   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
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                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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                     /db_xref="GI:29292684"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094214 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCCGGTCTTGTAATGCTTTGCATTCACGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTACACTGGGGCATTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAACCTGACGCCCCGGGAACACTAACACCCGTGTCTCCAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||||   |||||||||||||||||||||||||||
Db        242 ACACGTTTCATGAAGGATTTGCATTTTACCGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCTCTGACACTGTTCAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 128
AB094215
LOCUS       AB094215                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ4-1.
ACCESSION   AB094215
VERSION     AB094215.1  GI:29292685
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
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                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /protein_id="BAC66238.1"
                     /db_xref="GI:29292686"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
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Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094215 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACTTCCGGTCTTGTGATGCTTTGTATTCATGGTTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAATCTGACACCCGGGAACACTAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACAGGTTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGTTTTATGAAAGATCTGCATTTTACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATTGCTCTGACACTGTTTAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 CTGATTTCGTCGGCTGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 129
AB094216
LOCUS       AB094216                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ5-1.
ACCESSION   AB094216
VERSION     AB094216.1  GI:29292687
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ5-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66239.1"
                     /db_xref="GI:29292688"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094216 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCCGAGGAGGAGGCGACATCGGGGCTGGTCATGCTTTGTATTCATGGTTCCCCTGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTACACCAACACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTCAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCTTGCGCCGTGGCGCCGACGGAACCGCCGAGCTTACGACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACTAATGGCGTTGGTGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATAGCTCTGACTTTATTCAACCTTGCTGATACACTTCTCGGCGGCTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGCCAGCTCTTTTACTCCCGTCCAGTCGTCTCG 412

RESULT 130
AB094217
LOCUS       AB094217                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ6-1.
ACCESSION   AB094217
VERSION     AB094217.1  GI:29292689
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ6-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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                     /protein_id="BAC66240.1"
                     /db_xref="GI:29292690"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
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Query Match:            24.04%      Indels:        0
DB:                     1           Gaps:          0

US-09-769-066-16 (1-549) x AB094217 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACTTCCGGTCTGGTAATGCTTTGTATTCACGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGCGCATTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      |||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAATCTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTCACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        242 ACACGATTCATGAAGGACTTGCACTTTACTGGCACAAACGGTGTTGGTGAGGTGGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACGCTATTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 131
AB094218
LOCUS       AB094218                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ6-2.
ACCESSION   AB094218
VERSION     AB094218.1  GI:29292691
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /mol_type="genomic RNA"
                     /isolate="swJ6-2"
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                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /note="ORF2"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094218 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACTTCCGGTCTGGTAATGCTTTGTATTCACGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGCGCATTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      |||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAATCTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTCACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGATTCATGAAGGACTTGCACTTTACTGGCACAAACGGTGTTGGTGAGGTGGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACGCTATTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 132
AB094238
LOCUS       AB094238                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ10-1.
ACCESSION   AB094238
VERSION     AB094238.1  GI:29292731
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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          Fax:81-285-44-1557)
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                     /db_xref="taxon:63421"
                     /country="Japan"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB094238 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACTTCCGGTCTGGTAATGCTTTGTATTCATGGCTCCCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGCGCATTGGGGCTCCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||     |||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGAAATCTGACACCTGGGAACACTAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGCCGCGGTGCCGATGGGACCGCTGAGCTCACCACCACAGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||||    |||||||||||||||||||||||||
Db        242 ACACGATTCATGAAGGACTTGCACTTTACTGGCACAAACGGTGTCGGTGAGGTGGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||    |||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACGCTATTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAATTGTTCTACTCCCGCCCTGTTGTCTCG 412

RESULT 133
AB094239
LOCUS       AB094239                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ10-2.
ACCESSION   AB094239
VERSION     AB094239.1  GI:29292733
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:63421"
                     /country="Japan"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB094239 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACTTCCGGTCTGGTAATGCTTTGTATTCATGGCTCCCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGCGCATTGGGGCTCCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||     |||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGAAATCTGACACCTGGGAACACTAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGCCGCGGTGCCGATGGGACCGCTGAGCTCACCACCACAGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||||    |||||||||||||||||||||||||
Db        242 ACACGATTCATGAAGGACTTGCACTTTACTGGCACAAACGGTGTCGGTGAGGTGGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||    |||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACGCTATTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAATTGTTCTACTCCCGCCCTGTTGTCTCG 412

RESULT 134
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AB094240
LOCUS       AB094240                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ11-1.
ACCESSION   AB094240
VERSION     AB094240.1  GI:29292735
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ11-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66263.1"
                     /db_xref="GI:29292736"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094240 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCYCCCGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAACACACCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||  ||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        242 ACACGCTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCCCTGACATTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 135
AB094241
LOCUS       AB094241                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ11-2.
ACCESSION   AB094241
VERSION     AB094241.1  GI:29292737
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ11-2"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66264.1"
                     /db_xref="GI:29292738"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094241 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCTCCYGTTAAT 61
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAACACACCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        242 ACACGCTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCCCTGACATTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412
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RESULT 136
AB094242
LOCUS AB094242 412 bp RNA linear VRL 27-MAR-2003
DEFINITION Swine hepatitis E virus ORF2 gene for capsid protein, partial cds, isolate:swJ11-3.
ACCESSION AB094242
VERSION AB094242.1 GI:29292739
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T., Tsuda,F. and Okamoto,H.
TITLE Swine hepatitis E virus strains in Japan form four phylogenetic clusters comparable with those of Japanese isolates of human hepatitis E virus
JOURNAL J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
PUBMED 12655086
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School, Immunology Division and Division of Molecular Virology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
FEATURES Location/Qualifiers
source 1. .412
/organism="Swine hepatitis E virus"
/virion
/mol_type="genomic RNA"
/isolate="swJ11-3"
/isolation_source="swine serum"
/specific_host="farm pig"
/db_xref="taxon:63421"
/country="Japan"
CDS <1. .>412
/note="ORF2"
/codon_start=2
/product="capsid protein"
/protein_id="BAC66265.1"
/db_xref="GI:29292740"
/translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

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Alignment Scores:
Pred. No.:              204          Length:          412
Score:                  132.00       Matches:         132
Percent Similarity:     96.35%       Conservative:    0
Best Local Similarity:  96.35%       Mismatches:      5
Query Match:            24.04%       Indels:          0
DB:                     1            Gaps:            0

US-09-769-066-16 (1-549) x AB094242 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAACACACCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        242 ACACGCTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCCCTGACATTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412
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RESULT 137
AB094243
LOCUS AB094243 412 bp RNA linear VRL 27-MAR-2003
DEFINITION Swine hepatitis E virus ORF2 gene for capsid protein, partial cds, isolate:swJ11-4.
ACCESSION AB094243
VERSION AB094243.1 GI:29292741
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T., Tsuda,F. and Okamoto,H.
TITLE Swine hepatitis E virus strains in Japan form four phylogenetic clusters comparable with those of Japanese isolates of human hepatitis E virus
JOURNAL J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
PUBMED 12655086
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School, Immunology Division and Division of Molecular Virology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
FEATURES Location/Qualifiers
source 1. .412
/organism="Swine hepatitis E virus"
/virion
/mol_type="genomic RNA"
/isolate="swJ11-4"
/isolation_source="swine serum"

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                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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                     /db_xref="GI:29292742"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB094243 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCTCCCGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAACACACCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        242 ACACGCTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCCCTGACATTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 138
AB094244
LOCUS       AB094244                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ11-5.
ACCESSION   AB094244
VERSION     AB094244.1  GI:29292743
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES              Location/Qualifiers
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                      /organism="Swine hepatitis E virus"
                      /virion
                      /mol_type="genomic RNA"
                      /isolate="swJ11-5"
                      /isolation_source="swine serum"
                      /specific_host="farm pig"
                      /db_xref="taxon:63421"
                      /country="Japan"
     CDS              <1. .>412
                      /note="ORF2"
                      /codon_start=2
                      /product="capsid protein"
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                      /db_xref="GI:29292744"
                      /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                      ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB094244 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCTCCCGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAACACACCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        242 ACACGCTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCCCTGACATTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 139
AB094245
LOCUS       AB094245                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ11-6.
ACCESSION   AB094245
VERSION     AB094245.1  GI:29292745
KEYWORDS    .
SOURCE      Swine hepatitis E virus
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  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ11-6"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66268.1"
                     /db_xref="GI:29292746"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    132.00          Matches:        132
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Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB094245 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCTCCCGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAACACACCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGCTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTGGGTCGT 301

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Db        302 GGTATCGCCCTGACATTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 140
AB094246
LOCUS       AB094246                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ11-7.
ACCESSION   AB094246
VERSION     AB094246.1  GI:29292747
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ11-7"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
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                     /protein_id="BAC66269.1"
                     /db_xref="GI:29292748"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB094246 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCTCCCGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGCTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 141
AB094247
LOCUS       AB094247                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ11-8.
ACCESSION   AB094247
VERSION     AB094247.1  GI:29292749
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
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Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0
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US-09-769-066-16 (1-549) x AB094247 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCTCCCGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAACACACCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Db        242 ACACGCTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   |||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCCCTGACATTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 142
AB094248
LOCUS       AB094248                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ11-9.
ACCESSION   AB094248
VERSION     AB094248.1  GI:29292751
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094248 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCTCCCGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAACACACCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGCTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCCCTGACATTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCTCGCCCTGTTGTCTCG 412

RESULT 143
AB094249
LOCUS       AB094249                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ11-10.
ACCESSION   AB094249
VERSION     AB094249.1  GI:29292753
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094249 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTAATGCTTTGTATTCATGGCTCTCCCGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAAYACACCTTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||    ||||||
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTTCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        242 ACACGCTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCCCTGACATTGTTTAATCTCGCTGAYACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 144
AB094250
LOCUS       AB094250                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ12-1.
ACCESSION   AB094250
VERSION     AB094250.1  GI:29292755
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
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           hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
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            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66273.1"
                     /db_xref="GI:29292756"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:                204          Length:         412
Score:                    132.00       Matches:        132
Percent Similarity:       96.35%       Conservative:   0
Best Local Similarity:    96.35%       Mismatches:     5
Query Match:              24.04%       Indels:         0
DB:                       1            Gaps:           0

US-09-769-066-16 (1-549) x AB094250 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAAGAGGAGGCAACATCGGGTCTGGTCATGCTCTGTATTCATGGTTCTCCCGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTACACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCTTACGTCGTGGCGCCGACGGAACTGCCGAGCTTACGACCACTGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGCTTCATGAAGGATCTGCATTTTACTGGGATGAATGGCGTTGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATAGCCCTAACTCTATTCAACCTTGCTGATACACTTCTTGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGAGGCCAGCTCTTTTACTCCCGCCCAGTCGTCTCG 412

RESULT 145
AB094251
LOCUS       AB094251                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ12-2.
ACCESSION   AB094251
VERSION     AB094251.1  GI:29292757
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ12-2"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66274.1"
                     /db_xref="GI:29292758"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204          Length:         412
Score:                    132.00       Matches:        132
Percent Similarity:       96.35%       Conservative:   0
Best Local Similarity:    96.35%       Mismatches:     5
Query Match:              24.04%       Indels:         0
DB:                       1            Gaps:           0

US-09-769-066-16 (1-549) x AB094251 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAAGAGGAGGCAACATCGGGTCTGGTCATGCTCTGTATTCATGGTTCTCCCGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCTTACGTCGTGGCGCCGACGGAACTGCCGAGCTTACGACCACTGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGCTTCATGAAGGATCTGCATTTTACTGGGATGAATGGCGTTGGCGAGGTGGGCCGT 301
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Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTCTATTCAACCTTGCTGATACACTTCTTGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGCCAGCTCTTTTACTCCCGCCCAGTCGTCTCG 412

RESULT 146
AB094252
LOCUS       AB094252                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ12-3.
ACCESSION   AB094252
VERSION     AB094252.1  GI:29292759
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
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                     /mol_type="genomic RNA"
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                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094252 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAAGAGGAGGCAACATCGGGTCTGGTCATGCTCTGTATTCATGGTTCTCCCGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         62 TCCTACACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||  ||||||
Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCTTACGTCGTGGCGCCGACGGAACTGCCGAGCTTACGACCACTGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        242 ACGCGCTTCATGAAGGATTTGCATTTTACTGGGATGAATGGCGTTGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTCTATTCAACCTTGCTGATACACTTCTTGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGCCAGCTCTTTTACTCCCGCCCAGTCGTCTCG 412

RESULT 147
AB094253
LOCUS       AB094253                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ12-4.
ACCESSION   AB094253
VERSION     AB094253.1  GI:29292761
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
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Percent Similarity:     96.35%          Conservative:  0
Best Local Similarity:  96.35%          Mismatches:    5
Query Match:            24.04%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-16 (1-549) x AB094253 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCAACATCGGGTCTGGTCATGCTCTGTATTCATGGTTCTCCCGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      |||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCTTACGTCGTGGCGCCGACGGAACTGCCGAGCTTACGACCACTGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGCTTCATGAAGGATCTGCATTTTACTGGGATGAATGGCGTTGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTCTATTCAACCTTGCTGATACACTTCTTGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGCCAGCTCTTTTACTCCCGCCCAGTCGTCTCG 412

RESULT 148
AB094256
LOCUS       AB094256                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-1.
ACCESSION   AB094256
VERSION     AB094256.1  GI:29292767
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:63421"
                     /country="Japan"
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Alignment Scores:
Pred. No.:              204             Length:        412
Score:                  132.00          Matches:       132
Percent Similarity:     96.35%          Conservative:  0
Best Local Similarity:  96.35%          Mismatches:    5
Query Match:            24.04%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-16 (1-549) x AB094256 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCCCTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGTCGTGGRGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        242 ACGCGTTTCATGAAGGACCTGCACTTTACTGGCACGAAYGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAACCTTGCTGATACACTTCTCGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 CTGATTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 149
AB094257
LOCUS       AB094257                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-2.
ACCESSION   AB094257
VERSION     AB094257.1  GI:29292769
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
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          Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
          Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
          Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:63421"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204          Length:          412
Score:                    132.00       Matches:         132
Percent Similarity:       96.35%       Conservative:    0
Best Local Similarity:    96.35%       Mismatches:      5
Query Match:              24.04%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-16 (1-549) x AB094257 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCTTACACTGGTGCCCTGGGGCTTCTTGATTTTGCAYTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGTCGTGGAGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        242 ACGCGTTTCATGAAGGACCTGCACTTTACTGGCACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAACCTTGCTGATACACTTCTCGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CTGATTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 150
AB094259
LOCUS       AB094259                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-4.
ACCESSION   AB094259
VERSION     AB094259.1  GI:29292773
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.

REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
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                     /isolate="swJ15-4"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
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                     /db_xref="GI:29292774"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204          Length:          412
Score:                    132.00       Matches:         132
Percent Similarity:       96.35%       Conservative:    0
Best Local Similarity:    96.35%       Mismatches:      5
Query Match:              24.04%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-16 (1-549) x AB094259 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCTCTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGTCGTGGAGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        242 ACGCGTTTCATGAAGGACCTGCACTTTACTGGCACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAACCTAGCTGATACACTTCTCGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 CTGATTTCGTCGGCCGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412
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RESULT 151
AB094260
LOCUS       AB094260                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-5.
ACCESSION   AB094260
VERSION     AB094260.1  GI:29292775
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ15-5"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
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                     /protein_id="BAC66283.1"
                     /db_xref="GI:29292776"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204          Length:        412
Score:                  132.00       Matches:       132
Percent Similarity:     96.35%       Conservative:  0
Best Local Similarity:  96.35%       Mismatches:    5
Query Match:            24.04%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-16 (1-549) x AB094260 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCCCTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        182 GCCCGCCATCGGCTGCGTCGTGGAGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        242 ACGCGTTTCATGAAGGACCTGCACTTTACTGGCACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAACCTTGCTGATACACTTCTCGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CTGATTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 152
AB094261
LOCUS       AB094261                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-6.
ACCESSION   AB094261
VERSION     AB094261.1  GI:29292777
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
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                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204          Length:        412
Score:                  132.00       Matches:       132
Percent Similarity:     96.35%       Conservative:  0
Best Local Similarity:  96.35%       Mismatches:    5
Query Match:            24.04%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-16 (1-549) x AB094261 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195

Db         62 TCCTATACTAATACACCTTACACTGGTGCCCTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215

Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235

Db        182 GCCCGCCATCGGCTGCGTCGTGGAGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255

Db        242 ACGCGTTTCATGAAGGACCTGCACTTTACTGGCACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275

Db        302 GGTATTGCTCTGACACTGTTCAACCTTGCTGATACACTTCTCGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292

Db        362 CTGATTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 153
AB094262
LOCUS       AB094262                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-7.
ACCESSION   AB094262
VERSION     AB094262.1  GI:29292779
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /db_xref="GI:29292780"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204          Length:          412
Score:                  132.00       Matches:         132
Percent Similarity:     96.35%       Conservative:    0
Best Local Similarity:  96.35%       Mismatches:      5
Query Match:            24.04%       Indels:          0
DB:                     1            Gaps:            0

US-09-769-066-16 (1-549) x AB094262 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175

Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195

Db         62 TCCTATACTAATACACCTTACACTGGTGCCCTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215

Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235

Db        182 GCCCGCCATCGGCTGCGTCGTGGAGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255

Db        242 ACGCGTTTCATGAAGGACCTGCACTTTACTGGCACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275

Db        302 GGTATTGCTCTGACACTGTTCAACCTTGCTGATACACTTCTCGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292

Db        362 CTGATTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 154
AB094263
LOCUS       AB094263                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-8.
ACCESSION   AB094263
VERSION     AB094263.1  GI:29292781
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
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                     /isolate="swJ15-8"
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Alignment Scores:
Pred. No.:              204           Length:         412
Score:                  132.00        Matches:        132
Percent Similarity:     96.35%        Conservative:   0
Best Local Similarity:  96.35%        Mismatches:     5
Query Match:            24.04%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AB094263 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACACCCGTGTGTCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGTCGTGGTGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        242 ACGCGATTCATGAAGGACCTGCACTTTACTGGCACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAACCTAGCTGATACGCTTCTCGGCGGACTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CTGATTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCG 412

RESULT 155
AB094264
LOCUS       AB094264                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-9.
ACCESSION   AB094264
VERSION     AB094264.1  GI:29292783
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086

REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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Alignment Scores:
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US-09-769-066-16 (1-549) x AB094264 (1-412)

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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-10.
ACCESSION   AB094265
VERSION     AB094265.1  GI:29292785
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KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              204          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
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US-09-769-066-16 (1-549) x AB094265 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        362 CTGATTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 157
AB094266
LOCUS       AB094266                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-11.
ACCESSION   AB094266
VERSION     AB094266.1  GI:29292787
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              204          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB094266 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        302 GGTATTGCTCTGACACTGTTCAACCTAGCTGATACACTTCTCGGCGGTCTGCCGACAGAA 361

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Db        362 CTGATTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 158
AB094267
LOCUS       AB094267                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
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ACCESSION   AB094267
VERSION     AB094267.1  GI:29292789
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
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REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
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  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
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Alignment Scores:
Pred. No.:              204          Length:        412
Score:                  132.00       Matches:       132
Percent Similarity:     96.35%       Conservative:  0
Best Local Similarity:  96.35%       Mismatches:    5
Query Match:            24.04%       Indels:        0

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US-09-769-066-16 (1-549) x AB094267 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTCTACTCCCGCCCTGTCGTCTCG 412

RESULT 159
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LOCUS       AB094268                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ16-2.
ACCESSION   AB094268
VERSION     AB094268.1  GI:29292791
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
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   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
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            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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Alignment Scores:
Pred. No.:                  204             Length:         412
Score:                      132.00          Matches:        132
Percent Similarity:         96.35%          Conservative:   0
Best Local Similarity:      96.35%          Mismatches:     5
Query Match:                24.04%          Indels:         0
DB:                         1               Gaps:           0

US-09-769-066-16 (1-549) x AB094268 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCCGGTCTCGTCATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATCGCTCTGACACTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTCTACTCCCGCCCTGTTGTCTCG 412

RESULT 160
AB094269
LOCUS       AB094269                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ16-3.
ACCESSION   AB094269
VERSION     AB094269.1  GI:29292793
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
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            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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FEATURES            Location/Qualifiers
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Alignment Scores:
Pred. No.:                  204             Length:         412
Score:                      132.00          Matches:        132
Percent Similarity:         96.35%          Conservative:   0
Best Local Similarity:      96.35%          Mismatches:     5
Query Match:                24.04%          Indels:         0
DB:                         1               Gaps:           0

US-09-769-066-16 (1-549) x AB094269 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCCGGTCTCGTCATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTACACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGCCGCGGTGCTGACGGGACTGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGTTTCATGAAGGATCTGCATTTCACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATCGCTCTGACACTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTCTACTCCCGCCCTGTTGTCTCG 412

RESULT 161
AB094270
LOCUS       AB094270                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ16-4.
ACCESSION   AB094270
VERSION     AB094270.1  GI:29292795
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
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  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
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                     /isolate="swJ16-4"
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                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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                     /db_xref="GI:29292796"
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Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094270 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCCGGTCTCGTCATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGCCGCGGTGCTGACGGGACTGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGTTTCATGAAGGATCTGCATTTCACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATCGCTCTGACACTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTCTACTCCCGCCCTGTTGTCTCG 412

RESULT 162
AB094271
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LOCUS       AB094271                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ16-5.
ACCESSION   AB094271
VERSION     AB094271.1  GI:29292797
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
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                     /isolate="swJ16-5"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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                     /db_xref="GI:29292798"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094271 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCCACCTCCGGTCTCGTAATGCTTTGCATCCACGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGCCGTGGTGCTGATGGGACTGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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                 ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        242 ACACGTTTCATGAAGGATCTGCATTTCACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                 ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCTCTGACACTGTTCAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                 ||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CTGATTTCGTCGGCTGGGGGTCAACTATTCTACTCCCGCCCTGTTGTCTCG 412

RESULT 163
AB094272
LOCUS       AB094272                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ17-1.
ACCESSION   AB094272
VERSION     AB094272.1  GI:29292799
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
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Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094272 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTCGTTATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||   ||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAACTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTACACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGTTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGTTTCATGAAGGATCTGCATTTCACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTTAATCTTGCTGATACGCTCCTTGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 164
AB094273
LOCUS       AB094273                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ17-2.
ACCESSION   AB094273
VERSION     AB094273.1  GI:29292801
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
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Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094273 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTCGTTATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAACTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTACACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGTTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        242 ACACGTTTCATGAAGGATCTGCATTTCACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTTAATCTTGCTGATACGCTCCTTGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 165
AB094274
LOCUS       AB094274                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ17-3.
ACCESSION   AB094274
VERSION     AB094274.1  GI:29292803
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094274 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTCGTTATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAACTTGACACCCGGGAACACCAACACCCGTGTTTCCAGGTACACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGTTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        242 ACACGTTTCATGAAGGATCTGCATTTCACTGGCACGAACGGCGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTTAATCTTGCTGATACGCTCCTTGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAATTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 166
AB094276
LOCUS       AB094276                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ18-2.
ACCESSION   AB094276
VERSION     AB094276.1  GI:29292807
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
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  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ18-2"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66299.1"
                     /db_xref="GI:29292808"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB094276 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||      ||||||||||||||||||||||||||||||||||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGCCGTGGTGCCGACGGGACTGCCGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAGGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 167
AB094277
LOCUS       AB094277                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ18-3.
ACCESSION   AB094277
VERSION     AB094277.1  GI:29292809
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ18-3"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66300.1"
                     /db_xref="GI:29292810"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB094277 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||      ||||||||||||||||||||||||||||||||||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCCGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAGGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 168
AB094278
LOCUS       AB094278                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ18-4.
ACCESSION   AB094278
VERSION     AB094278.1  GI:29292811
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ18-4"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66301.1"
                     /db_xref="GI:29292812"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094278 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCCGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAGGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 169
AB094279
LOCUS       AB094279                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ19-1.
ACCESSION   AB094279
VERSION     AB094279.1  GI:29292813
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
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                     /country="Japan"
     CDS             <1. .>412
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Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094279 (1-412)
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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTTTGGTGATGCTTTGCATCCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTTGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||     |||||||||||||||||||||||||||    ||||||
Db        122 GAGTTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGTCGTGGCGCCGATGGGACAGCTGAGCTTACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||    |||||||||||||||||||||||||
Db        242 ACACGTTTCATGAAGGACTTGCATTTTACTGGTACGAATGGGGTTGGTGAGGTGGGTCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTTTGACATTGTTCAATCTTGCTGATACGCTTCTCGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCG 412
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RESULT 170
AB094280
LOCUS AB094280 412 bp RNA linear VRL 27-MAR-2003
DEFINITION Swine hepatitis E virus ORF2 gene for capsid protein, partial cds, isolate:swJ19-2.
ACCESSION AB094280
VERSION AB094280.1 GI:29292815
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T., Tsuda,F. and Okamoto,H.
TITLE Swine hepatitis E virus strains in Japan form four phylogenetic clusters comparable with those of Japanese isolates of human hepatitis E virus
JOURNAL J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
PUBMED 12655086
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School, Immunology Division and Division of Molecular Virology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
FEATURES Location/Qualifiers
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/organism="Swine hepatitis E virus"
/virion
/mol_type="genomic RNA"
/isolate="swJ19-2"
/isolation_source="swine serum"
/specific_host="farm pig"
/db_xref="taxon:63421"
/country="Japan"
CDS <1. .>412
/note="ORF2"
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/db_xref="GI:29292816"
/translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:

Pred. No.:	204	Length:	412
Score:	132.00	Matches:	132
Percent Similarity:	96.35%	Conservative:	0
Best Local Similarity:	96.35%	Mismatches:	5
Query Match:	24.04%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AB094280 (1-412)

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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTTTGGTGATGCTTTGCATCCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTTGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||     |||||||||||||||||||||||||||    ||||||
Db        122 GAGTTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGTCGTGGCGCCGATGGGACAGCTGAGCTTACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||    |||||||||||||||||||||||||
Db        242 ACACGTTTCATGAAGGACTTGCATTTTACTGGTACGAATGGGGTTGGTGAGGTGGGTCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTTTGACATTGTTCAATCTTGCTGATACGCTTCTCGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCG 412
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RESULT 171
AB094281
LOCUS AB094281 412 bp RNA linear VRL 27-MAR-2003
DEFINITION Swine hepatitis E virus ORF2 gene for capsid protein, partial cds, isolate:swJ19-3.
ACCESSION AB094281
VERSION AB094281.1 GI:29292817
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T., Tsuda,F. and Okamoto,H.
TITLE Swine hepatitis E virus strains in Japan form four phylogenetic clusters comparable with those of Japanese isolates of human hepatitis E virus
JOURNAL J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
PUBMED 12655086
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School, Immunology Division and Division of Molecular Virology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              204             Length:         412
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Best Local Similarity:  96.35%          Mismatches:     5
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US-09-769-066-16 (1-549) x AB094281 (1-412)

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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ19-4.
ACCESSION   AB094282
VERSION     AB094282.1  GI:29292819
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
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US-09-769-066-16 (1-549) x AB094282 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
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SOURCE      Swine hepatitis E virus
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            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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Alignment Scores:
Pred. No.:              204          Length:        412
Score:                  132.00       Matches:       132
Percent Similarity:     96.35%       Conservative:  0
Best Local Similarity:  96.35%       Mismatches:    5
Query Match:            24.04%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-16 (1-549) x AB094283 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTTTGGTGATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        302 GGTATTGCTCTGACATTGTTCAATCTTGCTGATACGCTTCTCGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCG 412

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LOCUS       AB094284                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
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VERSION     AB094284.1  GI:29292823
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
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REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
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Alignment Scores:
Pred. No.:              204          Length:        412
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Best Local Similarity:  96.35%       Mismatches:    5
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US-09-769-066-16 (1-549) x AB094284 (1-412)

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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        242 ACACGYTTCATGAAGGACTTGCATTTTACTGGTACGAATGGGGTTGGTGAGGTGGGTCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATTGCTYTGACATTGTTCAATCTTGCTGATACGCTTCTCGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCG 412

RESULT 175
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LOCUS       AB094285                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
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ACCESSION   AB094285
VERSION     AB094285.1  GI:29292825
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
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Alignment Scores:
Pred. No.:              204          Length:        412
Score:                  132.00       Matches:       132
Percent Similarity:     96.35%       Conservative:  0
Best Local Similarity:  96.35%       Mismatches:    5
Query Match:            24.04%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-16 (1-549) x AB094285 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTTTGGTGATGCTTTGCATCCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGTCGTGGCGCCGATGGGACAGCTGAGCTTACCACCACGGCTGCC 241

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Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATTGCTTTGACATTGTTCAATCTTGCTGATACGCTTCTCGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCG 412

RESULT 176
AB094286
LOCUS       AB094286                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ19-8.
ACCESSION   AB094286
VERSION     AB094286.1  GI:29292827
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
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  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
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            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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                ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
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Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094286 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTTTGGTGATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTTGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGTCGTGGCGCTGATGGGACAGCTGAGCTTACCACCACGGCCGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGCTTCATGAAGGACTTGCATTTTACTGGTACGAATGGGGTTGGTGAGGTGGGTCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACATTGTTCAATCTTGCTGATACGCTTCTCGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCG 412

RESULT 177
AB094287
LOCUS       AB094287                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ19-9.
ACCESSION   AB094287
VERSION     AB094287.1  GI:29292829
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES            Location/Qualifiers
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                    /organism="Swine hepatitis E virus"
                    /virion
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                    /specific_host="farm pig"
                    /db_xref="taxon:63421"
                    /country="Japan"
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                    /codon_start=2
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                    /db_xref="GI:29292830"
                    /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                    ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094287 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTTTGGTGATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAATACACCTTACACTGGTGCACTTGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||    ||||||
Db        122 GAGTTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGTCGTGGCGCTGATGGGACAGCTGAGCTTACCACCACGGCYGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        242 ACACGCTTCATGAAGGACTTGCATTTTACTGGTACGAATGGGGTTGGTGAGGTGGGTCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACATTGTTCAATCTTGCTGATACGCTTCTCGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCG 412

RESULT 178
AB094288
LOCUS       AB094288                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ19-10.
ACCESSION   AB094288
VERSION     AB094288.1  GI:29292831
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
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  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ19-10"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /db_xref="GI:29292832"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094288 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTTTGGTGATGCTTTGCATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTTGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAGTTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGTCGTGGCGCTGATGGGACAGCTGAGCTTACCACCACGGCCGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        242 ACACGCTTCATGAAGGACTTGCATTTTACTGGTACGAATGGGGTTGGTGAGGTGGGTCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATTGCTCTGACATTGTTCAATCTTGCTGATACGCTTCTCGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCG 412
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RESULT 179
AB094290
LOCUS       AB094290                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ20-1.
ACCESSION   AB094290
VERSION     AB094290.1  GI:29292835
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
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                     /db_xref="taxon:63421"
                     /country="Japan"
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Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094290 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCCGGTTTGGTAATGCTTTGCATTCATGGGTCCCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTACGCCGCGGTGCCGACGGGACCGCTGAGCTTACTACCACAGCAGCC 241
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Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGTTTTATGAAGGATCTGCACTTTACCGGTACGAATGGCGTTGGTGAGGTGGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATTGCCCTGACACTGTTTAATCTTGCCGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCCGTTGTCTCG 412

RESULT 180
AB094291
LOCUS       AB094291                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ20-2.
ACCESSION   AB094291
VERSION     AB094291.1  GI:29292837
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094291 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCCGGTTTGGTAATGCTTTGCATTCATGGGTCCCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||  ||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTACGCCGCGGTGCCGACGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGTTTTATGAAGGATCTGCACTTTACCGGTACGAATGGCGTTGGTGAGGTGGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCCCTGACACTGTTTAATCTTGCCGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCCGTTGTCTCG 412

RESULT 181
AB094292
LOCUS       AB094292                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ20-3.
ACCESSION   AB094292
VERSION     AB094292.1  GI:29292839
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094292 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCCGGTTTGGTAATGCTTTGCATTCATGGGTCCCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      |||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTACGCCGCGGTGCCGACGGGACCGCTGAGCTTACTACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||||||   |||||||||||||||||||||||
Db        242 ACACGTTTTATGAAGGATCTGCACTTTACCGGTACGAATGGCGTTGGTGAGGTGGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCCCTGACACTGTTTAATCTTGCCGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCCGTTGTCTCG 412

RESULT 182
AB094293
LOCUS       AB094293                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-1.
ACCESSION   AB094293
VERSION     AB094293.1  GI:29292841
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ22-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66316.1"
                     /db_xref="GI:29292842"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094293 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      |||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATCTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||||||   |||||||||||||||||||||||
Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACATTGTTCAATCTTGCTGACACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCA 412

RESULT 183
AB094294
LOCUS       AB094294                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-2.
ACCESSION   AB094294
VERSION     AB094294.1  GI:29292843
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
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  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ22-2"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66317.1"
                     /db_xref="GI:29292844"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB094294 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATCTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACATTGTTCAATCTTGCTGACACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCA 412

RESULT 184
AB094295
LOCUS       AB094295                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-3.
ACCESSION   AB094295
VERSION     AB094295.1  GI:29292845
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
  PUBMED    12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ22-3"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /db_xref="GI:29292846"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB094295 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTYTGACATTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTGCCGACAGAA 361
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Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 185
AB094296
LOCUS       AB094296                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-4.
ACCESSION   AB094296
VERSION     AB094296.1  GI:29292847
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
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                     /country="Japan"
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Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094296 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACYGGTGCATTGGGMCTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAATYTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACATTGTTCAATCTTGCTGAYACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCA 412

RESULT 186
AB094298
LOCUS       AB094298                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-6.
ACCESSION   AB094298
VERSION     AB094298.1  GI:29292851
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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     CDS             <1. .>412
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                     /db_xref="GI:29292852"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0
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US-09-769-066-16 (1-549) x AB094298 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||      |||||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACATTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 187
AB094299
LOCUS       AB094299                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-7.
ACCESSION   AB094299
VERSION     AB094299.1  GI:29292853
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ22-7"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66322.1"
                     /db_xref="GI:29292854"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094299 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||      |||||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACATTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 188
AB094301
LOCUS       AB094301                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-9.
ACCESSION   AB094301
VERSION     AB094301.1  GI:29292857
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ22-9"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66324.1"
                     /db_xref="GI:29292858"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB094301 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATCTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACATTGTTCAATCTTGCTGACACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCA 412

RESULT 189
AB094302
LOCUS       AB094302                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-10.
ACCESSION   AB094302
VERSION     AB094302.1  GI:29292859
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
  PUBMED    12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ22-10"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66325.1"
                     /db_xref="GI:29292860"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB094302 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACATTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCA 412

RESULT 190
AB094303
LOCUS       AB094303                412 bp    RNA     linear   VRL 27-MAR-2003
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DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-11.
ACCESSION   AB094303
VERSION     AB094303.1  GI:29292861
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ22-11"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204          Length:        412
Score:                    132.00       Matches:       132
Percent Similarity:       96.35%       Conservative:  0
Best Local Similarity:    96.35%       Mismatches:    5
Query Match:              24.04%       Indels:        0
DB:                       1            Gaps:          0

US-09-769-066-16 (1-549) x AB094303 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACATTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCA 412

RESULT 191
AB094304
LOCUS       AB094304                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-12.
ACCESSION   AB094304
VERSION     AB094304.1  GI:29292863
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ22-12"
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                     /country="Japan"
     CDS             <1. .>412
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                     /codon_start=2
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                     /protein_id="BAC66327.1"
                     /db_xref="GI:29292864"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204          Length:        412
Score:                    132.00       Matches:       132
Percent Similarity:       96.35%       Conservative:  0
Best Local Similarity:    96.35%       Mismatches:    5
Query Match:              24.04%       Indels:        0
DB:                       1            Gaps:          0

US-09-769-066-16 (1-549) x AB094304 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 TCTTATACTAATACACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGCTT 121

Qy         196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
                |||||||||||||||||||      |||||||||||||||||||||||||||    ||||||
Db         122 GAATTTAGGAATTTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy         216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy         236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
                |||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Db         242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy         256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                |||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db         302 GGCATTGCTCTGACATTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy         276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCA 412

RESULT 192
AB094305
LOCUS       AB094305                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ23-1.
ACCESSION   AB094305
VERSION     AB094305.1  GI:29292865
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ23-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /note="ORF2"
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                     /product="capsid protein"
                     /protein_id="BAC66328.1"
                     /db_xref="GI:29292866"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              204           Length:        412
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Score:                  132.00        Matches:       132
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Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094305 (1-412)

Qy         156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db           2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCTCCCGTTAAT 61

Qy         176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db          62 TCTTACACTAATACACCCTACACTGGTGCACTTGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy         196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db         122 GAATTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy         216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db         182 GCCCGCCATCGGCTGCGTCGTGGCGCCGATGGGACCGCTGAGCTCACCACCACGGCGGCT 241

Qy         236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db         242 ACTCGTTTCATGAAGGACCTGCACTTTACCGGCACGAATGGGGTTGGCGAGGTGGGTAGA 301

Qy         256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db         302 GGTATTGCTCTGACATTGTTCAATCTTGCTGATACGCTTCTCGGCGGTCTGCCGACAGAA 361

Qy         276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db         362 TTGATTTCGTCGGCCGGGGGTCAGTTATTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 193
AB094306
LOCUS       AB094306                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-1.
ACCESSION   AB094306
VERSION     AB094306.1  GI:29292867
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ24-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
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                /country="Japan"
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                /db_xref="GI:29292868"
                /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094306 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATTCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAATACACCCTATACTGGTGCACTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATTGCCTTGACACTTTTTAATCTTGCTGACACGCTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 194
AB094307
LOCUS       AB094307                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-2.
ACCESSION   AB094307
VERSION     AB094307.1  GI:29292869
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES            Location/Qualifiers
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                    /organism="Swine hepatitis E virus"
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                    /db_xref="taxon:63421"
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Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094307 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATTCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCACTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||      ||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATTGCCTTGACACTTTTTAATCTTGCTGACACGCTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 195
AB094308
LOCUS       AB094308                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-3.
ACCESSION   AB094308
VERSION     AB094308.1  GI:29292871
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
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          Hepevirus.
REFERENCE 1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE 2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
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                     /db_xref="taxon:63421"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204           Length:         412
Score:                  132.00        Matches:        132
Percent Similarity:     96.35%        Conservative:   0
Best Local Similarity:  96.35%        Mismatches:     5
Query Match:            24.04%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AB094308 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATCCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCACTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCCTTGACACTTTTYAATCTTGCTGACACGCTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 196
AB094309
LOCUS       AB094309                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-4.
ACCESSION   AB094309
VERSION     AB094309.1  GI:29292873
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              204           Length:         412
Score:                  132.00        Matches:        132
Percent Similarity:     96.35%        Conservative:   0
Best Local Similarity:  96.35%        Mismatches:     5
Query Match:            24.04%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AB094309 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATTCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCGCTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATTGCCTTGACACTTTTTAATCTTGCTGACACGCTCCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 197
AB094310
LOCUS       AB094310                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-5.
ACCESSION   AB094310
VERSION     AB094310.1  GI:29292875
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              204          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB094310 (1-412)
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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATTCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAATACACCCTATACTGGTGCRCTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
                ||||||||||||||||||  ||||||||||||||||||||||||||||||  ||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTATCCCGATAYACTAGYACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
                |||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        242 ACACGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCCTTGACACTTTTTAATCTTGCTGACACGCTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 198
AB094311
LOCUS       AB094311                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-6.
ACCESSION   AB094311
VERSION     AB094311.1  GI:29292877
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ24-6"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66334.1"
                     /db_xref="GI:29292878"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094311 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATTCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCACTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAAYTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCCTTGACACTTTTTAATCTTGCTGACACGCTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 199
AB094312
LOCUS       AB094312                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-7.
ACCESSION   AB094312
VERSION     AB094312.1  GI:29292879
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ24-7"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66335.1"
                     /db_xref="GI:29292880"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094312 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATTCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCACTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        242 ACACGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCCTTGACACTTTTTAATCTTGCTGACACGCTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 200
AB094313
LOCUS       AB094313                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-8.
ACCESSION   AB094313
VERSION     AB094313.1  GI:29292881
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
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   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
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                     /db_xref="taxon:63421"
                     /country="Japan"
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Alignment Scores:
Pred. No.:                204          Length:         412
Score:                    132.00       Matches:        132
Percent Similarity:       96.35%       Conservative:   0
Best Local Similarity:    96.35%       Mismatches:     5
Query Match:              24.04%       Indels:         0
DB:                       1            Gaps:           0

US-09-769-066-16 (1-549) x AB094313 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATTCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCRCTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATYTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGAYGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        242 ACACGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCCTTGACACTTTTTAATCTTGCTGACACGCTYCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 201
AB094314
LOCUS       AB094314                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-9.
ACCESSION   AB094314
VERSION     AB094314.1  GI:29292883
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
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                     /db_xref="GI:29292884"
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Alignment Scores:
Pred. No.:                204          Length:         412
Score:                    132.00       Matches:        132
Percent Similarity:       96.35%       Conservative:   0
Best Local Similarity:    96.35%       Mismatches:     5
Query Match:              24.04%       Indels:         0
DB:                       1            Gaps:           0

US-09-769-066-16 (1-549) x AB094314 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATTCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCACTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        242 ACACGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATTGCCTTGACACTTTTTAATCTTGCTGACACGCTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 202
AB094315
LOCUS       AB094315                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-10.
ACCESSION   AB094315
VERSION     AB094315.1  GI:29292885
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /country="Japan"
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                     /db_xref="GI:29292886"
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Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094315 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATTCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCACTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||  ||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGRACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        242 ACACGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCCTTGACACTTTTTAATCTTGCTGACACGCTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 203
AB094316
LOCUS       AB094316                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ24-11.
ACCESSION   AB094316
VERSION     AB094316.1  GI:29292887
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ24-11"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66339.1"
                     /db_xref="GI:29292888"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
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Query Match:            24.04%      Indels:        0
DB:                     1           Gaps:          0

US-09-769-066-16 (1-549) x AB094316 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTAATGCTCTGTATTCATGGTTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCACTGGGACTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACACGTTTTATGAAGGACCTGCATTTCACTGGTACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCCTTGACACTTTTTAATCTTGCTGACACGCTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 204
AB094317
LOCUS       AB094317                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-1.
ACCESSION   AB094317
VERSION     AB094317.1  GI:29292889
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66340.1"
                     /db_xref="GI:29292890"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094317 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTRGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||      |||||||||||||||||||||||||||   ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||||      |||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 205
AB094318
LOCUS       AB094318                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-2.
ACCESSION   AB094318
VERSION     AB094318.1  GI:29292891
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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          Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-2"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66341.1"
                     /db_xref="GI:29292892"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204          Length:        412
Score:                  132.00       Matches:       132
Percent Similarity:     96.35%       Conservative:  0
Best Local Similarity:  96.35%       Mismatches:    5
Query Match:            24.04%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-16 (1-549) x AB094318 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 206
AB094319
LOCUS       AB094319                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-3.
ACCESSION   AB094319
VERSION     AB094319.1  GI:29292893
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
  PUBMED    12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-3"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
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                     /db_xref="GI:29292894"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204          Length:        412
Score:                  132.00       Matches:       132
Percent Similarity:     96.35%       Conservative:  0
Best Local Similarity:  96.35%       Mismatches:    5
Query Match:            24.04%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-16 (1-549) x AB094319 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACYAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRCGGCGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACRCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 207
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AB094321
LOCUS       AB094321                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-5.
ACCESSION   AB094321
VERSION     AB094321.1  GI:29292897
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-5"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66344.1"
                     /db_xref="GI:29292898"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB094321 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||    ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCCGTCGTCTCA 412

RESULT 208
AB094322
LOCUS       AB094322                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-6.
ACCESSION   AB094322
VERSION     AB094322.1  GI:29292899
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-6"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66345.1"
                     /db_xref="GI:29292900"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB094322 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACAGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 209
AB094323
LOCUS       AB094323                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-7.
ACCESSION   AB094323
VERSION     AB094323.1  GI:29292901
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-7"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66346.1"
                     /db_xref="GI:29292902"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              204          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB094323 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTYAGGAATTTAACYCCCGGGAACACTAACACCCGTGTATCCCGATATACYAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRCGGCGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACRCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 210
AB094324
LOCUS       AB094324                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-8.
ACCESSION   AB094324
VERSION     AB094324.1  GI:29292903
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Swine hepatitis E virus"
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                     /isolation_source="swine serum"
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                     /specific_host="farm pig"
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Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094324 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||  ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACYAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 211
AB094325
LOCUS       AB094325                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-9.
ACCESSION   AB094325
VERSION     AB094325.1  GI:29292905
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES              Location/Qualifiers
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                      /country="Japan"
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                      ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094325 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTCAGGAATTTAACTCCCGGGAACACTAACACCCGTGTATCCCGATATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACACTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 212
AB094327
LOCUS       AB094327                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-11.
ACCESSION   AB094327
VERSION     AB094327.1  GI:29292909
KEYWORDS    .
SOURCE      Swine hepatitis E virus
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  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094327 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCCGTCGTCTCA 412

RESULT 213
AB094328
LOCUS       AB094328                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-12.
ACCESSION   AB094328
VERSION     AB094328.1  GI:29292911
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
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            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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     CDS             <1. .>412
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                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66351.1"
                     /db_xref="GI:29292912"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094328 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACAGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 214
AB094329
LOCUS       AB094329                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-13.
ACCESSION   AB094329
VERSION     AB094329.1  GI:29292913
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-13"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66352.1"
                     /db_xref="GI:29292914"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0
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US-09-769-066-16 (1-549) x AB094329 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCAYGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAAYACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||   ||||||||||||||||||||||||||||||   ||||||
Db        122 GAATTCAGGAATTTAACYCCCGGGAACACTAACACCCGTGTATCCCGATATACYAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACRCTACTYGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 215
AB094330
LOCUS       AB094330                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-14.
ACCESSION   AB094330
VERSION     AB094330.1  GI:29292915
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
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                     /isolate="swJ25-14"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /codon_start=2
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094330 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAAYACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTCAGGAATTTAACYCCCGGGAACACTAACACCCGTGTATCCCGATATACYAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCAYCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRGCRGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACRCTACTYGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 216
AB094331
LOCUS       AB094331                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-15.
ACCESSION   AB094331
VERSION     AB094331.1  GI:29292917
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /virion
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                     /isolate="swJ25-15"
                     /isolation_source="swine serum"
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                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /note="ORF2"
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094331 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTMTCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 217
AB094332
LOCUS       AB094332                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-16.
ACCESSION   AB094332
VERSION     AB094332.1  GI:29292919
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
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          hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /db_xref="GI:29292920"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB094332 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTCAGGAATTTAACYCCCGGGAACACTAACACCCGTGTATCCCGATATACYAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRCGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACRCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 218
AB094333
LOCUS       AB094333                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-17.
ACCESSION   AB094333
VERSION     AB094333.1  GI:29292921
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /country="Japan"
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Alignment Scores:
Pred. No.:              204          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB094333 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAACACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301
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Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTACTTGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 219
AB094334
LOCUS       AB094334                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-18.
ACCESSION   AB094334
VERSION     AB094334.1  GI:29292923
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-18"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66357.1"
                     /db_xref="GI:29292924"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
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Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094334 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||  ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTRTCCCGATATACYAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACRCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 220
AB094335
LOCUS       AB094335                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-19.
ACCESSION   AB094335
VERSION     AB094335.1  GI:29292925
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-19"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66358.1"
                     /db_xref="GI:29292926"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
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Percent Similarity:     96.35%          Conservative:  0
Best Local Similarity:  96.35%          Mismatches:    5
Query Match:            24.04%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-16 (1-549) x AB094335 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||    ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTRTCCCGATATACYAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACRCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 221
AB094336
LOCUS       AB094336                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-20.
ACCESSION   AB094336
VERSION     AB094336.1  GI:29292927
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-20"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
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                     /product="capsid protein"
                     /protein_id="BAC66359.1"
                     /db_xref="GI:29292928"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:        412
Score:                  132.00          Matches:       132
Percent Similarity:     96.35%          Conservative:  0
Best Local Similarity:  96.35%          Mismatches:    5
Query Match:            24.04%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-16 (1-549) x AB094336 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||    ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACRCTACTTGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 222
AB094337
LOCUS       AB094337                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-21.
ACCESSION   AB094337
VERSION     AB094337.1  GI:29292929
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
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           Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
           Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
           Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
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                     /db_xref="taxon:63421"
                     /country="Japan"
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Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094337 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCCTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||   ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACAGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGATACGCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 223
AB094338
LOCUS       AB094338                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-22.
ACCESSION   AB094338
VERSION     AB094338.1  GI:29292931
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /organism="Swine hepatitis E virus"
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                     /country="Japan"
     CDS             <1. .>412
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094338 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||   ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTRTCCCGATATACYAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRCGGCCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACRCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412
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RESULT 224
AB094339
LOCUS       AB094339                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-23.
ACCESSION   AB094339
VERSION     AB094339.1  GI:29292933
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-23"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66362.1"
                     /db_xref="GI:29292934"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB094339 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||  ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 225
AB105891
LOCUS       AB105891                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JA15.
ACCESSION   AB105891
VERSION     AB105891.1  GI:34097983
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JA15"
                     /isolation_source="human serum"
                     /db_xref="taxon:12461"
                     /country="Japan:Hokkaido"
                     /note="genotype III; sporadic acute hepatitis E"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC82168.1"
                     /db_xref="GI:34097984"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204             Length:         412
Score:                    132.00          Matches:        132
Percent Similarity:       96.35%          Conservative:   0
Best Local Similarity:    96.35%          Mismatches:     5
Query Match:              24.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB105891 (1-412)
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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTGGTAATGCTTTGYATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAATCTGACACCCGGGAACACAAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCACCGGCTGCGCCGCGGTGCTGATGGGACTGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        242 ACACGTTTCATGAAGGATTTACATTTTACTGGCACGAATGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCTYTGACATTGTTTAATCTCGCTGACACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCG 412
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RESULT 226
AB105892
LOCUS AB105892 412 bp RNA linear VRL 22-AUG-2003
DEFINITION Hepatitis E virus ORF2 gene for capsid protein, partial cds, isolate:HE-JA16.
ACCESSION AB105892
VERSION AB105892.1 GI:34097985
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N., Gotanda,Y. and Okamoto,H.
TITLE Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be food-borne, as suggested by the presence of hepatitis E virus in pig liver as food
JOURNAL J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
PUBMED 12917455
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School, Immunology Division and Division of Molecular Virology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
FEATURES Location/Qualifiers
source 1. .412
/organism="Hepatitis E virus"
/virion
/mol_type="genomic RNA"
/isolate="HE-JA16"
/isolation_source="human serum"
/db_xref="taxon:12461"
/country="Japan:Hokkaido"
/note="genotype III; sporadic acute hepatitis E"
gene 1. .412
/gene="ORF2"
CDS <1. .>412
/gene="ORF2"
/codon_start=2
/product="capsid protein"
/protein_id="BAC82169.1"
/db_xref="GI:34097986"
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ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:

Pred. No.:	204	Length:	412
Score:	132.00	Matches:	132
Percent Similarity:	96.35%	Conservative:	0
Best Local Similarity:	96.35%	Mismatches:	5
Query Match:	24.04%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AB105892 (1-412)

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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCCGAGGAGGAGGCTACTTCTGGTCTGGTAATGCTTTGTATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAATCTGACACCCGGGAACACAAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGTTTCATGAAGGATTTACATTTTACTGGCACGAACGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATCGCCCTGACATTGTTTAATCTCGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTTTACTCCCGCCCTGTTGTCTCG 412
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RESULT 227
AB105898
LOCUS AB105898 412 bp RNA linear VRL 22-AUG-2003
DEFINITION Swine hepatitis E virus ORF2 gene for capsid protein, partial cds, isolate:swJL82.
ACCESSION AB105898
VERSION AB105898.1 GI:34097997
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N., Gotanda,Y. and Okamoto,H.
TITLE Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be food-borne, as suggested by the presence of hepatitis E virus in pig liver as food
JOURNAL J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
PUBMED 12917455
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School, Immunology Division and Division of Molecular Virology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
FEATURES Location/Qualifiers

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                     /country="Japan:Hokkaido"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB105898 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTAGTGATGCTTTGCATTCATGGCTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCTTACACTGGTGCACTGGGGCTTCTCGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||  ||||||
Db        122 GAGTTTAGGAATTTGACACCCGGGAACACTAATACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGTCGTGGTGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGTTTTATGAAAGATCTGCACTTTACTGGCACAAATGGGGTTGGTGAGGTTGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACATTGTTTAACCTTGCTGATACGCTTCTCGGTGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGCTGTTCTACTCCCGCCCTGTCGTCTCG 412

RESULT 228
AB105899
LOCUS       AB105899                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJL97.
ACCESSION   AB105899
VERSION     AB105899.1  GI:34097999
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /country="Japan:Hokkaido"
                     /note="genotype III"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB105899 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGCCTGGTGATGCTTTGCATTCATGGCTCCCCCGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACGCCCTATACTGGTGCACTAGGGCTTCTTGATTTCGCATTAGAGCTC 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||  ||||||
Db        122 GAATTTAGGAATTTAACACCCGGGAACACCAACACCCGTGTATCCCGATATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGAGGTGCCGACGGGACCGCTGAGCTCACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGTTTTATGAAGGACCTGCATTTCACCGGCACGAATGGGGTCGGTGAAGTCGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACGCTGTTCAATCTAGCTGACACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 229
AB105900
LOCUS       AB105900                 412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJL98.
ACCESSION   AB105900
VERSION     AB105900.1  GI:34098001
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJL98"
                     /isolation_source="pig liver"
                     /specific_host="swine"
                     /db_xref="taxon:63421"
                     /country="Japan:Hokkaido"
                     /note="genotype III"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC82177.1"
                     /db_xref="GI:34098002"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB105900 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGCCTGGTGATGCTTTGCATTCATGGCTCCCCCGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAATACGCCCTATACTGGTGCACTAGGGCTTCTTGATTTCGCATTAGAGCTC 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTAACACCCGGGAACACCAACACCCGTGTATCCCGATATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGAGGTGCCGACGGGACCGCTGAGCTCACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGTTTTATGAAGGACCTGCATTTCACCGGCACGAATGGGGTCGGTGAAGTCGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATTGCTCTGACGCTGTTCAATCTAGCTGACACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 230
AB105901
LOCUS       AB105901                 412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJL131.
ACCESSION   AB105901
VERSION     AB105901.1  GI:34098003
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /isolate="swJL131"
                     /isolation_source="pig liver"
                     /specific_host="swine"
                     /db_xref="taxon:63421"
                     /country="Japan:Hokkaido"
                     /note="genotype III"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
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                     /codon_start=2
                     /product="capsid protein"
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                     /db_xref="GI:34098004"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
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Percent Similarity:     96.35%          Conservative:  0
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Query Match:            24.04%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-16 (1-549) x AB105901 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACTTCTGGTTTGGTAATGCTTTGTATTCATGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAATACACCTTACACTGGTGCATTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTGTCCCGGTACACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGTCGTGGTGCTGACGGTACCGCTGAGCTTACTACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATTGCCTTGACACTGTTCAATCTTGCTGATACGCTTCTTGGTGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTAATTTCGTCGGCTGGGGGTCAATTATTTTACTCCCGCCCTGTCGTCTCG 412

RESULT 231
AB105903
LOCUS       AB105903                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJL234.
ACCESSION   AB105903
VERSION     AB105903.1  GI:34098007
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /isolate="swJL234"
                     /isolation_source="pig liver"
                     /specific_host="swine"
                     /db_xref="taxon:63421"
                     /country="Japan:Hokkaido"
                     /note="genotype III"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
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                     /product="capsid protein"
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Alignment Scores:
Pred. No.:              204             Length:        412
Score:                  132.00          Matches:       132
Percent Similarity:     96.35%          Conservative:  0
Best Local Similarity:  96.35%          Mismatches:    5
Query Match:            24.04%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-16 (1-549) x AB105903 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTGGTAATGCTTTGTATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCYTACACTAATACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAATCTGACACCCGGGAACACAAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCACCGGCTGCGCCGCGGTGCTGATGGGACYGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGTTTCATGAAGGATTTACATTTTACTGGCACGAAYGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATCGCYCTGACATTGTTTAATCTCGCTGAYACGCTTCTCGGTGGTYTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 232
AB105904
LOCUS       AB105904                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJL325.
ACCESSION   AB105904
VERSION     AB105904.1  GI:34098009
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
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  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:63421"
                     /country="Japan:Hokkaido"
                     /note="genotype III"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
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                     /protein_id="BAC82181.1"
                     /db_xref="GI:34098010"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB105904 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTGGTAATGCTTTGTATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCYTACACTAATACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGAAATCTGACACCCGGGAACACAAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCACCGGCTGCGCCGCGGTGCTGATGGGACYGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGTTTCATGAAGGATTTACATTTTACTGGCACGAAYGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        302 GGCATCGCYCTGACATTGTTTAATCTCGCTGAYACGCTTCTCGGTGGTYTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 233
AB107366
LOCUS       AB107366                412 bp    RNA     linear   VRL 07-APR-2004
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate: HE-JAS1.
ACCESSION   AB107366
VERSION     AB107366.1  GI:46250706
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yamamoto,T., Suzuki,H., Toyota,T., Takahashi,M. and Okamoto,H.
  TITLE     Three male patients with sporadic acute hepatitis E in Sendai, who
            were domestically infected with hepatitis E virus of genotype III
            or IV
  JOURNAL   J. Gastroenterol. 39, 292-298 (2004)
   PUBMED   15065009
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-APR-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /mol_type="genomic RNA"
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                     /db_xref="taxon:12461"
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                     /note="genotype III"
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              204          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB107366 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGTATTCACGGCTCCCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTATACTGGTGCTTTGGGGCTTCTTGATTTTGCATTAGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGCCGCGGCGCTGATGGGACCGCTGAGCTCACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
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Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCCCTGACACTGTTTAATCTTGCTGATACGCTTCTTGGTGGCTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAATTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 234
AB107368
LOCUS       AB107368                412 bp    RNA     linear   VRL 07-APR-2004
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate: HE-JAS3.
ACCESSION   AB107368
VERSION     AB107368.1  GI:46250710
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yamamoto,T., Suzuki,H., Toyota,T., Takahashi,M. and Okamoto,H.
  TITLE     Three male patients with sporadic acute hepatitis E in Sendai, who
            were domestically infected with hepatitis E virus of genotype III
            or IV
  JOURNAL   J. Gastroenterol. 39, 292-298 (2004)
   PUBMED   15065009
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
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            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /country="Japan:Sendai"
                     /note="genotype III"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD15081.1"
                     /db_xref="GI:46250711"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              204             Length:         412
Score:                  132.00          Matches:        132
Percent Similarity:     96.35%          Conservative:   0
Best Local Similarity:  96.35%          Mismatches:     5
Query Match:            24.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB107368 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCCGAGGAGGAGGCTACCTCCGGCCTGGTAATGCTTTGTATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAACTA 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||  ||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        242 ACACGTTTTATGAAGGATTTGCATTTTACTGGCACGAACGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATCGCTCTGACATTGTTTAATCTTGCTGATACGCTTCTTGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 235
AB112743
LOCUS       AB112743                412 bp    RNA     linear   VRL 22-JUN-2004
DEFINITION  Hepatitis E virus ORF2 gene for capsid, partial cds,
            isolate:HE-JBD1.
ACCESSION   AB112743
VERSION     AB112743.1  GI:49022381
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Fukuda,S., Sunaga,J., Saito,N., Fujimura,K., Itoh,Y., Sasaki,M.,
            Tsuda,F., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Prevalence of antibodies to hepatitis E virus among Japanese blood
            donors: identification of three blood donors infected with a
            genotype 3 hepatitis E virus
  JOURNAL   J. Med. Virol. 73, 554-561 (2004)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JUN-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JBD1"
                     /isolation_source="human serum"
                     /db_xref="taxon:12461"
                     /country="Japan: Tochigi"
                     /note="genotype III"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid"
                     /protein_id="BAD23989.1"
                     /db_xref="GI:49022382"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"
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Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB112743 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGCCTGGTAATGCTTTGCATTCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACAAATACACCTTATACTGGGGCTTTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACACCTGGGAACACTAACACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGCCGTGGAGCCGACGGGACCGCTGAGCTCACCACTACAGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGTTTTATGAAGGACTTGCATTTCACCGGTACGAATGGAGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCCCTGACACTGTTTAATCTTGCTGATACGCTTCTCGGTGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 236
AB115541
LOCUS       AB115541                412 bp    RNA     linear   VRL 22-JUL-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds,
            isolate:HE-JA20.
ACCESSION   AB115541
VERSION     AB115541.1  GI:50507839
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Sainokami,S., Abe,K., Kumagai,I., Miyasaka,A., Endo,R.,
            Takikawa,Y., Suzuki,K., Mizuo,H., Sugai,Y., Akahane,Y., Koizumi,Y.,
            Yajima,Y. and Okamoto,H.
  TITLE     Epidemiological and clinical study of sporadic acute hepatitis E
            caused by indigenous strains of hepatitis E virus in Japan compared
            with acute hepatitis A
  JOURNAL   J. Gastroenterol. 39, 640-648 (2004)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
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                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Japan:Iwate"
                     /note="Genotype III"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              204           Length:        412
Score:                  132.00        Matches:       132
Percent Similarity:     96.35%        Conservative:  0
Best Local Similarity:  96.35%        Mismatches:    5
Query Match:            24.04%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB115541 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCTACCTCCGGCCTGGTAATGCTTTGTATTCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAACTA 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGAAATTTGACACCCGGGAACACTAACACTCGTGTTTCCCGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGTTTTATGAAGGATTTGCATTTTACTGGCACGAACGGTGTTGGTGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATCGCTCTGACATTGTTTAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCCCGTCCTGTTGTCTCG 412

RESULT 237
AB115542
LOCUS       AB115542                412 bp    RNA     linear   VRL 22-JUL-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds,
            isolate:HE-JA21.
ACCESSION   AB115542
VERSION     AB115542.1  GI:50507841
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Sainokami,S., Abe,K., Kumagai,I., Miyasaka,A., Endo,R.,
            Takikawa,Y., Suzuki,K., Mizuo,H., Sugai,Y., Akahane,Y., Koizumi,Y.,
            Yajima,Y. and Okamoto,H.
  TITLE     Epidemiological and clinical study of sporadic acute hepatitis E
            caused by indigenous strains of hepatitis E virus in Japan compared
            with acute hepatitis A
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  JOURNAL   J. Gastroenterol. 39, 640-648 (2004)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
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                     /isolation_source="serum"
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                     /db_xref="taxon:12461"
                     /country="Japan:Iwate"
                     /note="Genotype III"
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                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204          Length:         412
Score:                    132.00       Matches:        132
Percent Similarity:       96.35%       Conservative:   0
Best Local Similarity:    96.35%       Mismatches:     5
Query Match:              24.04%       Indels:         0
DB:                       1            Gaps:           0

US-09-769-066-16 (1-549) x AB115542 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCTACCTCCGGCCTGGTGATGCTTTGCATTCATGGCTCCCCCGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACCGGTGCATTGGGGCTTCTTGATTTTGCACTGGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||   ||||||
Db        122 GAGTTTAGGAACTTGACACCTGGGAACACTAACACCCGTGTATCCCGATATACCAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGCGGTGCCGATGGAACAGCTGAGCTCACTACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACCTGCATTTCACTGGCACGAATGGGGTTGGAGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATCGCCCTGACATTATTCAATCTTGCTGATACGCTTCTCGGTGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTCTTTTACTCCCGCCCCGTCGTCTCG 412

RESULT 238
AB115543
LOCUS       AB115543                412 bp    RNA     linear   VRL 22-JUL-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds,
            isolate:HE-JA22.
ACCESSION   AB115543
VERSION     AB115543.1  GI:50507843
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Sainokami,S., Abe,K., Kumagai,I., Miyasaka,A., Endo,R.,
            Takikawa,Y., Suzuki,K., Mizuo,H., Sugai,Y., Akahane,Y., Koizumi,Y.,
            Yajima,Y. and Okamoto,H.
  TITLE     Epidemiological and clinical study of sporadic acute hepatitis E
            caused by indigenous strains of hepatitis E virus in Japan compared
            with acute hepatitis A
  JOURNAL   J. Gastroenterol. 39, 640-648 (2004)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
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                     /country="Japan:Iwate"
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                     /gene="ORF2"
     CDS             <1. .>412
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                     /codon_start=2
                     /product="capsid protein"
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                     /db_xref="GI:50507844"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                204          Length:         412
Score:                    132.00       Matches:        132
Percent Similarity:       96.35%       Conservative:   0
Best Local Similarity:    96.35%       Mismatches:     5
Query Match:              24.04%       Indels:         0
DB:                       1            Gaps:           0

US-09-769-066-16 (1-549) x AB115543 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCTACTTCCGGTCTGGTAATGCTTTGTATCCACGGCTCCCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCTTATACTGGTGCTTTGGGGCTTCTTGATTTTGCATTAGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGAAACCTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGCCGCGGCGCTGATGGGACCGCTGAGCTCACCACCACAGCAGCC 241
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Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Db        242 ACACGTTTTATGAAGGATTTGCATTTTACTGGCACGAATGGCGTTGGAGAGGTGGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCCCTGACACTGTTTAATCTTGCTGATACGCTTCTTGGTGGCTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAATTGTTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 239
AB115544
LOCUS       AB115544                412 bp    RNA     linear   VRL 22-JUL-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds,
            isolate:HE-JA23.
ACCESSION   AB115544
VERSION     AB115544.1  GI:50507845
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Sainokami,S., Abe,K., Kumagai,I., Miyasaka,A., Endo,R.,
            Takikawa,Y., Suzuki,K., Mizuo,H., Sugai,Y., Akahane,Y., Koizumi,Y.,
            Yajima,Y. and Okamoto,H.
  TITLE     Epidemiological and clinical study of sporadic acute hepatitis E
            caused by indigenous strains of hepatitis E virus in Japan compared
            with acute hepatitis A
  JOURNAL   J. Gastroenterol. 39, 640-648 (2004)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:12461"
                     /country="Japan:Nagano"
                     /note="Genotype III"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
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                     /product="capsid protein"
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                     /db_xref="GI:50507846"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              204          Length:         412
Score:                  132.00       Matches:        132
Percent Similarity:     96.35%       Conservative:   0
Best Local Similarity:  96.35%       Mismatches:     5
Query Match:            24.04%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB115544 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCACGGCTCTCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAACACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||   ||||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACCAATACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGGTTTATGAAAGACCTGCACTTCACTGGCACGAACGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGCATCGCTCTGACACTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 240
AB154829
LOCUS       AB154829                412 bp    RNA     linear   VRL 22-JUN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds,
            isolate:HE-JBD2.
ACCESSION   AB154829
VERSION     AB154829.1  GI:49022580
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Fukuda,S., Sunaga,J., Saito,N., Fujimura,K., Itoh,Y., Sasaki,M.,
            Tsuda,F., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Prevalence of antibodies to hepatitis E virus among Japanese blood
            donors: identification of three blood donors infected with a
            genotype 3 hepatitis E virus
  JOURNAL   J. Med. Virol. 73, 554-561 (2004)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-DEC-2003) Hiroaki Okamoto, Jichi Medical School,
            Department of Infection and Immunity; 3311-1 Yakushiji,
            Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498, Japan
            (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JBD2"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Japan:Tochigi"
                     /note="genotype 3"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
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                     /db_xref="GI:49022581"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:

Pred. No.:	204	Length:	412
Score:	132.00	Matches:	132
Percent Similarity:	96.35%	Conservative:	0
Best Local Similarity:	96.35%	Mismatches:	5
Query Match:	24.04%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AB154829 (1-412)

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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGCTTGGTAATGCTCTGCATACATGGTTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACAAATACACCTTATACTGGAGCACTGGGGCTCCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||     |||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATTTGACACCTGGGAACACTAATACCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGTTGCGTCGTGGTGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||||    |||||||||||||||||||||||||
Db        242 ACACGTTTTATGAAGGATCTGCACTTCACCGGTACGAATGGGGTTGGCGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCCCTGACACTGTTTAATCTTGCTGATACGCTTCTCGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGGGGTCAGCTATTTTACTCCCGCCCTGTCGTCTCA 412
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RESULT 241
AB154830
LOCUS AB154830 412 bp RNA linear VRL 22-JUN-2004
DEFINITION Hepatitis E virus gene for capsid protein, partial cds, isolate:HE-JBD3.
ACCESSION AB154830
VERSION AB154830.1 GI:49022585
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Fukuda,S., Sunaga,J., Saito,N., Fujimura,K., Itoh,Y., Sasaki,M., Tsuda,F., Takahashi,M., Nishizawa,T. and Okamoto,H.
TITLE Prevalence of antibodies to hepatitis E virus among Japanese blood donors: identification of three blood donors infected with a genotype 3 hepatitis E virus
JOURNAL J. Med. Virol. 73, 554-561 (2004)
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (19-DEC-2003) Hiroaki Okamoto, Jichi Medical School, Department of Infection and Immunity; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
FEATURES Location/Qualifiers
source 1. .412
/organism="Hepatitis E virus"
/virion
/mol_type="genomic RNA"
/isolate="HE-JBD3"
/specific_host="human"
/db_xref="taxon:12461"
/country="Japan:Tochigi"
/note="genotype 3"
CDS <1. .>412
/note="ORF2"
/codon_start=2
/product="capsid protein"
/protein_id="BAD23991.1"
/db_xref="GI:49022586"
/translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:

Pred. No.:	204	Length:	412
Score:	132.00	Matches:	132
Percent Similarity:	96.35%	Conservative:	0
Best Local Similarity:	96.35%	Mismatches:	5
Query Match:	24.04%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AB154830 (1-412)

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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACTTCCGGCCTTGTAATGCTTTGCATTCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCACTGGGGCTCCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||     |||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACTAACACCCGTGTATCCCGATACACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGTCGTGGTGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGTTTTATGAAAGACCTGCATTTTACCGGCACAAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACACTGTTTAATCTTGCTGATACGCTCCTTGGCGGCTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCG 412
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RESULT 242
AB082567
LOCUS AB082567 412 bp RNA linear VRL 03-SEP-2002
DEFINITION Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA11.
ACCESSION AB082567
VERSION AB082567.1 GI:22759630
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y., Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
TITLE Polyphyletic Strains of Hepatitis E Virus Are Responsible for Sporadic Cases of Acute Hepatitis in Japan
JOURNAL J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
PUBMED 12202555
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.

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  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /clone="HE-JA11-2"
                     /country="Japan:Yamanashi, Kofu"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /protein_id="BAC10966.1"
                     /db_xref="GI:22759631"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              207           Length:         412
Score:                  131.00        Matches:        131
Percent Similarity:     95.62%        Conservative:   0
Best Local Similarity:  95.62%        Mismatches:     6
Query Match:            23.86%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AB082567 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCCGAGGAGGAGGCTACCTCTGGCCTGGTAATGCTTTGTATTCATGGCTCCCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTCAGGAATTTAACACCCGGGAACACTAACACCCGTGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGCCGTGGTGYCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        242 ACGCGTTTCATGAAGGATCTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTTTGACATTGTTCAATCTTGCTGATACGCTTCTCGGTGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCCGTCGTCTCA 412

RESULT 243
AB094204
LOCUS       AB094204                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ1-2.
ACCESSION   AB094204
VERSION     AB094204.1  GI:29292663
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              207           Length:         412
Score:                  131.00        Matches:        131
Percent Similarity:     95.62%        Conservative:   0
Best Local Similarity:  95.62%        Mismatches:     6
Query Match:            23.86%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AB094204 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAGGAGGAGGCTACTTCCGGTCTCGTAATGCTTTGCATTCATGGTTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTAGAAATTTGACACCCGGGAACACCAACACCCGCGTTTCCAGGTATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACCACAGCAGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGTTTCATGAAGGATCTGCATTTTACTGGCACGAATGGCGTTGGTGAGGTAGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATCGCTCTTACACWGTTTAATCTTGCTGATACGCTTCTCGGTGGTTTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGGGGTCAACTATTTTACTCCCGCCCTGTTGTCTCG 412

RESULT 244
AB094226
LOCUS       AB094226                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-1.
ACCESSION   AB094226
VERSION     AB094226.1  GI:29292707
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
  .PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /protein_id="BAC66249.1"
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Alignment Scores:
Pred. No.:              207           Length:        412
Score:                  131.00        Matches:       131
Percent Similarity:     95.62%        Conservative:  0
Best Local Similarity:  95.62%        Mismatches:    6
Query Match:            23.86%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094226 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCCGAGGAGGAGGCAACATCAGGTCTGGTCATGCTTTGCATTCATGGTTCCCCCGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||  ||||||
Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCCGAACTTACTACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGTGTTGGCGAAGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTTTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 245
AB094227
LOCUS       AB094227                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-2.
ACCESSION   AB094227
VERSION     AB094227.1  GI:29292709
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
  PUBMED    12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ8-2"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66250.1"
                     /db_xref="GI:29292710"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              207           Length:        412
Score:                  131.00        Matches:       131
Percent Similarity:     95.62%        Conservative:  0
Best Local Similarity:  95.62%        Mismatches:    6
Query Match:            23.86%        Indels:        0
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DB:                 1           Gaps:          0

US-09-769-066-16 (1-549) x AB094227 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCCGAGGAGGAGGCAACATCTGGTCTGGTCATGCTTTGCATCCATGGTTCTCCCGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      |||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCTGAACTTACCACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||   |||||||||||||||||||||||||||
Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTCGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTTTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 246
AB094228
LOCUS       AB094228                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-3.
ACCESSION   AB094228
VERSION     AB094228.1  GI:29292711
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ8-3"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66251.1"
                     /db_xref="GI:29292712"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              207           Length:         412
Score:                  131.00        Matches:        131
Percent Similarity:     95.62%        Conservative:   0
Best Local Similarity:  95.62%        Mismatches:     6
Query Match:            23.86%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AB094228 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCAACATCTGGTCTGGTCATGCTTTGCATCCATGGTTCTCCCGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      |||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCTGAACTTACCACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||   |||||||||||||||||||||||||||
Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTCGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTTTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 247
AB094229
LOCUS       AB094229                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-4.
ACCESSION   AB094229
VERSION     AB094229.1  GI:29292713
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ8-4"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                207          Length:          412
Score:                    131.00       Matches:         131
Percent Similarity:       95.62%       Conservative:    0
Best Local Similarity:    95.62%       Mismatches:      6
Query Match:              23.86%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-16 (1-549) x AB094229 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCAACATCTGGTCTGGTCATGCTTTGCATCCATGGTTCTCCCGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCTGAACTTACCACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTCGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTTTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 248
AB094230
LOCUS       AB094230                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-5.
ACCESSION   AB094230
VERSION     AB094230.1  GI:29292715
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
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                     /db_xref="taxon:63421"
                     /country="Japan"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                207          Length:          412
Score:                    131.00       Matches:         131
Percent Similarity:       95.62%       Conservative:    0
Best Local Similarity:    95.62%       Mismatches:      6
Query Match:              23.86%       Indels:          0
DB:                       1            Gaps:            0

US-09-769-066-16 (1-549) x AB094230 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCAACATCTGGTCTGGTCATGCTTTGCATTCATGGTTCCCCCGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCCGAACTTACCACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTTGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTTTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 249
AB094231
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LOCUS       AB094231                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-6.
ACCESSION   AB094231
VERSION     AB094231.1  GI:29292717
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /country="Japan"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              207           Length:         412
Score:                  131.00        Matches:        131
Percent Similarity:     95.62%        Conservative:   0
Best Local Similarity:  95.62%        Mismatches:     6
Query Match:            23.86%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AB094231 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAGGAGGCAACATCTGGTCTGGTCATGCTTTGTATTCATGGTTCTCCCGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGGCTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCTGAACTTACCACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTTGGYGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTGACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTTTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 250
AB094232
LOCUS       AB094232                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-7.
ACCESSION   AB094232
VERSION     AB094232.1  GI:29292719
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /virion
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                     /country="Japan"
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                     /db_xref="GI:29292720"
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Alignment Scores:
Pred. No.:              207           Length:         412
Score:                  131.00        Matches:        131
Percent Similarity:     95.62%        Conservative:   0
Best Local Similarity:  95.62%        Mismatches:     6
Query Match:            23.86%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AB094232 (1-412)

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Db          2 GCCGAGGAGGAGGCAACATCTGGTCTGGTCATGCTTTGCATCCATGGTTCTCCCGTCAAC 61
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 YTGATTTCGTCGGCTGGAGGTCAGCTTTTCTACTCCCGACCAGTCGTCTCG 412
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RESULT 251
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LOCUS AB094233 412 bp RNA linear VRL 27-MAR-2003
DEFINITION Swine hepatitis E virus ORF2 gene for capsid protein, partial cds, isolate:swJ8-8.
ACCESSION AB094233
VERSION AB094233.1 GI:29292721
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T., Tsuda,F. and Okamoto,H.
TITLE Swine hepatitis E virus strains in Japan form four phylogenetic clusters comparable with those of Japanese isolates of human hepatitis E virus
JOURNAL J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
PUBMED 12655086
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School, Immunology Division and Division of Molecular Virology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
FEATURES Location/Qualifiers
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/virion
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/specific_host="farm pig"
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Alignment Scores:

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Query Match: 23.86% Indels: 0
DB: 1 Gaps: 0

US-09-769-066-16 (1-549) x AB094233 (1-412)

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Db          2 GCCGAGGAGGAGGCAACATCAGGTCTGGTCATGCTTTGCATTCATGGTTCCCCCGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTAYACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTTTTCTACTCCCGACCAGTCGTCTCG 412
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RESULT 252
AB094234
LOCUS AB094234 412 bp RNA linear VRL 27-MAR-2003
DEFINITION Swine hepatitis E virus ORF2 gene for capsid protein, partial cds, isolate:swJ8-9.
ACCESSION AB094234
VERSION AB094234.1 GI:29292723
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T., Tsuda,F. and Okamoto,H.
TITLE Swine hepatitis E virus strains in Japan form four phylogenetic clusters comparable with those of Japanese isolates of human hepatitis E virus
JOURNAL J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
PUBMED 12655086
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School, Immunology Division and Division of Molecular Virology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
FEATURES Location/Qualifiers
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/organism="Swine hepatitis E virus"
/virion
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/isolate="swJ8-9"
/isolation_source="swine serum"
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Alignment Scores:
Pred. No.:              207           Length:        412
Score:                  131.00        Matches:       131
Percent Similarity:     95.62%        Conservative:  0
Best Local Similarity:  95.62%        Mismatches:    6
Query Match:            23.86%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094234 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCCGAACTTACTACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTTGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTTTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 253
AB094235
LOCUS       AB094235                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-10.
ACCESSION   AB094235
VERSION     AB094235.1  GI:29292725
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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Alignment Scores:
Pred. No.:              207           Length:        412
Score:                  131.00        Matches:       131
Percent Similarity:     95.62%        Conservative:  0
Best Local Similarity:  95.62%        Mismatches:    6
Query Match:            23.86%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094235 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCCGAGGAAGAGGCAACTTCAGGTCTGGTCATGCTTTGCATTCATGGTTCCCCTGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCCGAACTTACTACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTTGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTCTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 254
AB094236
LOCUS       AB094236                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-11.
ACCESSION   AB094236
VERSION     AB094236.1  GI:29292727
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
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          Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
          Hepevirus.
REFERENCE 1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE 2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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Alignment Scores:
Pred. No.:              207          Length:         412
Score:                  131.00       Matches:        131
Percent Similarity:     95.62%       Conservative:   0
Best Local Similarity:  95.62%       Mismatches:     6
Query Match:            23.86%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB094236 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCGAGGAAGAGGCAACTTCAGGTCTGGTCATGCTTTGCATTCATGGTTCCCCTGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTTGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTCTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 255
AB094237
LOCUS       AB094237                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ8-12.
ACCESSION   AB094237
VERSION     AB094237.1  GI:29292729
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              207          Length:         412
Score:                  131.00       Matches:        131
Percent Similarity:     95.62%       Conservative:   0
Best Local Similarity:  95.62%       Mismatches:     6
Query Match:            23.86%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB094237 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCCGAGGAAGAGGCAACTTCAGGTCTGGTCATGCTTTGCATTCATGGTTCCCCTGTTAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACCAATACGCCCTATACTGGGGCATTGGGACTTCTTGACTTTGCACTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGGTATACTAGCACG 181
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGTCACCGCCTACGCCGTGGCCCCGACGGAACCGCCGAACTTACTACCACTGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        242 ACGCGCTTTATGAAGGACCTGCATTTTACTGGGACGAATGGCGTTGGCGAGGTGGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGCATAGCCCTAACTTTATTCAACCTTGCTGATACACTTCTCGGCGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGAGGTCAGCTCTTCTACTCCCGACCAGTCGTCTCG 412

RESULT 256
AB094258
LOCUS       AB094258                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ15-3.
ACCESSION   AB094258
VERSION     AB094258.1  GI:29292771
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ15-3"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66281.1"
                     /db_xref="GI:29292772"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
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Alignment Scores:
Pred. No.:              207             Length:         412
Score:                  131.00          Matches:        131
Percent Similarity:     95.62%          Conservative:   0
Best Local Similarity:  95.62%          Mismatches:     6
Query Match:            23.86%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094258 (1-412)
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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTGATGCTTTGCATTCACGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCCCTGGGGCTTCTTGATTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||    ||||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACTAGTACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCATCGGCTGCGTCGTGGAGCCGACGGGACCGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        242 ACGCGTTTCATGAAGGACCTGCACTTTACTGGCACGAATGGGGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAACCTTGCTGATACACTTCTCGGCGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              |||    ||||||||||||||||||||||||||||||||||||||||||||
Db        362 CTGRTTTCGTCGGCCGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 257
AB094275
LOCUS       AB094275                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ18-1.
ACCESSION   AB094275
VERSION     AB094275.1  GI:29292805
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ18-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
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                     /db_xref="GI:29292806"
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISPAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                207             Length:         412
Score:                    131.00          Matches:        131
Percent Similarity:       95.62%          Conservative:   0
Best Local Similarity:    95.62%          Mismatches:     6
Query Match:              23.86%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB094275 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCCGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAGGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              |||||||||   ||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGCCGGCTGGTGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 258
AB094289
LOCUS       AB094289                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ19-11.
ACCESSION   AB094289
VERSION     AB094289.1  GI:29292833
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
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                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                207             Length:         412
Score:                    131.00          Matches:        131
Percent Similarity:       95.62%          Conservative:   0
Best Local Similarity:    95.62%          Mismatches:     6
Query Match:              23.86%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB094289 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTTTGGTGATGCTTTGCATYCATGGCTCTCCTGTTAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTACACTGGTGCACTTGGGCTTCTTGATTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||      ||||||||||||||||||||||||||   ||||||
Db        122 GAGTTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTATCCCGATATACCAGYACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCACCGGCTGCGTCGTGGCGCYGATGGGACAGCTGAGCTTACCACCACGGCYGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        242 AYACGYTTCATGAAGGACTTGCATTTTACTGGTACGAATGGGGTTGGTGAGGTGGGTCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTYTGACATTGTTCAATCTTGCTGATACGCTTCTCGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCG 412

RESULT 259
AB094297
LOCUS       AB094297                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-5.
ACCESSION   AB094297
VERSION     AB094297.1  GI:29292849
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
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  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /organism="Swine hepatitis E virus"
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                     /country="Japan"
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Alignment Scores:
Pred. No.:              207           Length:        412
Score:                  131.00        Matches:       131
Percent Similarity:     95.62%        Conservative:  0
Best Local Similarity:  95.62%        Mismatches:    6
Query Match:            23.86%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094297 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGYTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATTTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACATTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCA 412

RESULT 260
AB094300
LOCUS       AB094300                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ22-8.
ACCESSION   AB094300
VERSION     AB094300.1  GI:29292855
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              207           Length:        412
Score:                  131.00        Matches:       131
Percent Similarity:     95.62%        Conservative:  0
Best Local Similarity:  95.62%        Mismatches:    6
Query Match:            23.86%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB094300 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCTACTTCCGGCCTGGTAATGCTTTGCATCCATGGCTCTCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||    ||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATRCACCTTATACTGGTGCATTGGGACTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||    ||||||
Db        122 GAATTTAGGAATCTGACACCCGGGAACACCAACACCCGAGTATCCCGGTATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACTGCTGAGCTTACCACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        242 ACGCGGTTTATGAAGGACCTGCATTTCACTGGCACGAATGGAGTTGGCGAAGTAGGCCGG 301
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Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACATTGTTCAATCTTGCTGACACGCTTCTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGGGGTCAGTTGTTCTACTCCCGCCCTGTCGTCTCA 412

RESULT 261
AB094320
LOCUS       AB094320                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-4.
ACCESSION   AB094320
VERSION     AB094320.1  GI:29292895
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-4"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66343.1"
                     /db_xref="GI:29292896"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNXRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              207             Length:         412
Score:                  131.00          Matches:        131
Percent Similarity:     95.62%          Conservative:   0
Best Local Similarity:  95.62%          Mismatches:     6
Query Match:            23.86%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094320 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTAGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  |||||||||  ||||||||||||||  ||||||
Db        122 GAATTCAGGAATTTAACTCCCGGGAACACTAACAYCCGTGTATCCCGATATACTAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACACACTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 262
AB094326
LOCUS       AB094326                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ25-10.
ACCESSION   AB094326
VERSION     AB094326.1  GI:29292907
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ25-10"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66349.1"
                     /db_xref="GI:29292908"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYTSTARHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADXLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              207             Length:         412
Score:                  131.00          Matches:        131
Percent Similarity:     95.62%          Conservative:   0
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Best Local Similarity:  95.62%          Mismatches:    6
Query Match:            23.86%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-16 (1-549) x AB094326 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACCTCAGGCTTGGTAATGCTTTGTATTCACGGCTCCCCTGTCAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGACTTTGCATTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      |||||||||||||||||||||||||||   ||||||
Db        122 GAATTCAGGAATTTAACCCCCGGGAACACTAACACCCGTGTATCCCGATATACYAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGTCATCGGCTGCGCCGTGGTGCCGACGGGACCGCTGAGCTTACCACCACRGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAAGACTTGCATTTCACTGGCACGAATGGGGTTGGTGAAGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||   |||||||||||||||||||||||||
Db        302 GGTATTGCTCTGACACTGTTCAATCTTGCTGACRCRCTACTCGGTGGTTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 263
AB096756
LOCUS       AB096756                412 bp    RNA     linear   VRL 11-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate: swJC1990.
ACCESSION   AB096756
VERSION     AB096756.1  GI:28971695
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Identification of a Genotype III Swine Hepatitis E Virus That Was
            Isolated from a Japanese Pig Born in 1990 and That Is Most Closely
            Related to Japanese Isolates of Human Hepatitis E Virus
  JOURNAL   J. Clin. Microbiol. 41 (3), 1342-1343 (2003)
  MEDLINE   22511089
   PUBMED   12624083
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-NOV-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJC1990"
                     /isolation_source="serum"
                     /specific_host="pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
                     /note="genotype III"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC65323.1"
                     /db_xref="GI:28971696"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              207             Length:        412
Score:                  131.00          Matches:       131
Percent Similarity:     95.62%          Conservative:  0
Best Local Similarity:  95.62%          Mismatches:    6
Query Match:            23.86%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-16 (1-549) x AB096756 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTGGTAATGCTTTGTATCCATGGCTCCCCTGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGACTTTGCACTAGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      |||||||||   |||||||||||||   ||||||
Db        122 GAATTTAGGAACTTGACACCCGGGAACACTAACTCCCGTGTATCCCGATATACCAGCACA 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCCCGCCATCGGCTGCGCCGCGGTGCCGACGGGACCGCTGAGCTTACTACTACGGCGGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Db        242 ACGCGTTTTATGAAGGACTTGCATTTCACTGGCACGAATGGAGTTGGTGAGGTGGGCCGA 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        302 GGCATTGCTCTGACACTGTTTAATCTTGCTGACACGCTTCTCGGTGGTCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGGGGTCAGCTGTTTTACTCCCGCCCTGTCGTCTCA 412

RESULT 264
AB079762
LOCUS       AB079762                412 bp    RNA     linear   VRL 06-NOV-2002
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JF1.
ACCESSION   AB079762
VERSION     AB079762.1  GI:24636297
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Suzuki,K., Aikawa,T. and Okamoto,H.
  TITLE     Fulminant hepatitis E in Japan
  JOURNAL   N. Engl. J. Med. 347 (18), 1456 (2002)
  MEDLINE   22297680
   PUBMED   12409557
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-FEB-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
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           Yakushiji, Minamikawachi-Machi, Kawachi, Tochigi 329-0498, Japan
           (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
           Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JF1"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Japan"
                     /note="HE-JF1 was isolated from a Japanese patient
                     (Patient 1) with fulminant hepatitis of unknown
                     etiology-genotype IV"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC22749.1"
                     /db_xref="GI:24636298"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209          Length:         412
Score:                  130.00       Matches:        130
Percent Similarity:     94.89%       Conservative:   0
Best Local Similarity:  94.89%       Mismatches:     7
Query Match:            23.68%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB079762 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCAGAGGAGGAGGCAACCTCCGGCCTTGTTATGCTTTGCATTCATGGATCGCCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACTGGTGCCCTTGGTTTGCTCGATTTTGCACTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAATTTGACACCTGGTAATACAAATACGCGCGTTTCCCGATACTCGAGCAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||  ||||||||||  ||||||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTTCGCCGCGGGCCCGACGGCACTGCTGAATTGACTACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        242 ACACGCTTTATGAAAGACCTTCACTTTACAGGGACTAATGGTGTTGGTGAGGTTGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGATACGCTTCTTGGCGGGCTTCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTAATTTCGTCGGCTGGTGGCCAGTTGTTTTACTCCCGCCCCGTCGTCTCA 412

RESULT 265
AB079764
LOCUS       AB079764                412 bp    RNA     linear   VRL 06-NOV-2002
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JF3.
ACCESSION   AB079764
VERSION     AB079764.1  GI:24636301
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Suzuki,K., Aikawa,T. and Okamoto,H.
  TITLE     Fulminant hepatitis E in Japan
  JOURNAL   N. Engl. J. Med. 347 (18), 1456 (2002)
  MEDLINE   22297680
   PUBMED   12409557
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-FEB-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi, Tochigi 329-0498, Japan
            (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="HE-JF3"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Japan"
                     /note="HE-JF3 was isolated from a Japanese patient
                     (Patient 3) with fulminant hepatitis of unknown
                     etiology-genotype IV"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC22751.1"
                     /db_xref="GI:24636302"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209          Length:         412
Score:                  130.00       Matches:        130
Percent Similarity:     94.89%       Conservative:   0
Best Local Similarity:  94.89%       Mismatches:     7
Query Match:            23.68%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB079764 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTTATGCTCTGCATCCATGGATCACCTGTGAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAATACACCTTATACTGGTGCTCTTGGCTTGCTCGATTTCGCACTTGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAATACGCGCGTTTCCCGTTATTCGAGTAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||  ||||||||||  ||||||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGYCGTGGGCCCGACGGTACTGCTGAGCTAACCACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        242 ACACGGTTTATGAAAGATCTTCACTTCACAGGGACCAATGGTGTTGGTGAGGTCGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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                ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTYCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 266
AB082557
LOCUS       AB082557                412 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA1.
ACCESSION   AB082557
VERSION     AB082557.1  GI:22759610
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /clone="HE-JA1-2"
                     /country="Japan:Hokkaido, Sapporo"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
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                     /codon_start=2
                     /protein_id="BAC10956.1"
                     /db_xref="GI:22759611"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB082557 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTTATGCTCTGCATCCATGGATCACCTGTGAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAATACGCGCGTTTCCCGTTATTCGAGTAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCGCGCCACAAGCTACGTCGTGGGCCCGACGGTACTGCTGAGCTAACCACCACTGCTGCT 241

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Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 267
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LOCUS       AB082558                412 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA2.
ACCESSION   AB082558
VERSION     AB082558.1  GI:22759612
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /isolate="HE-JA2"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /clone="HE-JA2-2"
                     /country="Japan:Hokkaido, Sapporo"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
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Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
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US-09-769-066-16 (1-549) x AB082558 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCACGCCACAAGTTACGCCGTGGGCCCGATGGTACTGCTGAATTGACTACTACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        362 TTGATTTCGTCGGCCGGCGGTCAACTGTTTTATTCTCGCCCCGTCGTCTCA 412

RESULT 268
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LOCUS       AB082559                412 bp    RNA     linear   VRL 03-SEP-2002
DEFINITION  Hepatitis E virus ORF2 gene, partial cds, isolate:HE-JA3.
ACCESSION   AB082559
VERSION     AB082559.1  GI:22759614
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Mizuo,H., Suzuki,K., Takikawa,Y., Sugai,Y., Tokita,H., Akahane,Y.,
            Itoh,K., Gotanda,Y., Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Polyphyletic Strains of Hepatitis E Virus Are Responsible for
            Sporadic Cases of Acute Hepatitis in Japan
  JOURNAL   J. Clin. Microbiol. 40 (9), 3209-3218 (2002)
   PUBMED   12202555
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
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Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB082559 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCATGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTCGAGCTC 121

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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTAACTACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGAAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATAGCGCTAACTCTGTTCAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTTTATTCTCGCCCCGTCGTCTCA 412

RESULT 269
AB085949
LOCUS       AB085949                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne014.
ACCESSION   AB085949
VERSION     AB085949.1  GI:27372320
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB085949 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 270
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LOCUS       AB085950                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne026.
ACCESSION   AB085950
VERSION     AB085950.1  GI:27372322
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB085950 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTTGGGCTGCTGGACTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 271
AB085951
LOCUS       AB085951                412 bp    RNA     linear   VRL 25-DEC-2002
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DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne037.
ACCESSION   AB085951
VERSION     AB085951.1  GI:27372324
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
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                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1a"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53673.1"
                     /db_xref="GI:27372325"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB085951 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAATCTTACCCCTGGCAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    ||||||      ||||||||||||||   |||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCTCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 272
AB085952
LOCUS       AB085952                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne049.
ACCESSION   AB085952
VERSION     AB085952.1  GI:27372326
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne049"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1a"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53674.1"
                     /db_xref="GI:27372327"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB085952 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAATCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 273
AB085953
LOCUS       AB085953                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne063.
ACCESSION   AB085953
VERSION     AB085953.1  GI:27372328
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne063"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E~subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53675.1"
                     /db_xref="GI:27372329"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209          Length:        412
Score:                  130.00       Matches:       130
Percent Similarity:     94.89%       Conservative:  0
Best Local Similarity:  94.89%       Mismatches:    7
Query Match:            23.68%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-16 (1-549) x AB085953 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 274
AB085954
LOCUS       AB085954                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne064.
ACCESSION   AB085954
VERSION     AB085954.1  GI:27372330
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
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                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
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                     E~subtype 1a"
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Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB085954 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAATCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||  ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 275
AB085955
LOCUS       AB085955                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne068.
ACCESSION   AB085955
VERSION     AB085955.1  GI:27372332
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES              Location/Qualifiers
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                      /tissue_type="serum"
                      /country="Nepal: Kathmandu"
                      /note="isolated from a patient with sporadic hepatitis
                      E-subtype 1a"
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Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB085955 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTC 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAATCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||  ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 276
AB085956
LOCUS       AB085956                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne069,
            clone:Ne069a.
ACCESSION   AB085956
VERSION     AB085956.1  GI:27372334
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
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          with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /clone="Ne069a"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
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Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB085956 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAATCTTACCCCTGGCAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCTCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 277
AB085957
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LOCUS       AB085957               412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne069,
            clone:Ne069c.
ACCESSION   AB085957
VERSION     AB085957.1  GI:27372336
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne069"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /clone="Ne069c"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53679.1"
                     /db_xref="GI:27372337"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB085957 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241
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Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 278
AB085958
LOCUS       AB085958                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne072.
ACCESSION   AB085958
VERSION     AB085958.1  GI:27372338
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne072"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1a"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53680.1"
                     /db_xref="GI:27372339"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209          Length:       412
Score:                  130.00       Matches:      130
Percent Similarity:     94.89%       Conservative: 0
Best Local Similarity:  94.89%       Mismatches:   7
Query Match:            23.68%       Indels:       0
DB:                     1            Gaps:         0

US-09-769-066-16 (1-549) x AB085958 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAATCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCTCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 279
AB085959
LOCUS       AB085959                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne074.
ACCESSION   AB085959
VERSION     AB085959.1  GI:27372340
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
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                     /protein_id="BAC53681.1"
                     /db_xref="GI:27372341"
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Alignment Scores:
Pred. No.:              209          Length:       412
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Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB085959 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||      ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||   ||||||      ||||||||||||||   ||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 280
AB085960
LOCUS       AB085960                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne080.
ACCESSION   AB085960
VERSION     AB085960.1  GI:27372342
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /specific_host="human"
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                     /note="isolated from a patient with sporadic hepatitis
                     E~subtype 1a"
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB085960 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTTGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||      ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAACCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||   ||||||      ||||||||||||||   ||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 281
AB085961
LOCUS       AB085961                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne081.
ACCESSION   AB085961
VERSION     AB085961.1  GI:27372344
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1a"
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB085961 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAATCTTACCCCTGGCAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 282
AB085962
LOCUS       AB085962                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne086.
ACCESSION   AB085962
VERSION     AB085962.1  GI:27372346
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne086"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53684.1"
                     /db_xref="GI:27372347"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB085962 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 283
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AB085963
LOCUS       AB085963                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne087.
ACCESSION   AB085963
VERSION     AB085963.1  GI:27372348
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne087"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E~subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53685.1"
                     /db_xref="GI:27372349"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209           Length:         412
Score:                  130.00        Matches:        130
Percent Similarity:     94.89%        Conservative:   0
Best Local Similarity:  94.89%        Mismatches:     7
Query Match:            23.68%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AB085963 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||  ||||||      ||||||||||||||||   ||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 284
AB085964
LOCUS       AB085964                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne090.
ACCESSION   AB085964
VERSION     AB085964.1  GI:27372350
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne090"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E~subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53686.1"
                     /db_xref="GI:27372351"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209           Length:         412
Score:                  130.00        Matches:        130
Percent Similarity:     94.89%        Conservative:   0
Best Local Similarity:  94.89%        Mismatches:     7
Query Match:            23.68%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AB085964 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
                ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
                ||||||||||||||||||||    ||||||      ||||||||||||||||   ||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                ||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 285
AB085965
LOCUS       AB085965                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne091.
ACCESSION   AB085965
VERSION     AB085965.1  GI:27372352
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="Ne091"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53687.1"
                     /db_xref="GI:27372353"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209          Length:        412
Score:                  130.00       Matches:       130
Percent Similarity:     94.89%       Conservative:  0
Best Local Similarity:  94.89%       Mismatches:    7
Query Match:            23.68%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-16 (1-549) x AB085965 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
                ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
                ||||||||||||||||||||    ||||||      ||||||||||||||||   ||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                ||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 286
AB085966
LOCUS       AB085966                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne105.
ACCESSION   AB085966
VERSION     AB085966.1  GI:27372354
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
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                     E-subtype 1a"
     CDS             <1. .>412
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                     /codon_start=2
                     /product="capsid protein"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                209           Length:         412
Score:                    130.00        Matches:        130
Percent Similarity:       94.89%        Conservative:   0
Best Local Similarity:    94.89%        Mismatches:     7
Query Match:              23.68%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-16 (1-549) x AB085966 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||       ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAATCTTACCCCTGGCAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||    ||||||      ||||||||||||||||   ||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 287
AB085967
LOCUS       AB085967                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne112.
ACCESSION   AB085967
VERSION     AB085967.1  GI:27372356
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
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                     /note="ORF2"
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                     /db_xref="GI:27372357"
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Alignment Scores:
Pred. No.:                209           Length:         412
Score:                    130.00        Matches:        130
Percent Similarity:       94.89%        Conservative:   0
Best Local Similarity:    94.89%        Mismatches:     7
Query Match:              23.68%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-16 (1-549) x AB085967 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTCGCAATCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACTACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

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Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 288
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LOCUS       AB085968                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne118.
ACCESSION   AB085968
VERSION     AB085968.1  GI:27372358
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
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  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1a"
     CDS             <1. .>412
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
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US-09-769-066-16 (1-549) x AB085968 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 289
AB085969
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DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne131.
ACCESSION   AB085969
VERSION     AB085969.1  GI:27372360
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
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Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB085969 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTCTCCCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGCCTTCGCCGCGGCGCAGACGGGACCGCCGAGCTCACCACCACGGCAGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGCGTCGGTGAGATCGGCCGC 301

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Db        302 GGGATAGCCCTCACCCTGTTTAACCTTGCTGACACTCTCCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 290
AB085970
LOCUS       AB085970                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne132.
ACCESSION   AB085970
VERSION     AB085970.1  GI:27372362
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
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REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB085970 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTCATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTCTCCCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGCCTTCGCCGCGGCGCAGACGGGACCGCCGAGCTCACCACCACGGCAGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGCGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTCACCCTGTTTAACCTTGCTGACACTCTCCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 291
AB085971
LOCUS       AB085971                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne133.
ACCESSION   AB085971
VERSION     AB085971.1  GI:27372364
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
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Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
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US-09-769-066-16 (1-549) x AB085971 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTCATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTCTCCCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGCCTTCGCCGCGGCGCAGACGGGACCGCCGAGCTCACCACCACGGCAGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGCGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTTAACCTTGCTGACACTCTCCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 292
AB085972
LOCUS       AB085972                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne134.
ACCESSION   AB085972
VERSION     AB085972.1  GI:27372366
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB085972 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTCATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTCTCCCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGCCTTCGCCGCGGCGCAGACGGGACCGCCGAGCTCACCACCACGGCAGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGCGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTTAACCTTGCTGACACTCTCCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 293
AB085973
LOCUS       AB085973                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne135.
ACCESSION   AB085973
VERSION     AB085973.1  GI:27372368
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
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                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="Ne135"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1a"
     CDS             <1. .>412
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                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53695.1"
                     /db_xref="GI:27372369"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB085973 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTCATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTCTCCCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCCCGCCACCGCCTTCGCCGCGGCGCAGACGGGACCGCCGAGCTCACCACCACGGCAGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGCGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTTAACCTTGCTGACACTCTCCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 294
AB085975
LOCUS       AB085975                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne136,
            clone:Ne136c.
ACCESSION   AB085975
VERSION     AB085975.1  GI:27372372
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="Ne136"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /clone="Ne136c"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53697.1"
                     /db_xref="GI:27372373"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB085975 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACTCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 295
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AB085976
LOCUS       AB085976                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne137.
ACCESSION   AB085976
VERSION     AB085976.1  GI:27372374
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="Ne137"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
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                     E-subtype 1c"
     CDS             <1. .>412
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                     /codon_start=2
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                     /protein_id="BAC53698.1"
                     /db_xref="GI:27372375"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB085976 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACTCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 296
AB085977
LOCUS       AB085977                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne146.
ACCESSION   AB085977
VERSION     AB085977.1  GI:27372376
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     E-subtype 1a"
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                     /codon_start=2
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                     /db_xref="GI:27372377"
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB085977 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 TCTTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy         196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db         122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181
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Qy         216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy         236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
                ||||||||||||||||||||   ||||||      ||||||||||||||||   ||||||
Db         242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy         256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                |||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db         302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy         276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 297
AB085978
LOCUS       AB085978                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne149.
ACCESSION   AB085978
VERSION     AB085978.1  GI:27372378
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /isolate="Ne149"
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                     /db_xref="taxon:12461"
                     /tissue_type="serum"
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                     /note="isolated from a patient with sporadic hepatitis
                     E~subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53700.1"
                     /db_xref="GI:27372379"
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Alignment Scores:
Pred. No.:              209          Length:       412
Score:                  130.00       Matches:      130
Percent Similarity:     94.89%       Conservative: 0
Best Local Similarity:  94.89%       Mismatches:   7
Query Match:            23.68%       Indels:       0
DB:                     1            Gaps:         0

US-09-769-066-16 (1-549) x AB085978 (1-412)

Qy         156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy         176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy         196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
               |||||||||||||||||     ||||||||||||||||||||||||||||||||||||||
Db         122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy         216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy         236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
               ||||||||||||||||||||   ||||||      ||||||||||||||||   ||||||
Db         242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy         256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
               |||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db         302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy         276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db         362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 298
AB085979
LOCUS       AB085979                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne150.
ACCESSION   AB085979
VERSION     AB085979.1  GI:27372380
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne150"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E~subtype 1c"
     CDS             <1. .>412
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                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53701.1"
                     /db_xref="GI:27372381"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB085979 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||     ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||   ||||||     ||||||||||||||   ||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 299
AB085980
LOCUS       AB085980                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne151.
ACCESSION   AB085980
VERSION     AB085980.1  GI:27372382
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES            Location/Qualifiers
     source         1. .412
                    /organism="Hepatitis E virus"
                    /virion
                    /mol_type="genomic RNA"
                    /isolate="Ne151"
                    /specific_host="human"
                    /db_xref="taxon:12461"
                    /tissue_type="serum"
                    /country="Nepal: Kathmandu"
                    /note="isolated from a patient with sporadic hepatitis
                    E-subtype 1c"
     CDS            <1. .>412
                    /note="ORF2"
                    /codon_start=2
                    /product="capsid protein"
                    /protein_id="BAC53702.1"
                    /db_xref="GI:27372383"
                    /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                    ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB085980 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||     ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||   ||||||     ||||||||||||||   ||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 300
AB085982
LOCUS       AB085982                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne154.
ACCESSION   AB085982
VERSION     AB085982.1  GI:27372386
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
```

```
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne154"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53704.1"
                     /db_xref="GI:27372387"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB085982 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||   ||||||      ||||||||||||||||   ||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 301
AB085983
LOCUS       AB085983                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne155.
ACCESSION   AB085983
VERSION     AB085983.1  GI:27372388
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
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                     /codon_start=2
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                     /protein_id="BAC53705.1"
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Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB085983 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 302
AB085984
LOCUS       AB085984                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne157.
ACCESSION   AB085984
VERSION     AB085984.1  GI:27372390
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
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                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53706.1"
                     /db_xref="GI:27372391"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB085984 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 303
AB085985
LOCUS       AB085985                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne159.
ACCESSION   AB085985
VERSION     AB085985.1  GI:27372392
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /db_xref="GI:27372393"
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
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Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB085985 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

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Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 304
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VERSION     AB085986.1  GI:27372394
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     E-subtype 1c"
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
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DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB085986 (1-412)

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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 305
AB085987
LOCUS       AB085987                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne164.
ACCESSION   AB085987
VERSION     AB085987.1  GI:27372396
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB085987 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 306
AB085988
LOCUS       AB085988                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne165.
ACCESSION   AB085988
VERSION     AB085988.1  GI:27372398
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB085988 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

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Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 307
AB085989
LOCUS       AB085989                412 bp    RNA     linear   VRL 25-DEC-2002
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DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne166.
ACCESSION   AB085989
VERSION     AB085989.1  GI:27372400
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
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Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB085989 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 308
AB085990
LOCUS       AB085990                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne169.
ACCESSION   AB085990
VERSION     AB085990.1  GI:27372402
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB085990 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 309
AB085991
LOCUS       AB085991                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne172.
ACCESSION   AB085991
VERSION     AB085991.1  GI:27372404
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="Ne172"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
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                     /codon_start=2
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Alignment Scores:
Pred. No.:              209          Length:        412
Score:                  130.00       Matches:       130
Percent Similarity:     94.89%       Conservative:  0
Best Local Similarity:  94.89%       Mismatches:    7
Query Match:            23.68%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-16 (1-549) x AB085991 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 310
AB085992
LOCUS       AB085992                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne174.
ACCESSION   AB085992
VERSION     AB085992.1  GI:27372406
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
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                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
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                     /protein_id="BAC53714.1"
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB085992 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 311
AB085993
LOCUS       AB085993                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne177.
ACCESSION   AB085993
VERSION     AB085993.1  GI:27372408
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
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                     /specific_host="human"
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                     /tissue_type="serum"
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                     E~subtype 1c"
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB085993 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 312
AB085994
LOCUS       AB085994                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne181.
ACCESSION   AB085994
VERSION     AB085994.1  GI:27372410
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
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  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     E-subtype 1c"
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Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB085994 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||  ||||||      ||||||||||||||   ||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 313
AB085995
LOCUS       AB085995                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne182.
ACCESSION   AB085995
VERSION     AB085995.1  GI:27372412
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
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                     E-subtype 1c"
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Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB085995 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||  ||||||      ||||||||||||||   ||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301
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Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 314
AB085996
LOCUS       AB085996                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne183.
ACCESSION   AB085996
VERSION     AB085996.1  GI:27372414
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne183"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53718.1"
                     /db_xref="GI:27372415"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB085996 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||  ||||||  ||||||||||||||  ||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 315
AB085997
LOCUS       AB085997                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne185.
ACCESSION   AB085997
VERSION     AB085997.1  GI:27372416
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne185"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53719.1"
                     /db_xref="GI:27372417"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
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DB:                    1              Gaps:          0

US-09-769-066-16 (1-549) x AB085997 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||       ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    ||||||      ||||||||||||||||    ||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 316
AB085998
LOCUS       AB085998                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne186.
ACCESSION   AB085998
VERSION     AB085998.1  GI:27372418
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne186"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="serum"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1c"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC53720.1"
                     /db_xref="GI:27372419"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB085998 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||       ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    ||||||      ||||||||||||||||    ||||||
Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 317
AB085999
LOCUS       AB085999                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne-A2.
ACCESSION   AB085999
VERSION     AB085999.1  GI:27372420
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="Ne-A2"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /tissue_type="stool"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1a"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /protein_id="BAC53721.1"
                     /db_xref="GI:27372421"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB085999 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTACACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||  ||||||      ||||||||||||||||  ||||||
Db        242 ACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 318
AB086000
LOCUS       AB086000                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds,
            isolate:Ne-A312.
ACCESSION   AB086000
VERSION     AB086000.1  GI:27372422
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /isolate="Ne-A312"
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                     /db_xref="taxon:12461"
                     /tissue_type="stool"
                     /country="Nepal: Kathmandu"
                     /note="isolated from a patient with sporadic hepatitis
                     E-subtype 1a"
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                     /product="capsid protein"
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                     /db_xref="GI:27372423"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB086000 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCTACTTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTACACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||  ||||||      ||||||||||||||||  ||||||
Db        242 ACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 319
AB094219
LOCUS       AB094219                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
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           isolate:swJ7-1.
ACCESSION  AB094219
VERSION    AB094219.1  GI:29292693
KEYWORDS   .
SOURCE     Swine hepatitis E virus
  ORGANISM Swine hepatitis E virus
           Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
           Hepevirus.
REFERENCE  1
  AUTHORS  Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
           Tsuda,F. and Okamoto,H.
  TITLE    Swine hepatitis E virus strains in Japan form four phylogenetic
           clusters comparable with those of Japanese isolates of human
           hepatitis E virus
  JOURNAL  J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED  12655086
REFERENCE  2  (bases 1 to 412)
  AUTHORS  Okamoto,H.
  TITLE    Direct Submission
  JOURNAL  Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
           Immunology Division and Division of Molecular Virology; 3311-1
           Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
           Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
           Fax:81-285-44-1557)
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                     /virion
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Best Local Similarity:  94.89%       Mismatches:     7
Query Match:            23.68%       Indels:         0
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US-09-769-066-16 (1-549) x AB094219 (1-412)

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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ7-2.
ACCESSION   AB094220
VERSION     AB094220.1  GI:29292695
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              209          Length:         412
Score:                  130.00       Matches:        130
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US-09-769-066-16 (1-549) x AB094220 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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LOCUS       AB094221                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
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ACCESSION   AB094221
VERSION     AB094221.1  GI:29292697
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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Alignment Scores:
Pred. No.:          209          Length:       412
Score:              130.00       Matches:      130
Percent Similarity:     94.89%       Conservative:  0
Best Local Similarity:  94.89%       Mismatches:    7
Query Match:            23.68%       Indels:        0
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US-09-769-066-16 (1-549) x AB094221 (1-412)

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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTTATGCTCTGCATTCATGGATCACCTGTGAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTACACTAATACACCTTATACTGGTGCTCTTGGCTTGCTTGATTTTGCACTTGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGCGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 322
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LOCUS       AB094222                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
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ACCESSION   AB094222
VERSION     AB094222.1  GI:29292699
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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Alignment Scores:
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Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094222 (1-412)

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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTTATGCTCTGCATTCATGGATCACCTGTGAAC 61

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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCGCGCCACAAGCTACGTCGTGGGCCCGACGGTACTGCTGAGCTAACCACCACTGCTGCT 241

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Db        242 ACACGGTTTATGAAAGACCTTCACTTCACAGGGACCAATGGTGTTGGTGAGGTCGGTCGC 301

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Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGCGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 323
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LOCUS       AB094223                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
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ACCESSION   AB094223
VERSION     AB094223.1  GI:29292701
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
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            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
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            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094223 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTTATGCTCTGCATTCATGGATCACCTGTGAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        182 GCGCGCCACAAGCTACGTCGTGGGCCCGACGGTACTGCTGAGCTAACCACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGGTTTATGAAAGACCTTCACTTCACAGGGACCAATGGTGTTGGTGAGGTCGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGCGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 324
AB094224
LOCUS       AB094224                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ7-6.
ACCESSION   AB094224
VERSION     AB094224.1  GI:29292703
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
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REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
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            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209           Length:         412
Score:                  130.00        Matches:        130
Percent Similarity:     94.89%        Conservative:   0
Best Local Similarity:  94.89%        Mismatches:     7
Query Match:            23.68%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AB094224 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTTATGCTCTGCATTCATGGATCACCTGTGAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAATACACCTTATACTGGTGCTCTTGGCTTGCTTGATTTTGCACTTGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAATTTGACACCCGGTAATACGAATACGCGCGTCTCCCGTTATTCGAGTAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||   ||||||||||   ||||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGTCGTGGGCCCGACGGTACTGCTGAGCTAACCACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGGTTTATGAAAGACCTTCACTTCACAGGGACCAATGGTGTTGGTGAGGTCGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCCGGCGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412
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RESULT 325
AB094225
LOCUS       AB094225                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ7-7.
ACCESSION   AB094225
VERSION     AB094225.1  GI:29292705
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ7-7"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC66248.1"
                     /db_xref="GI:29292706"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209           Length:         412
Score:                  130.00        Matches:        130
Percent Similarity:     94.89%        Conservative:   0
Best Local Similarity:  94.89%        Mismatches:     7
Query Match:            23.68%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AB094225 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTTATGCTCTGCATTCATGGATCACCTGTGAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAATACACCTTATACTGGTGCTCTTGGCTTGCTTGATTTTGCACTTGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAATTTGACACCCGGTAATACGAATACGCGCGTCTCCCGTTATTCGAGTAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCGCGCCACAAGCTACGTCGTGGGCCCGACGGTACTGCTGAGCTAACCACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        242 ACACGGTTTATGAAAGACCTTCACTTCACAGGGACCAATGGTGTTGGTGAGGTCGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCCGGCGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 326
AB094254
LOCUS       AB094254                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ13-1.
ACCESSION   AB094254
VERSION     AB094254.1  GI:29292763
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ13-1"
                     /isolation_source="swine serum"
                     /specific_host="farm pig"
                     /db_xref="taxon:63421"
                     /country="Japan"
     CDS             <1. .>412
                     /note="ORF2"
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                     /protein_id="BAC66277.1"
                     /db_xref="GI:29292764"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB094254 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTTATGCTCTGCATCCATGGATCACCTGTGAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAATACACCTTATACTGGTGCTCTTGGCTTGCTCGATTTCGCACTTGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAATACGCGCGTTTCCCGTTATTCGAGTAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||  ||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGTCGTGGGCCCGACGGTACTGCTGAGCTAACCACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        242 ACACGGTTTATGAAAGATCTTCACTTCACAGGGACCAATGGTGTTGGTGAGGTCGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 327
AB094255
LOCUS       AB094255                412 bp    RNA     linear   VRL 27-MAR-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJ13-2.
ACCESSION   AB094255
VERSION     AB094255.1  GI:29292765
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Takahashi,M., Nishizawa,T., Miyajima,H., Gotanda,Y., Iita,T.,
            Tsuda,F. and Okamoto,H.
  TITLE     Swine hepatitis E virus strains in Japan form four phylogenetic
            clusters comparable with those of Japanese isolates of human
            hepatitis E virus
  JOURNAL   J. Gen. Virol. 84 (Pt 4), 851-862 (2003)
   PUBMED   12655086
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJ13-2"
                     /isolation_source="swine serum"
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                     /db_xref="taxon:63421"
                     /country="Japan"
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                     /product="capsid protein"
                     /protein_id="BAC66278.1"
                     /db_xref="GI:29292766"
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                    ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB094255 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTTATGCTCTGCATCCATGGATCACCTGTGAAC 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAATACACCTTATACTGGTGCTCTTGGCTTGCTCGATTTCGCACTTGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAATACGCGCGTTTCCCGTTATTCGAGTAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||   ||||||||||   ||||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGTCGTGGGCCCGACGGTACTGCTGAGCTAACCACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        242 ACACGGTTTATGAAGGATCTTCACTTCACAGGGACCAATGGTGTTGGTGAGGTCGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTATTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 328
AB105888
LOCUS       AB105888                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JA12.
ACCESSION   AB105888
VERSION     AB105888.1  GI:34097977
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JA12"
                     /isolation_source="human serum"
                     /db_xref="taxon:12461"
                     /country="Japan:Hokkaido"
                     /note="genotype IV; sporadic acute hepatitis E"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
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                     /product="capsid protein"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB105888 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCATGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACCAATACGCCYTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTYGAGCTC 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAACACACGTGTTTCCCGCTACTCGAGTAGT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||   ||||||||||   ||||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTAACTACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGAAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTCAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 329
AB105889
LOCUS       AB105889                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JA13.
ACCESSION   AB105889
VERSION     AB105889.1  GI:34097979
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
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  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /isolation_source="human serum"
                     /db_xref="taxon:12461"
                     /country="Japan:Hokkaido"
                     /note="genotype IV; sporadic acute hepatitis E"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
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                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC82166.1"
                     /db_xref="GI:34097980"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB105889 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCATGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTCGAGCTC 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGYAATTTGACACCCGGTAACACGAACACACGTGTTTCCCGCTACTCGAGTAGT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTAACTACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGAAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTCAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 330
AB105893
LOCUS       AB105893                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JA17.
ACCESSION   AB105893
VERSION     AB105893.1  GI:34097987
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JA17"
                     /isolation_source="human serum"
                     /db_xref="taxon:12461"
                     /country="Japan:Hokkaido"
                     /note="genotype IV; sporadic acute hepatitis E"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC82170.1"
                     /db_xref="GI:34097988"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB105893 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCATGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTCGAGCTC 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAACACACGTGTTTCCCGCTACTCGAGTAGT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTAACTACCACTGCTGCT 241
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Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGAAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATAGCGCTAACTCTGTTCAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 331
AB105894
LOCUS       AB105894                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JA18.
ACCESSION   AB105894
VERSION     AB105894.1  GI:34097989
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JA18"
                     /isolation_source="human serum"
                     /db_xref="taxon:12461"
                     /country="Japan:Hokkaido"
                     /note="genotype IV; sporadic acute hepatitis E"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC82171.1"
                     /db_xref="GI:34097990"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209          Length:        412
Score:                  130.00       Matches:       130
Percent Similarity:     94.89%       Conservative:  0
Best Local Similarity:  94.89%       Mismatches:    7
Query Match:            23.68%       Indels:        0
DB:                     1            Gaps:          0

US-09-769-066-16 (1-549) x AB105894 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCACGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTCGAGCTC 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAACACACGTGTTTCCCGCTACTCGAGTAGT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||  ||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTAACTACGACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGAAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTCAACCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTTTATTCTCGCCCCGTCGTCTCA 412

RESULT 332
AB105895
LOCUS       AB105895                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JA19.
ACCESSION   AB105895
VERSION     AB105895.1  GI:34097991
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JA19"
                     /isolation_source="human serum"
                     /db_xref="taxon:12461"
                     /country="Japan:Hokkaido"
                     /note="genotype IV; sporadic acute hepatitis E"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB105895 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCATGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTCGAGCTC 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAACACACGTGTTTCCCGCTACTCGAGTAGT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||  ||||||||||  ||||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTGACTACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGAAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTTAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 333
AB105896
LOCUS       AB105896                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JF4.
ACCESSION   AB105896
VERSION     AB105896.1  GI:34097993
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="HE-JF4"
                     /isolation_source="human serum"
                     /db_xref="taxon:12461"
                     /country="Japan:Hokkaido"
                     /note="genotype IV; sporadic fulminant hepatitis E"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
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                     /product="capsid protein"
                     /protein_id="BAC82173.1"
                     /db_xref="GI:34097994"
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                     LTPGNTNTRVSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB105896 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCATGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTCGAGCTC 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAACACACGTGTTTCCCGCTACTCGAGTAGT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||  ||||||||||  ||||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTAACTACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGAAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGTTAACTCTGTTCAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 334
AB105897
LOCUS       AB105897                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JF5.
ACCESSION   AB105897
VERSION     AB105897.1  GI:34097995
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
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            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /isolate="HE-JF5"
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                     /country="Japan:Hokkaido"
                     /note="genotype IV; sporadic fulminant hepatitis E"
     gene            1. .412
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     CDS             <1. .>412
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                     /db_xref="GI:34097996"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB105897 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCATGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTCGAGCTC 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAACACACGTGTTTCCCGCTACTCGAGTAGT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              |||||||||   ||||||||||   ||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTAACTACCACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGAAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTCAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 335
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AB105902
LOCUS       AB105902                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:swJL145.
ACCESSION   AB105902
VERSION     AB105902.1  GI:34098005
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="swJL145"
                     /isolation_source="pig liver"
                     /specific_host="swine"
                     /db_xref="taxon:63421"
                     /country="Japan:Hokkaido"
                     /note="genotype IV"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAC82179.1"
                     /db_xref="GI:34098006"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB105902 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCACGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTCGAGCTC 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAACACACGTGTTTCCCGCTACTCGAGTAGT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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                ||||||||| ||||||||||| ||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTAACTACGACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGAAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTCAACCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTTTATTCTCGCCCCGTCGTCTCA 412

RESULT 336
AB107367
LOCUS       AB107367                412 bp    RNA     linear   VRL 07-APR-2004
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate: HE-JAS2.
ACCESSION   AB107367
VERSION     AB107367.1  GI:46250708
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yamamoto,T., Suzuki,H., Toyota,T., Takahashi,M. and Okamoto,H.
  TITLE     Three male patients with sporadic acute hepatitis E in Sendai, who
            were domestically infected with hepatitis E virus of genotype III
            or IV
  JOURNAL   J. Gastroenterol. 39, 292-298 (2004)
   PUBMED   15065009
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-APR-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="HE-JAS2"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Japan:Sendai"
                     /note="genotype IV"
     gene            1. .412
                     /gene="ORF2"
     CDS             <1. .>412
                     /gene="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD15080.1"
                     /db_xref="GI:46250709"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209          Length:         412
Score:                  130.00       Matches:        130
Percent Similarity:     94.89%       Conservative:   0
Best Local Similarity:  94.89%       Mismatches:     7
Query Match:            23.68%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB107367 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCATGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTCGCACTCGAGCTC 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAATTTGACACCCGGTAACACGAACACACGTGTTTCCCGCTACTCGAGTAGT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||| |||||||||| ||||||||||||||||||||||||||||||||||||||
Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTAACTACCACCGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGAAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCGCTAACTCTGTTCAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 337
AB116160
LOCUS       AB116160                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne015-1999.
ACCESSION   AB116160
VERSION     AB116160.1  GI:40809770
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne015-1999"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07300.1"
                     /db_xref="GI:40809771"
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB116160 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTTTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 338
AB116161
LOCUS       AB116161                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne018-1999.
ACCESSION   AB116161
VERSION     AB116161.1  GI:40809772
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne018-1999"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07301.1"
                     /db_xref="GI:40809773"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB116161 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGTATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAACCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGCCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 339
AB116162
LOCUS       AB116162                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne020-1999.
ACCESSION   AB116162
VERSION     AB116162.1  GI:40809774
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
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REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne020-1999"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07302.1"
                     /db_xref="GI:40809775"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB116162 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGTATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAACCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGCCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||  ||||||  ||||||||||||||  ||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 340
AB116163
LOCUS       AB116163                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne025-1999.
ACCESSION   AB116163
VERSION     AB116163.1  GI:40809776
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
  PUBMED    14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="Ne025-1999"
                     /isolation_source="serum"
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                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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                     /note="ORF2"
                     /codon_start=2
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                     /db_xref="GI:40809777"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB116163 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGTATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTCGCAACCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGCCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361
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Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 341
AB116164
LOCUS       AB116164                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne026-1999.
ACCESSION   AB116164
VERSION     AB116164.1  GI:40809778
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /db_xref="GI:40809779"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB116164 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGTATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTCGCAACCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGCCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 342
AB116165
LOCUS       AB116165                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116165
VERSION     AB116165.1  GI:40809780
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB116165 (1-412)
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGTATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTCGCAACCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGCCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412
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RESULT 343
AB116166
LOCUS AB116166 412 bp RNA linear VRL 14-JAN-2004
DEFINITION Hepatitis E virus gene for capsid protein, partial cds, isolate: Ne031-1999.
ACCESSION AB116166
VERSION AB116166.1 GI:40809782
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M., Gotanda,Y. and Okamoto,H.
TITLE Genetic changes in hepatitis E virus of subtype 1a in patients with sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
JOURNAL J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
PUBMED 14718624
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School, Division of Virology, Department of Infection and Immunity; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
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ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:

Pred. No.:	209	Length:	412
Score:	130.00	Matches:	130
Percent Similarity:	94.89%	Conservative:	0
Best Local Similarity:	94.89%	Mismatches:	7
Query Match:	23.68%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AB116166 (1-412)

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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGTATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAACCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGCCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412
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RESULT 344
AB116167
LOCUS AB116167 412 bp RNA linear VRL 14-JAN-2004
DEFINITION Hepatitis E virus gene for capsid protein, partial cds, isolate: Ne032-1999.
ACCESSION AB116167
VERSION AB116167.1 GI:40809784
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M., Gotanda,Y. and Okamoto,H.
TITLE Genetic changes in hepatitis E virus of subtype 1a in patients with sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
JOURNAL J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
PUBMED 14718624
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School, Division of Virology, Department of Infection and Immunity; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
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/virion
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Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB116167 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGTATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTCGCAACCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGCCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 345
AB116168
LOCUS       AB116168                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne033-1999.
ACCESSION   AB116168
VERSION     AB116168.1  GI:40809786
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES              Location/Qualifiers
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Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB116168 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGTATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTTCGCAACCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGCCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 346
AB116169
LOCUS       AB116169                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne034-1999.
ACCESSION   AB116169
VERSION     AB116169.1  GI:40809788
KEYWORDS    .
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SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
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                     /isolation_source="serum"
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                     /country="Nepal:Kathmandu"
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                     /codon_start=2
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                     /db_xref="GI:40809789"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB116169 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 347
AB116170
LOCUS       AB116170                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne035-1999.
ACCESSION   AB116170
VERSION     AB116170.1  GI:40809790
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /db_xref="GI:40809791"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB116170 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412
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RESULT 348
AB116171
LOCUS AB116171 412 bp RNA linear VRL 14-JAN-2004
DEFINITION Hepatitis E virus gene for capsid protein, partial cds, isolate: Ne036-1999.
ACCESSION AB116171
VERSION AB116171.1 GI:40809792
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M., Gotanda,Y. and Okamoto,H.
TITLE Genetic changes in hepatitis E virus of subtype 1a in patients with sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
JOURNAL J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
PUBMED 14718624
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School, Division of Virology, Department of Infection and Immunity; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
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/virion
/mol_type="genomic RNA"
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/db_xref="taxon:12461"
/country="Nepal:Kathmandu"
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ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:

Pred. No.:	209	Length:	412
Score:	130.00	Matches:	130
Percent Similarity:	94.89%	Conservative:	0
Best Local Similarity:	94.89%	Mismatches:	7
Query Match:	23.68%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AB116171 (1-412)

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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412
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RESULT 349
AB116172
LOCUS AB116172 412 bp RNA linear VRL 14-JAN-2004
DEFINITION Hepatitis E virus gene for capsid protein, partial cds, isolate: Ne037-1999.
ACCESSION AB116172
VERSION AB116172.1 GI:40809794
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M., Gotanda,Y. and Okamoto,H.
TITLE Genetic changes in hepatitis E virus of subtype 1a in patients with sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
JOURNAL J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
PUBMED 14718624
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School, Division of Virology, Department of Infection and Immunity; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
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                    ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB116172 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 350
AB116173
LOCUS       AB116173                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne038-1999.
ACCESSION   AB116173
VERSION     AB116173.1  GI:40809796
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB116173 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAATACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 351
AB116174
LOCUS       AB116174                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne040-1999.
ACCESSION   AB116174
VERSION     AB116174.1  GI:40809798
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
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  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne040-1999"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07314.1"
                     /db_xref="GI:40809799"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB116174 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||  ||||||      ||||||||||||||||  ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 352
AB116175
LOCUS       AB116175               412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne045-1999.
ACCESSION   AB116175
VERSION     AB116175.1  GI:40809800
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne045-1999"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07315.1"
                     /db_xref="GI:40809801"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB116175 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||  ||||||      ||||||||||||||||  ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412

RESULT 353
AB116176
LOCUS       AB116176                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne008-2000.
ACCESSION   AB116176
VERSION     AB116176.1  GI:40809802
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne008-2000"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07316.1"
                     /db_xref="GI:40809803"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB116176 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCTCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAACACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||  ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 354
AB116177
LOCUS       AB116177                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne032-2000.
ACCESSION   AB116177
VERSION     AB116177.1  GI:40809804
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /db_xref="taxon:12461"
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     CDS             <1. .>412
                     /note="ORF2"
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB116177 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db            2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy          176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCTCTTGAGCTT 121

Qy          196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
                |||||||||||||||||      ||||||||||||||||||||||||||||||||||||||
Db          122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy          216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy          236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
                |||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db          242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy          256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db          302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy          276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCG 412

RESULT 355
AB116178
LOCUS       AB116178                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne036-2000.
ACCESSION   AB116178
VERSION     AB116178.1  GI:40809806
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /organism="Hepatitis E virus"
                     /virion
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                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07318.1"
                     /db_xref="GI:40809807"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB116178 (1-412)

Qy          156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy          176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCTCTTGAGCTT 121

Qy          196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
                |||||||||||||||||      ||||||||||||||||||||||||||||||||||||||
Db          122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy          216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          182 GCTCGCCACCGCCTTCGTCGTGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy          236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
                |||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db          242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy          256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
                |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db          302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy          276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 356
AB116179
LOCUS       AB116179                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne037-2000.
ACCESSION   AB116179
VERSION     AB116179.1  GI:40809808
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne037-2000"
                     /isolation_source="serum"
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                     /specific_host="human"
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                     /country="Nepal:Kathmandu"
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                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
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                     /db_xref="GI:40809809"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB116179 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACAYGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAAYACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCTCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCYCGCCACCGCCTTCGTCGTGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 357
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LOCUS       AB116180                 412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne045-2000.
ACCESSION   AB116180
VERSION     AB116180.1  GI:40809810
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /isolation_source="serum"
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                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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                     /note="ORF2"
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
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Query Match:            23.68%          Indels:         0
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US-09-769-066-16 (1-549) x AB116180 (1-412)

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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCTCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGTGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 358
AB116181
LOCUS       AB116181                 412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116181
VERSION     AB116181.1  GI:40809812
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
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          Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
          Hepevirus.
REFERENCE 1
  AUTHORS Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
          Gotanda,Y. and Okamoto,H.
  TITLE   Genetic changes in hepatitis E virus of subtype 1a in patients with
          sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED 14718624
REFERENCE 2  (bases 1 to 412)
  AUTHORS Okamoto,H.
  TITLE   Direct Submission
  JOURNAL Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
          Division of Virology, Department of Infection and Immunity; 3311-1
          Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
          Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
          Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB116181 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCTCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACTCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 359
AB116182
LOCUS       AB116182                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116182
VERSION     AB116182.1  GI:40809814
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB116182 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCTCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACTCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 360
AB116183
LOCUS       AB116183                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116183
VERSION     AB116183.1  GI:40809816
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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Alignment Scores:
Pred. No.:              209          Length:         412
Score:                  130.00       Matches:        130
Percent Similarity:     94.89%       Conservative:   0
Best Local Similarity:  94.89%       Mismatches:     7
Query Match:            23.68%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB116183 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 361
AB116184
LOCUS       AB116184                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne055-2000.
ACCESSION   AB116184
VERSION     AB116184.1  GI:40809818
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"
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Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB116184 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 362
AB116185
LOCUS       AB116185                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne057-2000.
ACCESSION   AB116185
VERSION     AB116185.1  GI:40809820
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="Ne057-2000"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /db_xref="GI:40809821"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB116185 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||     ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||     ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 363
AB116186
LOCUS       AB116186                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne059-2000.
ACCESSION   AB116186
VERSION     AB116186.1  GI:40809822
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
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          Division of Virology, Department of Infection and Immunity; 3311-1
          Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
          Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
          Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
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                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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                     /note="ORF2"
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Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB116186 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATTCACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTTTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCAGACGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTTATGAAGGATCTTTATTTTACTAGTACTAATGGCGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTCGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 364
AB116187
LOCUS       AB116187                 412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne060-2000.
ACCESSION   AB116187
VERSION     AB116187.1  GI:40809825
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /db_xref="taxon:12461"
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Alignment Scores:
Pred. No.:                209             Length:         412
Score:                    130.00          Matches:        130
Percent Similarity:       94.89%          Conservative:   0
Best Local Similarity:    94.89%          Mismatches:     7
Query Match:              23.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB116187 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATTCACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTTTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCAGACGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTTATGAAGGATCTTTATTTTACTAGTACTAATGGCGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTCGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412
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RESULT 365
AB116188
LOCUS       AB116188                 412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne068-2000.
ACCESSION   AB116188
VERSION     AB116188.1  GI:40809829
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB116188 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||  ||||||      ||||||||||||||   ||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACCAGTACTAACGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 366
AB116189
LOCUS       AB116189                 412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne078-2000.
ACCESSION   AB116189
VERSION     AB116189.1  GI:40809831
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB116189 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTCCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||  ||||||  ||||||||||||||  ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGTCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 367
AB116190
LOCUS       AB116190                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne013-2002.
ACCESSION   AB116190
VERSION     AB116190.1  GI:40809834
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne013-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07330.1"
                     /db_xref="GI:40809835"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:

Pred. No.:                209             Length:          412
Score:                    130.00          Matches:         130
Percent Similarity:       94.89%          Conservative:    0
Best Local Similarity:    94.89%          Mismatches:      7
Query Match:              23.68%          Indels:          0
DB:                       1               Gaps:            0

US-09-769-066-16 (1-549) x AB116190 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTACACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTCGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAATACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCAGACGGGACTGCCGAGCTCACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||  ||||||  ||||||||||||||  ||||||
Db        242 ACCCGCTTTATGAAGGATCTTTATTTTACTAGTACTAATGGCGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTCGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 368
AB116191
LOCUS       AB116191                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne014-2002.
ACCESSION   AB116191
VERSION     AB116191.1  GI:40809839
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne014-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
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                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
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                     /protein_id="BAD07331.1"
                     /db_xref="GI:40809840"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                209           Length:        412
Score:                    130.00        Matches:       130
Percent Similarity:       94.89%        Conservative:  0
Best Local Similarity:    94.89%        Mismatches:    7
Query Match:              23.68%        Indels:        0
DB:                       1             Gaps:          0

US-09-769-066-16 (1-549) x AB116191 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTGCTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTCGTCTCA 412

RESULT 369
AB116192
LOCUS       AB116192                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne016-2002.
ACCESSION   AB116192
VERSION     AB116192.1  GI:40809843
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES              Location/Qualifiers
     source           1. .412
                      /organism="Hepatitis E virus"
                      /virion
                      /mol_type="genomic RNA"
                      /isolate="Ne016-2002"
                      /isolation_source="serum"
                      /specific_host="human"
                      /db_xref="taxon:12461"
                      /country="Nepal:Kathmandu"
     CDS              <1. .>412
                      /note="ORF2"
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Alignment Scores:
Pred. No.:                209           Length:        412
Score:                    130.00        Matches:       130
Percent Similarity:       94.89%        Conservative:  0
Best Local Similarity:    94.89%        Mismatches:    7
Query Match:              23.68%        Indels:        0
DB:                       1             Gaps:          0

US-09-769-066-16 (1-549) x AB116192 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTCAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTGCTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCTTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTCGTCTCA 412

RESULT 370
AB116197
LOCUS       AB116197                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne032-2002.
ACCESSION   AB116197
VERSION     AB116197.1  GI:40809853
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
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REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /country="Nepal:Kathmandu"
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                     /codon_start=2
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB116197 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412
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RESULT 371
AB116201
LOCUS       AB116201                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne039-2002.
ACCESSION   AB116201
VERSION     AB116201.1  GI:40809868
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /protein_id="BAD07341.1"
                     /db_xref="GI:40809869"
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB116201 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241
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Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||  ||||||      ||||||||||||||||   ||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412

RESULT 372
AB116204
LOCUS       AB116204                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne049-2002.
ACCESSION   AB116204
VERSION     AB116204.1  GI:40809874
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne049-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07344.1"
                     /db_xref="GI:40809875"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB116204 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||  ||||||      ||||||||||||||||   ||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412

RESULT 373
AB116214
LOCUS       AB116214                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne093-2002.
ACCESSION   AB116214
VERSION     AB116214.1  GI:40809896
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne093-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07354.1"
                     /db_xref="GI:40809897"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
                     LTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGI
                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              209           Length:        412
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Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB116214 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412

RESULT 374
AB116217
LOCUS       AB116217                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne105-2002.
ACCESSION   AB116217
VERSION     AB116217.1  GI:40809902
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="Ne105-2002"
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                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB116217 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||   ||||||      ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412

RESULT 375
AB116218
LOCUS       AB116218                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne107-2002.
ACCESSION   AB116218
VERSION     AB116218.1  GI:40809904
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
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           Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
           Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB116218 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412

RESULT 376
AB116219
LOCUS       AB116219                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne117-2002.
ACCESSION   AB116219
VERSION     AB116219.1  GI:40809906
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              209           Length:        412
Score:                  130.00        Matches:       130
Percent Similarity:     94.89%        Conservative:  0
Best Local Similarity:  94.89%        Mismatches:    7
Query Match:            23.68%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB116219 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTCCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412

RESULT 377
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AB116221
LOCUS       AB116221                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116221
VERSION     AB116221.1  GI:40809910
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="Ne122-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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                     /note="ORF2"
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                     /db_xref="GI:40809911"
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
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Query Match:            23.68%          Indels:         0
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US-09-769-066-16 (1-549) x AB116221 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAATCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412

RESULT 378
AB116224
LOCUS       AB116224                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne134-2002.
ACCESSION   AB116224
VERSION     AB116224.1  GI:40809916
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
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US-09-769-066-16 (1-549) x AB116224 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db          62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy         196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db         122 GAGTTCCGTAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy         216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db         182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy         236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db         242 ACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy         256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Qy         276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db         362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCTGTTGTCTCA 412

RESULT 379
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LOCUS       AB124818                412 bp    RNA     linear   VRL 25-MAR-2004
DEFINITION  Swine hepatitis E virus ORF2 gene for capsid protein, partial cds,
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ACCESSION   AB124818
VERSION     AB124818.1  GI:45736452
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wibawa,I.D., Muljono,D.H., Mulyanto, Suryadarma,I.G., Tsuda,F.,
            Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Prevalence of antibodies to hepatitis E virus among apparently
            healthy humans and pigs in Bali, Indonesia: Identification of a pig
            infected with a genotype 4 hepatitis E virus
  JOURNAL   J. Med. Virol. 73 (1), 38-44 (2004)
   PUBMED   15042646
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
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US-09-769-066-16 (1-549) x AB124818 (1-412)

Qy         156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Qy         176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 TCTTATACTAATACACCCTATACCGGCGCTCTTGGTCTGCTTGATTTTGCCCTTGAGCTT 121

Qy         196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db         122 GAGTTCCGTAATTTGACACCTGGTAACACGAATACGCGCGTCTCCCGTTATTCGAGTAGC 181

Qy         216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db         182 GCGCGTCATAAGTTACGCCGAGGGCCTGATGGTACAGCGGAGTTAACCACCACTGCTGCT 241

Qy         236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db         242 ACACGTTTTATGAAAGACCTCCATTTCACCGGGACTAATGGTGTTGGTGAGGTTGGTCGT 301

Qy         256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db         302 GGCATAGCACTAACCCTGTTCAATCTTGCTGATACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy         276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db         362 TTAATTTCGTCGGCTGGTGGCCAGCTGTTTTATTCCCGCCCCGTTGTCTCA 412

RESULT 380
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LOCUS       AB168096                412 bp    RNA     linear   VRL 07-AUG-2004
DEFINITION  Hepatitis E virus ORF2 gene for ORF2, partial cds.
ACCESSION   AB168096
VERSION     AB168096.1  GI:51036203
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Koizumi,Y., Isoda,N., Sato,Y., Iwaki,T., Ono,K., Ido,K., Sugano,K.,
            Takahashi,M., Nishizawa,T. and Okamoto,H.
  TITLE     Infection of a Japanese patient by genotype 4 hepatitis e virus
            while traveling in Vietnam
  JOURNAL   J. Clin. Microbiol. 42 (8), 3883-3885 (2004)
   PUBMED   15297556
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-MAR-2004) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                /country="Viet Nam"
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Alignment Scores:
Pred. No.:              209             Length:         412
Score:                  130.00          Matches:        130
Percent Similarity:     94.89%          Conservative:   0
Best Local Similarity:  94.89%          Mismatches:     7
Query Match:            23.68%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB168096 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAGGCCACCTCCGGCCTTGTTATGCTTTGTATTCATGGGTCACCTGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAATCTGACACCTGGTAATACGAACACGCGTGTCTCCCGTTATTCGAGTAGC 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCGCGTCATAAGTTACGCCGAGGGCCTGACGGCACTGCGGAGCTAACTACTACTGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGTTTTATGAAAGATCTTCATTTTACTGGGACTAATGGTGTTGGTGAAGTTGGCCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGTATAGCACTGACCCTGTTTAATCTTGCTGATACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTAATTTCGTCGGCTGGTGGTCAGCTGTTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 381
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LOCUS       AB085974                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne136,
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ACCESSION   AB085974
VERSION     AB085974.1  GI:27372370
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              212             Length:         412
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Best Local Similarity:  94.16%          Mismatches:     8
Query Match:            23.50%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB085974 (1-412)

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Db          2 GCTGAGGAGGAGGCCACCTCTGGTCTTGTCAAGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        182 GCCCGCCACCGCCTTCGCCGCGGCGCAGACGGGACCGCCGAGCTCACCACCACGGCAGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGCGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTCACCCTGTTTAACCTTGCTGACACTCTCCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 412

RESULT 382
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LOCUS       AB085981                412 bp    RNA     linear   VRL 25-DEC-2002
DEFINITION  Hepatitis E virus  for capsid protein, partial cds, isolate:Ne153.
ACCESSION   AB085981
VERSION     AB085981.1  GI:27372384
KEYWORDS    .
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SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Gotanda,Y.,
            Takeda,N. and Okamoto,H.
  TITLE     Molecular investigation of hepatitis E virus infection in patients
            with acute hepatitis in Kathmandu, Nepal
  JOURNAL   J. Med. Virol. 69, 207-214 (2003)
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2002) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              212           Length:        412
Score:                  129.00        Matches:       129
Percent Similarity:     94.16%        Conservative:  0
Best Local Similarity:  94.16%        Mismatches:    8
Query Match:            23.50%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB085981 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAAGAGGAGGCCACCTCTGGTCTCGTTATGCTTTGCATACATGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCCCTCGAACTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTACTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACCACGGCTGCC 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAGTGGTGTCGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTACCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGTCAGCTGTTCTACTCCCGTCCCGTCGTCTCA 412

RESULT 383
AB105890
LOCUS       AB105890                412 bp    RNA     linear   VRL 22-AUG-2003
DEFINITION  Hepatitis E virus ORF2 gene for capsid protein, partial cds,
            isolate:HE-JA14.
ACCESSION   AB105890
VERSION     AB105890.1  GI:34097981
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Yazaki,Y., Mizuo,H., Takahashi,M., Nishizawa,T., Sasaki,N.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Sporadic acute or fulminant hepatitis E in Hokkaido, Japan, may be
            food-borne, as suggested by the presence of hepatitis E virus in
            pig liver as food
  JOURNAL   J. Gen. Virol. 84 (Pt 9), 2351-2357 (2003)
   PUBMED   12917455
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2003) Hiroaki Okamoto, Jichi Medical School,
            Immunology Division and Division of Molecular Virology; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi-Ken 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /virion
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                     /isolate="HE-JA14"
                     /isolation_source="human serum"
                     /db_xref="taxon:12461"
                     /country="Japan:Hokkaido"
                     /note="genotype IV; sporadic acute hepatitis E"
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     CDS             <1. .>412
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                     /codon_start=2
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                     /db_xref="GI:34097982"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              212           Length:        412
Score:                  129.00        Matches:       129
Percent Similarity:     94.16%        Conservative:  0
Best Local Similarity:  94.16%        Mismatches:    8
Query Match:            23.50%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AB105890 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCGGAGGAGGAGGCGACCTCCGGCCTTGTCATGCTTTGCATCCATGGATCACCTGTGAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACCAATACGCCTTATACTGGTGCCCTTGGCTTGCTTGATTTTGCACTCGAGCTC 121
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTYCGCAATTTGACACCCGGTAACACGAACACACGTGTTTCCCGCTACTCGAGTAGT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCGCGCCACAAGCTACGCCGAGGGCCTGATGGCACTGCTGAGTTAACTACCACCGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACACGCTTTATGAAGGACCTTCATTTTACAGGGACTAATGGAGTTGGTGMAGTCGGTCGT 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGTATAGCGCTAACTCTGTTCAATCTTGCTGACACGCTTCTCGGCGGGCTCCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGTCAGTTGTTTTACTCTCGCCCCGTCGTCTCA 412

RESULT 384
AB116193
LOCUS       AB116193                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne021-2002.
ACCESSION   AB116193
VERSION     AB116193.1  GI:40809845
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="Ne021-2002"
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                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
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                     /db_xref="GI:40809846"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLPYSRPVVS"

Alignment Scores:
Pred. No.:              212          Length:         412
Score:                  129.00       Matches:        129
Percent Similarity:     94.16%       Conservative:   0
Best Local Similarity:  94.16%       Mismatches:     8
Query Match:            23.50%       Indels:         0

DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AB116193 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||  |||        ||||||||||||||   ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 385
AB116194
LOCUS       AB116194                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne023-2002.
ACCESSION   AB116194
VERSION     AB116194.1  GI:40809847
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              212           Length:         412
Score:                  129.00        Matches:        129
Percent Similarity:     94.16%        Conservative:   0
Best Local Similarity:  94.16%        Mismatches:     8
Query Match:            23.50%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AB116194 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCTGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 386
AB116195
LOCUS       AB116195                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116195
VERSION     AB116195.1  GI:40809849
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              212           Length:         412
Score:                  129.00        Matches:        129
Percent Similarity:     94.16%        Conservative:   0
Best Local Similarity:  94.16%        Mismatches:     8
Query Match:            23.50%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AB116195 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||  |||         ||||||||||||||   ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 387
AB116196
LOCUS       AB116196                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne029-2002.
ACCESSION   AB116196
VERSION     AB116196.1  GI:40809851
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
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  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:                212             Length:         412
Score:                    129.00          Matches:        129
Percent Similarity:       94.16%          Conservative:   0
Best Local Similarity:    94.16%          Mismatches:     8
Query Match:              23.50%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB116196 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGYTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGYAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGKTATTCYAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||  |||  ||||||||||||||  ||||||
Db        242 ACCCGCTTCATGAAGGACCTYTATTTTWCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCYGTTGTCTCA 412

RESULT 388
AB116198
LOCUS       AB116198                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne033-2002.

ACCESSION   AB116198
VERSION     AB116198.1  GI:40809860
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne033-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07338.1"
                     /db_xref="GI:40809861"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                212             Length:         412
Score:                    129.00          Matches:        129
Percent Similarity:       94.16%          Conservative:   0
Best Local Similarity:    94.16%          Mismatches:     8
Query Match:              23.50%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB116198 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||  |||  ||||||||||||||  ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
                  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 389
AB116200
LOCUS       AB116200                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne037-2002.
ACCESSION   AB116200
VERSION     AB116200.1  GI:40809866
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne037-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07340.1"
                     /db_xref="GI:40809867"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              212             Length:         412
Score:                  129.00          Matches:        129
Percent Similarity:     94.16%          Conservative:   0
Best Local Similarity:  94.16%          Mismatches:     8
Query Match:            23.50%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB116200 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
                  ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||  |||         ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 390
AB116202
LOCUS       AB116202                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne045-2002.
ACCESSION   AB116202
VERSION     AB116202.1  GI:40809870
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
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                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              212             Length:         412
Score:                  129.00          Matches:        129
Percent Similarity:     94.16%          Conservative:   0
Best Local Similarity:  94.16%          Mismatches:     8
Query Match:            23.50%          Indels:         0
DB:                     1               Gaps:           0
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US-09-769-066-16 (1-549) x AB116202 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||      ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    |||          ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 391
AB116203
LOCUS       AB116203                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne046-2002.
ACCESSION   AB116203
VERSION     AB116203.1  GI:40809872
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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                     /country="Nepal:Kathmandu"
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Alignment Scores:
Pred. No.:                212             Length:          412
Score:                    129.00          Matches:         129
Percent Similarity:       94.16%          Conservative:    0
Best Local Similarity:    94.16%          Mismatches:      8
Query Match:              23.50%          Indels:          0
DB:                       1               Gaps:            0

US-09-769-066-16 (1-549) x AB116203 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||||      ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||||    |||          ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 392
AB116205
LOCUS       AB116205                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne050-2002.
ACCESSION   AB116205
VERSION     AB116205.1  GI:40809877
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              212             Length:         412
Score:                  129.00          Matches:        129
Percent Similarity:     94.16%          Conservative:   0
Best Local Similarity:  94.16%          Mismatches:     8
Query Match:            23.50%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB116205 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||    |||          ||||||||||||||    ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 393
AB116206
LOCUS       AB116206                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne054-2002.
ACCESSION   AB116206
VERSION     AB116206.1  GI:40809879
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
    PUBMED  14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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                     /virion
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                     /db_xref="taxon:12461"
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                     /db_xref="GI:40809880"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Score:                  129.00          Matches:        129
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Query Match:            23.50%          Indels:         0
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US-09-769-066-16 (1-549) x AB116206 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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RESULT 394
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DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116208
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VERSION     AB116208.1  GI:40809884
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              212             Length:         412
Score:                  129.00          Matches:        129
Percent Similarity:     94.16%          Conservative:   0
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US-09-769-066-16 (1-549) x AB116208 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 395
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DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116209
VERSION     AB116209.1  GI:40809886
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              212             Length:         412
Score:                  129.00          Matches:        129
Percent Similarity:     94.16%          Conservative:   0
Best Local Similarity:  94.16%          Mismatches:     8
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US-09-769-066-16 (1-549) x AB116209 (1-412)

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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 396
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LOCUS       AB116210                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116210
VERSION     AB116210.1  GI:40809888
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
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            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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Alignment Scores:
Pred. No.:              212          Length:        412
Score:                  129.00       Matches:       129
Percent Similarity:     94.16%       Conservative:  0
Best Local Similarity:  94.16%       Mismatches:    8
Query Match:            23.50%       Indels:        0
DB:                     1            Gaps:          0
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US-09-769-066-16 (1-549) x AB116210 (1-412)

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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTTATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 397
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LOCUS       AB116211                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116211
VERSION     AB116211.1  GI:40809890
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
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Alignment Scores:
Pred. No.:              212             Length:         412
Score:                  129.00          Matches:        129
Percent Similarity:     94.16%          Conservative:   0
Best Local Similarity:  94.16%          Mismatches:     8
Query Match:            23.50%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB116211 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 398
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LOCUS       AB116212                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116212
VERSION     AB116212.1  GI:40809892
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
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                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:              212             Length:         412
Score:                  129.00          Matches:        129
Percent Similarity:     94.16%          Conservative:   0
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Query Match:            23.50%          Indels:         0
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US-09-769-066-16 (1-549) x AB116212 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 399
AB116213
LOCUS       AB116213                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116213
VERSION     AB116213.1  GI:40809894
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
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REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
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                     ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:              212           Length:         412
Score:                  129.00        Matches:        129
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Best Local Similarity:  94.16%        Mismatches:     8
Query Match:            23.50%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AB116213 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 400
AB116215
LOCUS       AB116215                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne095-2002.
ACCESSION   AB116215
VERSION     AB116215.1  GI:40809898
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              212           Length:         412
Score:                  129.00        Matches:        129
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Best Local Similarity:  94.16%        Mismatches:     8
Query Match:            23.50%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AB116215 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361
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Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 401
AB116216
LOCUS       AB116216                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne098-2002.
ACCESSION   AB116216
VERSION     AB116216.1  GI:40809900
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:                212             Length:         412
Score:                    129.00          Matches:        129
Percent Similarity:       94.16%          Conservative:   0
Best Local Similarity:    94.16%          Mismatches:     8
Query Match:              23.50%          Indels:         0
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US-09-769-066-16 (1-549) x AB116216 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 402
AB116220
LOCUS       AB116220                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne118-2002.
ACCESSION   AB116220
VERSION     AB116220.1  GI:40809908
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:                212             Length:         412
Score:                    129.00          Matches:        129
Percent Similarity:       94.16%          Conservative:   0
Best Local Similarity:    94.16%          Mismatches:     8
Query Match:              23.50%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB116220 (1-412)
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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412
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RESULT 403
AB116222
LOCUS AB116222 412 bp RNA linear VRL 14-JAN-2004
DEFINITION Hepatitis E virus gene for capsid protein, partial cds, isolate: Ne131-2002.
ACCESSION AB116222
VERSION AB116222.1 GI:40809912
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M., Gotanda,Y. and Okamoto,H.
TITLE Genetic changes in hepatitis E virus of subtype 1a in patients with sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
JOURNAL J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
PUBMED 14718624
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School, Division of Virology, Department of Infection and Immunity; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
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Alignment Scores:

Pred. No.:	212	Length:	412
Score:	129.00	Matches:	129
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Query Match:	23.50%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AB116222 (1-412)

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Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
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Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412
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RESULT 404
AB116223
LOCUS AB116223 412 bp RNA linear VRL 14-JAN-2004
DEFINITION Hepatitis E virus gene for capsid protein, partial cds, isolate: Ne133-2002.
ACCESSION AB116223
VERSION AB116223.1 GI:40809914
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1
AUTHORS Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M., Gotanda,Y. and Okamoto,H.
TITLE Genetic changes in hepatitis E virus of subtype 1a in patients with sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
JOURNAL J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
PUBMED 14718624
REFERENCE 2 (bases 1 to 412)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School, Division of Virology, Department of Infection and Immunity; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404, Fax:81-285-44-1557)
FEATURES Location/Qualifiers
source 1. .412
/organism="Hepatitis E virus"
/virion
/mol_type="genomic RNA"

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                /specific_host="human"
                /db_xref="taxon:12461"
                /country="Nepal:Kathmandu"
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                /note="ORF2"
                /codon_start=2
                /product="capsid protein"
                /protein_id="BAD07363.1"
                /db_xref="GI:40809915"
                /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRN
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Alignment Scores:
Pred. No.:                212             Length:         412
Score:                    129.00          Matches:        129
Percent Similarity:       94.16%          Conservative:   0
Best Local Similarity:    94.16%          Mismatches:     8
Query Match:              23.50%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB116223 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
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Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
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Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 405
AB116225
LOCUS       AB116225                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne135-2002.
ACCESSION   AB116225
VERSION     AB116225.1  GI:40809918
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES              Location/Qualifiers
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                      /organism="Hepatitis E virus"
                      /virion
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                      /isolate="Ne135-2002"
                      /isolation_source="serum"
                      /specific_host="human"
                      /db_xref="taxon:12461"
                      /country="Nepal:Kathmandu"
     CDS              <1. .>412
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                      /codon_start=2
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                      /db_xref="GI:40809919"
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                      ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.:                212             Length:         412
Score:                    129.00          Matches:        129
Percent Similarity:       94.16%          Conservative:   0
Best Local Similarity:    94.16%          Mismatches:     8
Query Match:              23.50%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AB116225 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTACACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||  |||  ||||||||||||||  ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 406
AB116226
LOCUS       AB116226                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne138-2002.
ACCESSION   AB116226
VERSION     AB116226.1  GI:40809920
KEYWORDS    .
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SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="Ne138-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
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Alignment Scores:
Pred. No.:              212             Length:         412
Score:                  129.00          Matches:        129
Percent Similarity:     94.16%          Conservative:   0
Best Local Similarity:  94.16%          Mismatches:     8
Query Match:            23.50%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB116226 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412

RESULT 407
AB116227
LOCUS       AB116227                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne139-2002.
ACCESSION   AB116227
VERSION     AB116227.1  GI:40809922
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              212             Length:         412
Score:                  129.00          Matches:        129
Percent Similarity:     94.16%          Conservative:   0
Best Local Similarity:  94.16%          Mismatches:     8
Query Match:            23.50%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB116227 (1-412)

Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||      ||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181
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Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
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Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
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Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTCACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412
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RESULT 408
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LOCUS       AB116199                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
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ACCESSION   AB116199
VERSION     AB116199.1  GI:40809864
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
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Alignment Scores:
Pred. No.:              215             Length:         412
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Best Local Similarity:  93.43%          Mismatches:     9
Query Match:            23.32%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AB116199 (1-412)
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Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTCTGCATACACGGCTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTCGCCCTTGAGCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGAATGCCGAGCTCACCACCACGGCTACT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              |||||||||||||||||||  ||||||      ||||||||||||||   ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTACTAGTACTAATGGTGTTGGTGAGATTGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCTCTCACCCTTTTCAATCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
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Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412
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RESULT 409
AB116207
LOCUS       AB116207                412 bp    RNA     linear   VRL 14-JAN-2004
DEFINITION  Hepatitis E virus gene for capsid protein, partial cds, isolate:
            Ne056-2002.
ACCESSION   AB116207
VERSION     AB116207.1  GI:40809882
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Shrestha,S.M., Shrestha,S., Tsuda,F., Nishizawa,T., Takahashi,M.,
            Gotanda,Y. and Okamoto,H.
  TITLE     Genetic changes in hepatitis E virus of subtype 1a in patients with
            sporadic acute hepatitis E in Kathmandu, Nepal, from 1997 to 2002
  JOURNAL   J. Gen. Virol. 85 (Pt 1), 97-104 (2004)
   PUBMED   14718624
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2003) Hiroaki Okamoto, Jichi Medical School,
            Division of Virology, Department of Infection and Immunity; 3311-1
            Yakushiji, Minamikawachi-Machi, Kawachi-Gun, Tochigi 329-0498,
            Japan (E-mail:hokamoto@jichi.ac.jp, Tel:81-285-58-7404,
            Fax:81-285-44-1557)
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="Ne056-2002"
                     /isolation_source="serum"
                     /specific_host="human"
                     /db_xref="taxon:12461"
                     /country="Nepal:Kathmandu"
     CDS             <1. .>412
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="BAD07347.1"
                     /db_xref="GI:40809883"
                     /translation="AEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALHLEFRN
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ALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVS"

Alignment Scores:
Pred. No.: 215 Length: 412
Score: 128.00 Matches: 128
Percent Similarity: 93.43% Conservative: 0
Best Local Similarity: 93.43% Mismatches: 9
Query Match: 23.32% Indels: 0
DB: 1 Gaps: 0

US-09-769-066-16 (1-549) x AB116207 (1-412)

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Qy        156 AlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsn 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTGAGGAGGAAGCTACCTCTGGTCTCGTTATGCTTTGCATACACGGTTCACCCGTAAAT 61

Qy        176 SerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeu 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db         62 TCTTATACTAACACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTCGCCCTTCATCTT 121

Qy        196 GluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThr 215
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        122 GAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGGTATTCTAGCACT 181

Qy        216 AlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAla 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTTACCACCACGGCTGCT 241

Qy        236 ThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArg 255
              ||||||||||||||||||  |||         ||||||||||||||   ||||||
Db        242 ACCCGCTTCATGAAGGACCTTTATTTTTCTAGTACTAATGGTGTTGGTGAGATCGGCCGC 301

Qy        256 GlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGlu 275
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        302 GGGATAGCCCTTACCCTTTTCAACCTTGCTGACACTCTGCTTGGTGGCCTGCCGACAGAA 361

Qy        276 LeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSer 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TTGATTTCGTCGGCTGGTGGCCAGCTGTTTTACTCCCGCCCCGTTGTCTCA 412
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RESULT 410
AY160125
LOCUS AY160125 438 bp mRNA linear VRL 26-DEC-2003
DEFINITION Hepatitis E virus capsid protein mRNA, partial cds.
ACCESSION AY160125
VERSION AY160125.1 GI:37724689
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 438)
AUTHORS He,J., Kuschner,R.A., Innis,B.L., Caudill,J.D. and Vaughn,D.W.
TITLE Molecular Detection and Sequence Analysis of a New Hepatitis E Virus Isolate from Pakistan
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 438)
AUTHORS He,J., Kuschner,R.A., Innis,B.L., Caudill,J.D. and Vaughn,D.W.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-2002) Department of Virus Diseases, Walter Reed Army Institute of Research, 504 Scott Street, Silver Spring, MD 20910, USA
FEATURES Location/Qualifiers
source 1. .438
/organism="Hepatitis E virus"
/mol_type="mRNA"
/db_xref="taxon:12461"
CDS <1. .>438
/note="ORF-2 structural protein"
/codon_start=1
/product="capsid protein"
/protein_id="AAO18364.1"
/db_xref="GI:37724690"

/translation="LDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGY
PYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSVLALLEDTMD
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Alignment Scores:
Pred. No.: 221 Length: 438
Score: 126.00 Matches: 126
Percent Similarity: 89.36% Conservative: 0
Best Local Similarity: 89.36% Mismatches: 15
Query Match: 22.95% Indels: 0
DB: 1 Gaps: 0

US-09-769-066-16 (1-549) x AY160125 (1-438)

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Qy        403 LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer 422
              |||||||||  ||||||||||||||||||||||||||  |||       |||||||||
Db          1 CTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAGTATTCA 60

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGAACTACT 120

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||  |||   ||||||
Db        121 AAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTTGAGAAT 180

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        181 GCCGCTGGGCATCGGGTTGCTATTTCCACCTACACTACTAGCCTGGGTGCTGGCCCCGTC 240

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502
              |||||||||  |||||||||||||||  |||  ||||||||||||||||||||||||||
Db        241 TCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCTGTGCTAGCATTGCTTGAGGATACC 300

Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522
              |||||||||  ||||||||||||||||||||||||||||||||||||||  |||
Db        301 ATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGCCCCCTT 360

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        361 GGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAG 420

Qy        543 Val 543
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Db        421 GTG 423
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RESULT 411
AF396860
LOCUS AF396860 405 bp RNA linear VRL 03-DEC-2002
DEFINITION Hepatitis E virus isolate 96-Nepalese structural protein 2 gene, partial cds.
ACCESSION AF396860
VERSION AF396860.1 GI:15088672
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 405)
AUTHORS He,J., Innis,B.L., Shrestha,M.P., Clayson,E.T., Scoot,R.M., Linthicum,K.J., Musser,G.G., Gigliotti,S.C., Binn,L.N., Kuschner,R.A. and Vaughn,D.W.
TITLE Evidence that Rodents Are a Reservoir of Hepatitis E Virus for Humans in Nepal
JOURNAL J. Clin. Microbiol. 40 (12), 4493-4498 (2002)
PUBMED 12454141
REFERENCE 2 (bases 1 to 405)
AUTHORS He,J., Shrestha,M.P., Innis,B.L., Scoot,R.M., Linthicum,K.J., Mussert,G.G., Clayson,E.T., Gigliotti,S.C., Binn,L.N., Kuschner,R.A. and Vaughn,D.W.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2001) Virus Diseases, Walter Reed Army Institute of Research, 503 Robert Grant Avenue, Silver Spring, MD 20910, USA

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FEATURES             Location/Qualifiers
     source          1. .405
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="96-Nepalese"
                     /db_xref="taxon:12461"
                     /country="Nepal"
                     /note="RT-PCR amplified from rodent serum"
     CDS             <1. .>405
                     /codon_start=1
                     /product="structural protein 2"
                     /protein_id="AAK84155.1"
                     /db_xref="GI:15088673"
                     /translation="AQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEA
                     GTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALA
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Alignment Scores:
Pred. No.:              239             Length:         405
Score:                  120.00          Matches:        120
Percent Similarity:     90.23%          Conservative:   0
Best Local Similarity:  90.23%          Mismatches:     13
Query Match:            21.86%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF396860 (1-405)

Qy        396 AlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeu 415
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db          1 GCGCAGGCCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACACTTGACGGCCGCCCCCTC 60

Qy        416 ProThrValGluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSer 435
              |||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCT 120

Qy        436 PheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSer 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCTGGGAGGCAGGCACAACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGC 180

Qy        456 AspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThr 475
              ||||||   |||   ||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACCAACTGCTCGTCGAGAATGCCGCCGGGCACCGGGTTGCTATTTCCACTTACACCACT 240

Qy        476 ArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAla 495
              |||||||||||||||||   |||||||||   ||||||||||||||||   ||||||
Db        241 AGCCTGGGTGCTGGACCCGTTTCCATTTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCG 300

Qy        496 LeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPhe 515
              ||||||||||||||||||||   |||||||||   ||||||||||||||||||||||||
Db        301 CTAGCATTGCTTGAGGATACCTTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTC 360

Qy        516 CysProGluCysArgAlaLeuGlyLeuGlnGlyCysAla 528
              ||||||||||||||||   ||||||||||||||||||||
Db        361 TGCCCAGAGTGCCGCCCCCTTGGCCTCCAGGGCTGTGCT 399

RESULT 412
AY568359
LOCUS       AY568359                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 I capsid protein mRNA, partial
            cds.
ACCESSION   AY568359
VERSION     AY568359.1  GI:46403184
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished

REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 I"
                     /country="Algeria"
                     /note="clinical isolate"
     CDS             <1. .>409
                     /codon_start=3
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                     /protein_id="AAS92612.1"
                     /db_xref="GI:46403185"
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Alignment Scores:
Pred. No.:              239             Length:         409
Score:                  120.00          Matches:        120
Percent Similarity:     89.55%          Conservative:   0
Best Local Similarity:  89.55%          Mismatches:     14
Query Match:            21.86%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AY568359 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrVal 418
              ||||||||||||||   |||   ||||||||||||||||||||||||||   |||
Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGTCGCCCTCTTTCTACTATT 65

Qy        419 GluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         66 CAGCAGTACTCTAAGACTTTCTTCGACCTGCCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIle 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGly 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        186 CTTATTGAGAACGCCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeu 498
              |||||||||||   |||||||||   ||||||||||||||   ||||||||||||||||
Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCGCTG 305

Qy        499 LeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||   |||||||||   ||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              ||||||   ||||||||||||||||||||||||||||||||
Db        366 TGCCGACCCCTTGGCCTTCAGGGCTGTGCTTTCCAGTCTACT 407

RESULT 413
AY568365
LOCUS       AY568365                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 A capsid protein mRNA, partial
            cds.
ACCESSION   AY568365
VERSION     AY568365.1  GI:46403196
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
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            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 A"
                     /country="Algeria"
                     /note="clinical isolate"
     CDS             <1. .>409
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                     /protein_id="AAS92618.1"
                     /db_xref="GI:46403197"
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                     EDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTV"

Alignment Scores:
Pred. No.:              239           Length:         409
Score:                  120.00        Matches:        120
Percent Similarity:     89.55%        Conservative:   0
Best Local Similarity:  89.55%        Mismatches:     14
Query Match:            21.86%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AY568365 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrVal 418
              ||||||||||||||||   |||   ||||||||||||||||||||||||||||||   |||
Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGTCGCCCTCTTTCTACTATT 65

Qy        419 GluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              |||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db         66 CAGCAGTACTCTAAGACTTTCTTCGACCTGCCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIle 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGly 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        186 CTTATTGAGAACGCCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeu 498
              |||||||||||   |||||||||   ||||||||||||||   ||||||||||||||||
Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCACTG 305

Qy        499 LeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||   |||||||||   ||||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              ||||||   |||||||||||||||||||||||||||||||||
Db        366 TGTCGCCCCCTTGGCCTTCAGGGATGCGCTTTCCAGTCTACT 407

RESULT 414
AY596463
LOCUS       AY596463                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 B capsid protein mRNA, partial
            cds.
ACCESSION   AY596463
VERSION     AY596463.1  GI:46403200
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Teyssou,R. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 B"
                     /country="Algeria"
                     /note="clinical isolate"
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                     /db_xref="GI:46403201"
                     /translation="TVARSLEWTKVTLDGRPLSTIQQYSKTFFDLPLRGKLSFWEAGT
                     TKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALL
                     EDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTV"

Alignment Scores:
Pred. No.:              239           Length:         409
Score:                  120.00        Matches:        120
Percent Similarity:     89.55%        Conservative:   0
Best Local Similarity:  89.55%        Mismatches:     14
Query Match:            21.86%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AY596463 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrVal 418
              ||||||||||||||||   |||   ||||||||||||||||||||||||||||||   |||
Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGTCGCCCTCTTTCTACTATT 65

Qy        419 GluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              |||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db         66 CAGCAGTACTCTAAGACTTTCTTCGACCTGCCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIle 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGly 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        186 CTTATTGAGAACGCCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeu 498
              |||||||||||   |||||||||   ||||||||||||||   ||||||||||||||||
Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCACTG 305

Qy        499 LeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||   |||||||||   ||||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              ||||||   |||||||||||||||||||||||||||||||||
Db        366 TGCCGGCCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACT 407
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RESULT 415
AF228532
LOCUS       AF228532                397 bp    RNA     linear   VRL 02-FEB-2001
DEFINITION  Hepatitis E virus isolate 95-RCA structural protein gene, partial
            cds.
ACCESSION   AF228532
VERSION     AF228532.1  GI:12656042
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 397)
  AUTHORS   van Cuyck,H. and Viret,J.
  TITLE     Introduction for a modelization of Hepatitis E virus (HEV)
            evolution
  JOURNAL   Acta Biotheor. (2000) In press
REFERENCE   2  (bases 1 to 397)
  AUTHORS   Buisson,Y., Grandadam,M. and Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Transmissible Agents, CRSSA, 24 Ave des
            Maquis du Gresivaudan, BP87, La Tronche 38702, France
FEATURES             Location/Qualifiers
     source          1. .397
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="95-RCA"
                     /db_xref="taxon:12461"
                     /country="Central African Republic"
                     /note="isolated from sporadic case in 1995"
     CDS             <1. .>397
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAK00717.1"
                     /db_xref="GI:12656043"
                     /translation="VARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTT
                     KAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLE
                     DTLDYPARAHTFDDFCPECRPLGLQGCAF"

Alignment Scores:
Pred. No.:              242          Length:         397
Score:                  119.00       Matches:        119
Percent Similarity:     90.84%       Conservative:   0
Best Local Similarity:  90.84%       Mismatches:     12
Query Match:            21.68%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AF228532 (1-397)

Qy        399 ValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrVal 418
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||   |||
Db          3 GTTGCCCGGTCACTCGACTGGACCAAGGTCACGCTCGATGGCCGCCCTCTTTCTACTATT 62

Qy        419 GluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CAGCAGTACTCTAAGACCTTCTTTGTCCTGCCGCTTCGTGGCAAGCTCTCTTTCTGGGAG 122

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIle 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GCGGGTACTACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGTGACCAATTG 182

Qy        459 LeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGly 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 CTCATTGAGAATGCCGCCGGACATCGGGTGGCTATTTCCACCTATACCACTAGCCTAGGT 242

Qy        479 AlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeu 498
              ||||||||||||  |||||||||  ||||||||||||||||  ||||||||||||||||
Db        243 GCTGGCCCTGTTTCCATCTCCGCGGTCGCTGTTTTAGCCCCCCACTCTGCTTTAGCACTG 302

Qy        499 LeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||  |||||||||  ||||||||||||||||||||||||||||||||||||
Db        303 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCACACTTTCGATGATTTCTGCCCGGAG 362

Qy        519 CysArgAlaLeuGlyLeuGlnGlyCysAlaPhe 529
              ||||||  ||||||||||||||||||||||||
Db        363 TGCCGCCCTCTTGGCCTCCAGGGCTGTGCTTTC 395

RESULT 416
AY568357
LOCUS       AY568357                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 K capsid protein mRNA, partial
            cds.
ACCESSION   AY568357
VERSION     AY568357.1  GI:46403180
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 K"
                     /country="Algeria"
                     /note="clinical isolate"
     CDS             <1. .>409
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAS92610.1"
                     /db_xref="GI:46403181"
                     /translation="TVARSLEWTKVTLDGRPLSTIQQYSKTFFDLPLRGKLSFWEAGT
                     TKAGYPYNYNTTASDQLLIENVAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALL
                     EDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTV"

Alignment Scores:
Pred. No.:              242          Length:         409
Score:                  119.00       Matches:        119
Percent Similarity:     88.81%       Conservative:   0
Best Local Similarity:  88.81%       Mismatches:     15
Query Match:            21.68%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AY568357 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrVal 418
              ||||||||||||||||  |||  ||||||||||||||||||||||||||   |||
Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGTCGCCCTCTTTCTACTATT 65

Qy        419 GluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db         66 CAGCAGTACTCTAAGACTTTCTTCGACCTGCCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIle 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGly 478
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||   ||||||
Db        186 CTTATTGAGAACGTCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245
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Qy        479 AlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeu 498
              ||||||||||||   |||||||||   ||||||||||||||||   ||||||||||||||||
Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCGCTG 305

Qy        499 LeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||   |||||||||   ||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              ||||||   ||||||||||||||||||||||||||||||||
Db        366 TGCCGACCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACT 407

RESULT 417
AY568358
LOCUS       AY568358               409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 J capsid protein mRNA, partial
            cds.
ACCESSION   AY568358
VERSION     AY568358.1  GI:46403182
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 J"
                     /country="Algeria"
                     /note="clinical isolate"
     CDS             <1. .>409
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAS92611.1"
                     /db_xref="GI:46403183"
                     /translation="TVARSLEWTKVTLDGRPLSTIQQYSKTFFDLPLRGKLSFWEAGT
                     TKAGYPYNYNTTASDQLLIENVAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALL
                     EDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTV"

Alignment Scores:
Pred. No.:              242           Length:         409
Score:                  119.00        Matches:        119
Percent Similarity:     88.81%        Conservative:   0
Best Local Similarity:  88.81%        Mismatches:     15
Query Match:            21.68%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AY568358 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrVal 418
              ||||||||||||||   |||   ||||||||||||||||||||||||||||   |||
Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGTCGCCCTCTTTCTACTATT 65

Qy        419 GluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         66 CAGCAGTACTCTAAGACTTTCTTCGACCTGCCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIle 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGly 478
              ||||||||||||   ||||||||||||||||||||||||||||||||||||   ||||||
Db        186 CTTATTGAGAACGTCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeu 498
              ||||||||||||   |||||||||   ||||||||||||||||   ||||||||||||||||
Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCACTG 305

Qy        499 LeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||   |||||||||   ||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              ||||||   ||||||||||||||||||||||||||||||||
Db        366 TGCCGGCCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACT 407

RESULT 418
AY568361
LOCUS       AY568361               409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 F capsid protein mRNA, partial
            cds.
ACCESSION   AY568361
VERSION     AY568361.1  GI:46403188
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 F"
                     /country="Algeria"
                     /note="clinical isolate"
     CDS             <1. .>409
                     /codon_start=3
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                     /protein_id="AAS92614.1"
                     /db_xref="GI:46403189"
                     /translation="TVARSLEWTKVTLDGRPLSTIQQYSKTFFDLPLRGKLSFWEAGT
                     TKAGYPYNYNTTASDQLLIENVAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALL
                     EDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTV"

Alignment Scores:
Pred. No.:              242           Length:         409
Score:                  119.00        Matches:        119
Percent Similarity:     88.81%        Conservative:   0
Best Local Similarity:  88.81%        Mismatches:     15
Query Match:            21.68%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AY568361 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrVal 418
              ||||||||||||||   |||   ||||||||||||||||||||||||||||   |||
Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGTCGCCCTCTTTCTACTATT 65
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Qy        419 GluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db         66 CAGCAGTACTCTAAGACTTTCTTCGACCTACCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIle 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGly 478
              ||||||||||||  |||||||||  ||||||||||||||||||||||||||||||||||||
Db        186 CTTATTGAGAACGTCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeu 498
              ||||||||||||  |||||||||  ||||||||||||||||||||||||||||||||||||
Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCACTG 305

Qy        499 LeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||  |||||||||  ||||||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              ||||||  ||||||||||||||||||||||||||||||||||
Db        366 TGTCGCCCCCTTGGCCTTCAGGGATGCGCTTTCCAGTCTACT 407

RESULT 419
AY568362
LOCUS       AY568362                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 E capsid protein mRNA, partial
            cds.
ACCESSION   AY568362
VERSION     AY568362.1  GI:46403190
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 E"
                     /country="Algeria"
                     /note="clinical isolate"
     CDS             <1. .>409
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                     /db_xref="GI:46403191"
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                     EDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTV"

Alignment Scores:
Pred. No.:              242          Length:         409
Score:                  119.00       Matches:        119
Percent Similarity:     88.81%       Conservative:   0
Best Local Similarity:  88.81%       Mismatches:     15
Query Match:            21.68%       Indels:         0
DB:                     1            Gaps:           0
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US-09-769-066-16 (1-549) x AY568362 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrVal 418
              ||||||||||||||||  |||  ||||||||||||||||||||||||||||  |||
Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGCCGGCCTCTTTCTACTATT 65

Qy        419 GluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db         66 CAGCAGTACTCTAAGACTTTCTTCGACCTACCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIle 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGly 478
              ||||||||||||  |||||||||  ||||||||||||||||||||||||||||||||||||
Db        186 CTTATTGAGAACGTCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeu 498
              ||||||||||||  |||||||||  ||||||||||||||||||||||||||||||||||||
Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCGCTG 305

Qy        499 LeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||  |||||||||  ||||||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              ||||||  ||||||||||||||||||||||||||||||||||
Db        366 TGCCGACCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACT 407

RESULT 420
AY568363
LOCUS       AY568363                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 D capsid protein mRNA, partial
            cds.
ACCESSION   AY568363
VERSION     AY568363.1  GI:46403192
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 D"
                     /country="Algeria"
                     /note="clinical isolate"
     CDS             <1. .>409
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAS92616.1"
                     /db_xref="GI:46403193"
                     /translation="TVARSLEWTKVTLDGRPLSTIQQYSKTFFDLPLRGKLSFWEAGT
                     TKAGYPYNYNTTASDQLLIENVAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALL
                     EDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTV"

Alignment Scores:
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Pred. No.:              242           Length:       409
Score:                  119.00        Matches:      119
Percent Similarity:     88.81%        Conservative: 0
Best Local Similarity:  88.81%        Mismatches:   15
Query Match:            21.68%        Indels:       0
DB:                     1             Gaps:         0

US-09-769-066-16 (1-549) x AY568363 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrVal 418
              ||||||||||||||||   |||   ||||||||||||||||||||||||||||||   |||
Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGTCGCCCTCTTTCTACTATT 65

Qy        419 GluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
                |||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db         66 CAGCAGTACTCTAAGACTTTCTTCGACCTACCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIle 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGly 478
              ||||||||||||   ||||||||||||||||||||||||||||||||||||   ||||||
Db        186 CTTATTGAGAACGTCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeu 498
              ||||||||||||   |||||||||   ||||||||||||||||   ||||||||||||||||
Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCACTG 305

Qy        499 LeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||   |||||||||   ||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              ||||||   ||||||||||||||||||||||||||||||||
Db        366 TGCCGACCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACT 407

RESULT 421
AY568364
LOCUS       AY568364                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 C capsid protein mRNA, partial
            cds.
ACCESSION   AY568364
VERSION     AY568364.1  GI:46403194
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 C"
                     /country="Algeria"
                     /note="clinical isolate"
     CDS             <1. .>409
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAS92617.1"
                     /db_xref="GI:46403195"
                     /translation="TVARSLEWTKVTLDGRPLSTIQQHSKTFFDLPLRGKLSFWEAGT
                     TKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALL
                     EDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTV"

Alignment Scores:
Pred. No.:              242           Length:       409
Score:                  119.00        Matches:      119
Percent Similarity:     88.81%        Conservative: 0
Best Local Similarity:  88.81%        Mismatches:   15
Query Match:            21.68%        Indels:       0
DB:                     1             Gaps:         0

US-09-769-066-16 (1-549) x AY568364 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrVal 418
              ||||||||||||||||   |||   ||||||||||||||||||||||||||||||   |||
Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGCCGCCCTCTTTCTACTATT 65

Qy        419 GluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
                |||   ||||||||||||||   ||||||||||||||||||||||||||||||||
Db         66 CAGCAGCACTCTAAGACTTTCTTCGACCTGCCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIle 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGly 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        186 CTTATTGAGAACGCCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeu 498
              ||||||||||||   |||||||||   ||||||||||||||||   ||||||||||||||||
Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCACTG 305

Qy        499 LeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||   |||||||||   ||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              ||||||   ||||||||||||||||||||||||||||||||
Db        366 TGCCGGCCCCTTGGCCTTCAGGGTTGCGCTTTCCAGTCTACT 407

RESULT 422
AY596462
LOCUS       AY596462                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 H capsid protein mRNA, partial
            cds.
ACCESSION   AY596462
VERSION     AY596462.1  GI:46403198
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Teyssou,R. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 H"
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                     /country="Algeria"
                     /note="clinical isolate"
     CDS             <1. .>409
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAS92619.1"
                     /db_xref="GI:46403199"
                     /translation="TVARSLEWTKVTLDGRPLSTIQQHSKTFFDLPLRGKLSFWEAGT
                     TKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALL
                     EDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTV"

Alignment Scores:
Pred. No.:                242             Length:         409
Score:                    119.00          Matches:        119
Percent Similarity:       88.81%          Conservative:   0
Best Local Similarity:    88.81%          Mismatches:     15
Query Match:              21.68%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AY596462 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrVal 418
              ||||||||||||||||   |||   ||||||||||||||||||||||||||||   |||
Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGGCCGCCCTCTTTCTACTATT 65

Qy        419 GluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              |||   ||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         66 CAGCAGCACTCTAAGACTTTCTTCGACCTGCCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIle 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGly 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        186 CTTATTGAGAACGCCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeu 498
              ||||||||||||   |||||||||   ||||||||||||||   ||||||||||||||||
Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCACTG 305

Qy        499 LeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||   |||||||||   ||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              ||||||   |||||||||||||||||||||||||||||||
Db        366 TGCCGACCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACT 407

RESULT 423
AY568360
LOCUS       AY568360                409 bp    mRNA    linear   VRL 27-APR-2004
DEFINITION  Hepatitis E virus clone Tanef 86/87 G capsid protein mRNA, partial
            cds.
ACCESSION   AY568360
VERSION     AY568360.1  GI:46403186
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Evidence for the Hepatitis E virus quasispecies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Grandadam,M., Tebbal,S., Caron,M., Siriwardana,M., Larouze,B.,
            Koeck,J.L., Buisson,Y., Enouf,V. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-2004) Lab. Biol. Med., Hospital Val de Grace, 74
            bd Port Royal, Paris 75230 cedex 05, France
FEATURES             Location/Qualifiers
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     source          1. .409
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Tanefdour 86/87 epidemic"
                     /db_xref="taxon:12461"
                     /clone="Tanef 86/87 G"
                     /country="Algeria"
                     /note="clinical isolate"
     CDS             <1. .>409
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAS92613.1"
                     /db_xref="GI:46403187"
                     /translation="TVARSLEWTKVTLDVRPLSTIQQYSKTFFDLPLRGKLSFWEAGT
                     TKAGYPYNYNTTASDQLLIENVAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALAQL
                     EDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTV"

Alignment Scores:
Pred. No.:                249             Length:         409
Score:                    117.00          Matches:        117
Percent Similarity:       87.31%          Conservative:   0
Best Local Similarity:    87.31%          Mismatches:     17
Query Match:              21.31%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AY568360 (1-409)

Qy        399 ValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrVal 418
              ||||||||||||||||   |||   ||||||||||||||||||   |||||||||   |||
Db          6 GTTGCACGGTCGCTCGAATGGACCAAGGTCACACTCGATGTCCGCCCTCTTTCTACTATT 65

Qy        419 GluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGlu 438
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         66 CAGCAGTACTCTAAGACTTTCTTCGACCTACCGCTCCGTGGTAAGCTCTCCTTCTGGGAG 125

Qy        439 AlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIle 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGCGACCAATTG 185

Qy        459 LeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGly 478
              ||||||||||||   ||||||||||||||||||||||||||||||||||||    ||||||
Db        186 CTTATTGAGAACGTCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACTAGCCTAGGT 245

Qy        479 AlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeu 498
              ||||||||||||   |||||||||   ||||||||||||||||   ||||||||||||||
Db        246 GCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCTTTAGCGCAG 305

Qy        499 LeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGlu 518
              ||||||||||||   |||||||||   ||||||||||||||||||||||||||||||||
Db        306 CTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAG 365

Qy        519 CysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThr 532
              ||||||   |||||||||||||||||||||||||||||||
Db        366 TGCCGTCCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACT 407

RESULT 424
AF172999
LOCUS       AF172999                359 bp    RNA     linear   VRL 14-APR-2000
DEFINITION  Hepatitis E virus isolate Nig1 capsid protein gene, partial cds.
ACCESSION   AF172999
VERSION     AF172999.1  GI:5764617
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Identification of a novel hepatitis E virus in Nigeria
  JOURNAL   J. Gen. Virol. 81 (Pt 4), 903-909 (2000)
  MEDLINE   20191950
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   PUBMED   10725415
REFERENCE   2  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUL-1999) Biology, Hopital Val-de-Grace, 74,
            boulevard de Port Royal, Paris 75005, France
FEATURES             Location/Qualifiers
     source          1. .359
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="Nig1"
                     /db_xref="taxon:12461"
                     /country="Nigeria: Port-Harcourt"
                     /note="strain isolated from a patient with acute
                     hepatitis"
     CDS             <1. .>359
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAD51341.1"
                     /db_xref="GI:5764618"
                     /translation="VTLDGRPLPTIEQYSKSFFVLPLRGKLSFWEAGTTKAGYPYNYN
                     TTASDQILIENAAGHRVAISTYTTSLGAGPVAISAAAVLAPRSALALLEDTLDYPARA
                     HTFDDFCPECRALGLQG"

Alignment Scores:
Pred. No.:                257           Length:         359
Score:                    114.00        Matches:        114
Percent Similarity:       95.80%        Conservative:   0
Best Local Similarity:    95.80%        Mismatches:     5
Query Match:              20.77%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-16 (1-549) x AF172999 (1-359)

Qy        408 ValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheVal 427
              ||||||||||||||||||||||||||||||   ||||||||||||||   |||||||||
Db          1 GTTACTCTTGACGGGCGGCCCCTCCCTACTATTGAGCAGTACTCCAAGTCATTCTTTGTG 60

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGCCCCTTCGCGGTAAGCTCTCTTTTTGGGAGGCTGGTACAACGAAAGCGGGCTACCCT 120

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TATAATTACAACACCACAGCTAGCGACCAGATTTTGATTGAGAATGCAGCCGGCCACCGA 180

Qy        468 ValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAla 487
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        181 GTTGCTATTTCGACCTATACCACCAGCCTTGGGGCTGGCCCGGTCGCAATCTCTGCGGCC 240

Qy        488 AlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGly 507
              ||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        241 GCAGTCTTAGCCCCCCGTTCGGCCTTGGCCCTTCTTGAGGATACCCTTGATTACCCGGCG 300

Qy        508 ArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGly 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGGGCCCATACGTTTGATGATTTTTGCCCTGAGTGCCGTGCCCTGGGTCTCCAGGGT 357

RESULT 425
AF173000
LOCUS       AF173000                359 bp    RNA     linear   VRL 14-APR-2000
DEFINITION  Hepatitis E virus isolate Nig4 capsid protein gene, partial cds.
ACCESSION   AF173000
VERSION     AF173000.1  GI:5764619
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursàget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Identification of a novel hepatitis E virus in Nigeria
  JOURNAL   J. Gen. Virol. 81 (Pt 4), 903-909 (2000)
  MEDLINE   20191950
   PUBMED   10725415
REFERENCE   2  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUL-1999) Biology, Hopital Val-de-Grace, 74,
            boulevard de Port Royal, Paris 75005, France
FEATURES             Location/Qualifiers
     source          1. .359
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="Nig4"
                     /db_xref="taxon:12461"
                     /country="Nigeria: Port-Harcourt"
                     /note="strain isolated from a patient with acute
                     hepatitis"
     CDS             <1. .>359
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                     /product="capsid protein"
                     /protein_id="AAD51342.1"
                     /db_xref="GI:5764620"
                     /translation="VTLDGRPLPTIEQYSKSFFVLPLRGKLSFWEAGTTKAGYPYNYN
                     TTASDQILIENAAGHRVAISTYTTSLGAGPVAISAAAVLAPRSALALLEDTLDYPARA
                     HTFDDFCPECRALGLQG"

Alignment Scores:
Pred. No.:                257           Length:         359
Score:                    114.00        Matches:        114
Percent Similarity:       95.80%        Conservative:   0
Best Local Similarity:    95.80%        Mismatches:     5
Query Match:              20.77%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-16 (1-549) x AF173000 (1-359)

Qy        408 ValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheVal 427
              ||||||||||||||||||||||||||||||   ||||||||||||||   |||||||||
Db          1 GTTACTCTTGACGGGCGGCCCCTCCCTACTATTGAGCAGTACTCCAAGTCATTCTTTGTG 60

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGCCCCTTCGCGGTAAGCTCTCTTTTTGGGAGGCTGGTACAACGAAAGCGGGCTACCCT 120

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TATAATTACAACACCACAGCTAGCGACCAGATTTTGATTGAGAATGCAGCCGGCCACCGA 180

Qy        468 ValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAla 487
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        181 GTTGCTATTTCGACCTATACCACCAGCCTTGGGGCTGGCCCGGTCGCAATCTCTGCGGCC 240

Qy        488 AlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGly 507
              ||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        241 GCAGTCTTAGCCCCCCGTTCGGCCTTGGCCCTTCTTGAGGATACCCTTGATTACCCGGCG 300

Qy        508 ArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGly 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGGGCCCATACGTTTGATGATTTTTGCCCTGAGTGCCGTGCCCTGGGTCTCCAGGGT 357

RESULT 426
AF173001
LOCUS       AF173001                359 bp    RNA     linear   VRL 14-APR-2000
DEFINITION  Hepatitis E virus isolate Nig5 capsid protein gene, partial cds.
ACCESSION   AF173001
VERSION     AF173001.1  GI:5764621
KEYWORDS    .
SOURCE      Hepatitis E virus
```

```
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Identification of a novel hepatitis E virus in Nigeria
  JOURNAL   J. Gen. Virol. 81 (Pt 4), 903-909 (2000)
  MEDLINE   20191950
   PUBMED   10725415
REFERENCE   2  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUL-1999) Biology, Hopital Val-de-Grace, 74,
            boulevard de Port Royal, Paris 75005, France
FEATURES             Location/Qualifiers
     source          1. .359
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="Nig5"
                     /db_xref="taxon:12461"
                     /country="Nigeria: Port-Harcourt"
                     /note="strain isolated from a patient with acute
                     hepatitis"
     CDS             <1. .>359
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAD51343.1"
                     /db_xref="GI:5764622"
                     /translation="VTLDGRPLPTIEQYSKSFFVLPLRGKLSFWEAGTTKAGYPYNYN
                     TTASDQILIENAAGHRVAISTYTTSLGAGPVAISAAAVLAPRSALALLEDTLDYPARA
                     HTFDDFCPECRALGLQG"

Alignment Scores:
Pred. No.:              257           Length:         359
Score:                  114.00        Matches:        114
Percent Similarity:     95.80%        Conservative:   0
Best Local Similarity:  95.80%        Mismatches:     5
Query Match:            20.77%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF173001 (1-359)

Qy        408 ValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheVal 427
              ||||||||||||||||||||||||||||||  ||||||||||||||  |||||||||
Db          1 GTTACTCTTGACGGGCGGCCCCTCCCTACTATTGAGCAGTACTCCAAGTCATTCTTTGTG 60

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGCCCCTTCGCGGTAAGCTCTCTTTTTGGGAGGCTGGTACAACGAAAGCGGGCTACCCT 120

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TATAATTACAACACCACAGCTAGCGACCAGATTTTGATTGAGAATGCAGCCGGCCACCGA 180

Qy        468 ValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAla 487
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        181 GTTGCTATTTCGACCTATACCACCAGCCTTGGGGCTGGCCCGGTCGCAATCTCTGCGGCC 240

Qy        488 AlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGly 507
              ||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db        241 GCAGTCTTAGCCCCCCGTTCGGCCTTGGCCCTTCTTGAGGATACCCTTGATTACCCGGCG 300

Qy        508 ArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGly 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGGGCCCATACGTTTGATGATTTTTGCCCTGAGTGCCGTGCCCTGGGTCTCCAGGGT 357

RESULT 427
AF173230
LOCUS       AF173230                359 bp    RNA     linear   VRL 14-APR-2000
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DEFINITION  Hepatitis E virus strain Nig6 capsid protein gene, partial cds.
ACCESSION   AF173230
VERSION     AF173230.1  GI:5764637
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Identification of a novel hepatitis E virus in Nigeria
  JOURNAL   J. Gen. Virol. 81 (Pt 4), 903-909 (2000)
  MEDLINE   20191950
   PUBMED   10725415
REFERENCE   2  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUL-1999) Biology, Hopital Val-de-Grace, 74,
            Boulevard de Port Royal, Paris 75005, France
FEATURES             Location/Qualifiers
     source          1. .359
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="Nig6"
                     /db_xref="taxon:12461"
                     /country="Nigeria: Port-Harcourt"
                     /note="isolated from a patient with acute hepatitis"
     CDS             <1. .>359
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAD51353.1"
                     /db_xref="GI:5764638"
                     /translation="VTLDGRPLPTIEQYSKSFFVLPLRGKLSFWEAGTTKAGYPYNYN
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                     HTFDDFCPECRALGLQG"

Alignment Scores:
Pred. No.:              257           Length:         359
Score:                  114.00        Matches:        114
Percent Similarity:     95.80%        Conservative:   0
Best Local Similarity:  95.80%        Mismatches:     5
Query Match:            20.77%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF173230 (1-359)

Qy        408 ValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheVal 427
              ||||||||||||||||||||||||||||||  ||||||||||||||  |||||||||
Db          1 GTTACTCTTGACGGGCGGCCCCTCCCTACTATTGAGCAGTACTCCAAGTCATTCTTTGTG 60

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGCCCCTTCGCGGTAAGCTCTCTTTTTGGGAGGCTGGTACAACGAAAGCGGGCTACCCT 120

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TATAATTACAACACCACAGCTAGCGACCAGATTTTGATTGAGAATGCAGCCGGCCACCGA 180

Qy        468 ValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAla 487
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        181 GTTGCTATTTCGACCTATACCACCAGCCTTGGGGCTGGCCCGGTCGCAATCTCTGCGGCC 240

Qy        488 AlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGly 507
              ||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db        241 GCAGTCTTAGCCCCCCGTTCGGCCTTGGCCCTTCTTGAGGATACCCTTGATTACCCGGCG 300

Qy        508 ArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGly 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        301 CGGGCCCATACGTTTGATGATTTTTGCCCTGAGTGCCGTGCCCTGGGTCTCCAGGGT 357

RESULT 428
AF173231
LOCUS       AF173231                359 bp    RNA     linear   VRL 14-APR-2000
DEFINITION  Hepatitis E virus strain Nig7 capsid protein gene, partial cds.
ACCESSION   AF173231
VERSION     AF173231.1  GI:5764639
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Identification of a novel hepatitis E virus in Nigeria
  JOURNAL   J. Gen. Virol. 81 (Pt 4), 903-909 (2000)
  MEDLINE   20191950
   PUBMED   10725415
REFERENCE   2  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUL-1999) Biology, Hopital Val-de-Grace, 74,
            Boulevard de Port Royal, Paris 75005, France
FEATURES             Location/Qualifiers
     source          1. .359
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="Nig7"
                     /db_xref="taxon:12461"
                     /country="Nigeria: Port-Harcourt"
                     /note="isolated from a patient with acute hepatitis"
     CDS             <1. .>359
                     /note="ORF2"
                     /codon_start=1
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                     /protein_id="AAD51354.1"
                     /db_xref="GI:5764640"
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                     HTFDDFCPECRALGLQG"

Alignment Scores:
Pred. No.:              257           Length:         359
Score:                  114.00        Matches:        114
Percent Similarity:     95.80%        Conservative:   0
Best Local Similarity:  95.80%        Mismatches:     5
Query Match:            20.77%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF173231 (1-359)

Qy        408 ValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheVal 427
              ||||||||||||||||||||||||||||||  ||||||||||||||  |||||||||
Db          1 GTTACTCTTGACGGGCGGCCCCTCCCTACTATTGAGCAGTACTCCAAGTCATTCTTTGTG 60

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGCCCCTTCGCGGTAAGCTCTCTTTTTGGGAGGCTGGTACAACGAAAGCGGGCTACCCT 120

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TATAATTACAACACCACAGCTAGCGACCAGATTTTGATTGAGAATGCAGCCGGCCACCGA 180

Qy        468 ValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAla 487
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        181 GTTGCTATTTCGACCTATACCACCAGCCTTGGGGCTGGCCCGGTCGCAATCTCTGCGGCC 240

Qy        488 AlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGly 507
              ||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db        241 GCAGTCTTAGCCCCCCGTTCGGCCTTGGCCCTTCTTGAGGATACCCTTGATTACCCGGCG 300

Qy        508 ArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGly 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGGGCCCATACGTTTGATGATTTTTGCCCTGAGTGCCGTGCCCTGGGTCTCCAGGGT 357

RESULT 429
AF173232
LOCUS       AF173232                359 bp    RNA     linear   VRL 14-APR-2000
DEFINITION  Hepatitis E virus strain Nig9 capsid protein gene, partial cds.
ACCESSION   AF173232
VERSION     AF173232.1  GI:5764641
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Identification of a novel hepatitis E virus in Nigeria
  JOURNAL   J. Gen. Virol. 81 (Pt 4), 903-909 (2000)
  MEDLINE   20191950
   PUBMED   10725415
REFERENCE   2  (bases 1 to 359)
  AUTHORS   Buisson,Y., Grandadam,M., Nicand,E., Cheval,P., van
            Cuyck-Gandre,H., Innis,B., Rehel,P., Coursaget,P., Teyssou,R. and
            Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUL-1999) Biology, Hopital Val-de-Grace, 74,
            Boulevard de Port Royal, Paris 75005, France
FEATURES             Location/Qualifiers
     source          1. .359
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="Nig9"
                     /db_xref="taxon:12461"
                     /country="Nigeria: Port-Harcourt"
                     /note="isolated from a patient with acute hepatitis"
     CDS             <1. .>359
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAD51355.1"
                     /db_xref="GI:5764642"
                     /translation="VTLDGRPLPTIEQYSKSFFVLPLRGKLSFWEAGTTKAGYPYNYN
                     TTASDQILIENAAGHRVAISTYTTSLGAGPVAISAAAVLAPRSALALLEDTLDYPARA
                     HTFDDFCPECRALGLQG"

Alignment Scores:
Pred. No.:              257           Length:         359
Score:                  114.00        Matches:        114
Percent Similarity:     95.80%        Conservative:   0
Best Local Similarity:  95.80%        Mismatches:     5
Query Match:            20.77%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF173232 (1-359)

Qy        408 ValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheVal 427
              ||||||||||||||||||||||||||||||  ||||||||||||||  |||||||||
Db          1 GTTACTCTTGACGGGCGGCCCCTCCCTACTATTGAGCAGTATTCCAAGTCATTCTTTGTG 60

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGCCCCTTCGCGGTAAGCTCTCTTTTTGGGAGGCTGGTACAACGAAAGCGGGCTACCCT 120

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TATAATTACAACACCACAGCTAGCGATCAGATTTTGATCGAGAATGCAGCCGGCCACCGA 180
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Qy        468 ValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAla 487
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        181 GTTGCTATTTCGACCTATACCACCAGTCTTGGGGCTGGCCCGGTCGCAATCTCTGCGGCC 240

Qy        488 AlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGly 507
              ||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||
Db        241 GCGGTCTTAGCCCCCCGTTCGGCCTTGGCCCTTCTTGAGGATACGCTTGATTACCCGGCG 300

Qy        508 ArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGly 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGGGCCCATACATTTGATGATTTTTGCCCTGAGTGCCGTGCCCTGGGTCTCCAGGGT 357

RESULT 430
AR150919
LOCUS       AR150919                449 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 13 from patent US 6229005.
ACCESSION   AR150919
VERSION     AR150919.1  GI:15115510
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 449)
  AUTHORS   Reyes,G.R., Yarbough,P.O., Bradley,D.W., Krawczynski,K.Z., Tam,A.W.
            and Fry,K.E.
  TITLE     DNA sequences of enterically transmitted non-A/non-B hepatitis
            viral agent
  JOURNAL   Patent: US 6229005-A 13 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .449
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:                260             Length:         449
Score:                    114.00          Matches:        114
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              20.77%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AR150919 (1-449)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 165

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 225

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 285

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 345

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
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Db        346 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 405

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsn 114
              ||||||||||||||||||||||||||||||||||||||||||
Db        406 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAAT 447

RESULT 431
AR207637
LOCUS       AR207637                449 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 13 from patent US 6379891.
ACCESSION   AR207637
VERSION     AR207637.1  GI:21507443
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 449)
  AUTHORS   Reyes,G.R., Yarbough,P.O., Bradley,D.W., Krawczynski,K.Z., Tam,A.
            and Fry,K.E.
  TITLE     Method of detecting HEV infection
  JOURNAL   Patent: US 6379891-A 13 30-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .449
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                     /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:                260             Length:         449
Score:                    114.00          Matches:        114
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              20.77%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AR207637 (1-449)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 165

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 225

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 285

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 345

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 405

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsn 114
              ||||||||||||||||||||||||||||||||||||||||||
Db        406 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAAT 447

RESULT 432
AY621097
LOCUS       AY621097                348 bp    RNA     linear   VRL 27-JUN-2004
DEFINITION  Swine hepatitis E virus isolate swCH116 capsid protein gene,
            partial cds.
ACCESSION   AY621097
VERSION     AY621097.1  GI:49036116
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
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                /mol_type="genomic RNA"
                /isolate="swCH116"
                /isolation_source="pig feces"
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     CDS        <1. .>348
                /note="ORF2"
                /codon_start=1
                /product="capsid protein"
                /protein_id="AAT48731.1"
                /db_xref="GI:49036117"
                /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              270             Length:         348
Score:                  110.00          Matches:        110
Percent Similarity:     94.83%          Conservative:   0
Best Local Similarity:  94.83%          Mismatches:     6
Query Match:            20.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AY621097 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCATGCTTTGCATACATGGCTCACCTGTGAATTCTTACACTAATACACCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              |||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGCCTACTTGATTTCGCACTTGAGCTTGAGTTCCGTAACTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||||||||   |||||||||   ||||||||||||||
Db        121 ACTAATACGCGTGTTTCTCGTTACTCGAGTAGCGCGCGACACAAATTGCGCCGAGGGGCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGTACTGCTGAGCTTACTACCACTGCTGCCACACGTTTTATGAAAGACCTTCACTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACGGGAACTAATGGTGTTGGCGAGGTCGGTCGTGGTATAGCGTTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGACACGCTTCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348

RESULT 433
AY621100
LOCUS       AY621100                348 bp    RNA     linear   VRL 27-JUN-2004
DEFINITION  Swine hepatitis E virus isolate swCH110 capsid protein gene,
            partial cds.
ACCESSION   AY621100
VERSION     AY621100.1  GI:49036122
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="swCH110"
                     /isolation_source="pig feces"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT48734.1"
                     /db_xref="GI:49036123"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              270             Length:         348
Score:                  110.00          Matches:        110
Percent Similarity:     94.83%          Conservative:   0
Best Local Similarity:  94.83%          Mismatches:     6
Query Match:            20.04%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AY621100 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTTATGCTTTGCATACATGGCTCACCTGTGAATTCTTACACTAATACACCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
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Db         61 GCCCTCGGCCTACTTGATTTCGCACTTGAGCTTGAGTTCCGTAATTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||||||||   |||||||||   ||||||||||||||
Db        121 ACTAATACGCGTGTTTCTCGTTACTCGAGTAGCGCGCGACACAAATTGCGCCGAGGGGCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGTACTGCTGAGCTTACTACCACTGCTGCCACACGTTTTATGAAAGACCTTCACTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACGGGAACTAATGGTGTTGGCGAGGTCGGTCGTGGTATAGCGTTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCCGACACGCTTCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 434
HEE344171
LOCUS       HEE344171               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 87.
ACCESSION   AJ344171
VERSION     AJ344171.1  GI:15282367
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
```

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  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="mRNA"
                     /isolate="87"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51490.1"
                     /db_xref="GI:15282368"
                     /db_xref="GOA:Q91ED0"
                     /db_xref="UniProt/TrEMBL:Q91ED0"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:                270             Length:         348
Score:                    110.00          Matches:        110
Percent Similarity:       94.83%          Conservative:   0
Best Local Similarity:    94.83%          Mismatches:     6
Query Match:              20.04%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x HEE344171 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCATGCTTTGCATACATGGCTCACCTGTGAACTCCTATACCAATACACCTTATACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTTGGCCTGCTCGATTTTGCGCTTGAGCTTGAGTTTCGTAATTTGACACCCGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||    |||||||||    ||||||||||||||||
Db        121 ACAAACACGCGCGTTTCTCGTTATTCGAGCAGTGCGCGCCACAAACTGCGCCGGGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGGCACTGCTGAGCTAACTACTACTGCTGCCACACGGTTTATGAAGGATCTTCATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||    ||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        241 ACAGGGACTAATGGTGTTGGTGAGGTCGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGACACACTTCTCGGCGGGCTTCCGACAGAATTGATTTCGTCGGCT 348

RESULT 435
AF117275
LOCUS       AF117275                346 bp    mRNA    linear   VRL 12-SEP-2000
DEFINITION  Hepatitis E virus strain TW8E-2 nucleocapsid protein mRNA, partial
            cds.
ACCESSION   AF117275
VERSION     AF117275.1  GI:10086226
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 346)
  AUTHORS   Wu,J.C., Chen,C.M., Chiang,T.Y., Sheen,I.J., Chen,J.Y., Tsai,W.H.,
            Huang,Y.H. and Lee,S.D.
  TITLE     Clinical and epidemiological implications of swine hepatitis E
            virus infection
  JOURNAL   J. Med. Virol. 60 (2), 166-171 (2000)
  MEDLINE   20062925
   PUBMED   10596016
REFERENCE   2  (bases 1 to 346)
  AUTHORS   Wu,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-DEC-1998) Division of Gastroenterology, Department of
            Medicine, Graduate Institute of Clinical Medicine, Veterans General
            Hospital-Taipei, National Yang-Ming University School of Medicine,
            Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .346
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="TW8E-2"
                     /db_xref="taxon:12461"
                     /country="Taiwan"
                     /note="isolated from a patient with acute hepatitis"
     CDS             <1. .>346
                     /note="ORF2"
                     /codon_start=1
                     /product="nucleocapsid protein"
                     /protein_id="AAG12448.1"
                     /db_xref="GI:10086227"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISS"

Alignment Scores:
Pred. No.:                274             Length:         346
Score:                    109.00          Matches:        109
Percent Similarity:       94.78%          Conservative:   0
Best Local Similarity:    94.78%          Mismatches:     6
Query Match:              19.85%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF117275 (1-346)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTATGCTTTGCATACATGGCTCACCTGTGAACTCCTATACCAATACACCTTATACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCTCTCGGCCTGCTCGACTTCGCGCTTGAGCTTGAGTTTCGTAATTTGACACCTGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||    |||||||||    ||||||||||||||||
Db        121 ACAAACACGCGCGTTTCTCGTTATTCGAGCAGTGCACGCCACAAATTGCGCCGAGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGGCACCGCTGAGCTAACTACTACTGCTGCTACACGGTTTATGAAGGATCTTCATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||    ||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        241 ACAGGGACTAATGGTGTTGGTGAGGTTGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSer 279
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACACTTCTCGGCGGGCTCCCGACAGAATTGATTTCGTCG 345

RESULT 436
AF117278
LOCUS       AF117278                346 bp    mRNA    linear   VRL 12-SEP-2000
DEFINITION  Hepatitis E virus strain TW6196E nucleocapsid protein mRNA, partial
            cds.
ACCESSION   AF117278
VERSION     AF117278.1  GI:10086232
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
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           Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
           Hepevirus.
REFERENCE  1  (bases 1 to 346)
  AUTHORS  Wu,J.C., Chen,C.M., Chiang,T.Y., Sheen,I.J., Chen,J.Y., Tsai,W.H.,
           Huang,Y.H. and Lee,S.D.
  TITLE    Clinical and epidemiological implications of swine hepatitis E
           virus infection
  JOURNAL  J. Med. Virol. 60 (2), 166-171 (2000)
  MEDLINE  20062925
   PUBMED  10596016
REFERENCE  2  (bases 1 to 346)
  AUTHORS  Wu,J.C.
  TITLE    Direct Submission
  JOURNAL  Submitted (31-DEC-1998) Division of Gastroenterology, Department of
           Medicine, Graduate Institute of Clinical Medicine, Veterans General
           Hospital-Taipei, National Yang-Ming University School of Medicine,
           Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .346
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="TW6196E"
                     /db_xref="taxon:12461"
                     /country="Taiwan"
                     /note="isolated from a patient with acute hepatitis"
     CDS             <1. .>346
                     /codon_start=1
                     /product="nucleocapsid protein"
                     /protein_id="AAG12451.1"
                     /db_xref="GI:10086233"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                     TLLGGLPTELISS"

Alignment Scores:
Pred. No.:              274           Length:         346
Score:                  109.00        Matches:        109
Percent Similarity:     94.78%        Conservative:   0
Best Local Similarity:  94.78%        Mismatches:     6
Query Match:            19.85%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF117278 (1-346)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTTATGCTTTGCATACATGGCTCACCTGTGAACTCCTATACCAATACACCTTATACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCTCTCGGCCTGCTCGACTTCGCGCTTGAGCTTGAGTTTCGTAATTTGACACCTGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||||    |||||||||    ||||||||||||||||
Db        121 ACAAACACGCGCGTTTCTCGTTATTCGAGCAGTGCACGCCACAAATTGCGCCGAGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
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Db        181 GACGGCACCGCTGAGCTAACTACTACTGCTGCTACACGGTTTATGAAGGATCTTCATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACAGGGACTAATGGTGTTGGTGAGGTTGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSer 279
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACACTTCTCGGCGGGCTCCCGACAGAATTGATTTCGTCG 345

RESULT 437
AF117279
LOCUS       AF117279                346 bp    mRNA    linear   VRL 12-SEP-2000
DEFINITION  Hepatitis E virus strain TW6310E nucleocapsid protein mRNA, partial
            cds.
ACCESSION   AF117279
VERSION     AF117279.1  GI:10086234
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 346)
  AUTHORS   Wu,J.C., Chen,C.M., Chiang,T.Y., Sheen,I.J., Chen,J.Y., Tsai,W.H.,
            Huang,Y.H. and Lee,S.D.
  TITLE     Clinical and epidemiological implications of swine hepatitis E
            virus infection
  JOURNAL   J. Med. Virol. 60 (2), 166-171 (2000)
  MEDLINE   20062925
   PUBMED   10596016
REFERENCE   2  (bases 1 to 346)
  AUTHORS   Wu,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-DEC-1998) Division of Gastroenterology, Department of
            Medicine, Graduate Institute of Clinical Medicine, Veterans General
            Hospital-Taipei, National Yang-Ming University School of Medicine,
            Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .346
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="TW6310E"
                     /db_xref="taxon:12461"
                     /country="Taiwan"
                     /note="isolated from a patient with acute hepatitis"
     CDS             <1. .>346
                     /note="ORF2"
                     /codon_start=1
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                     TLLGGLPTELISS"

Alignment Scores:
Pred. No.:              274           Length:         346
Score:                  109.00        Matches:        109
Percent Similarity:     94.78%        Conservative:   0
Best Local Similarity:  94.78%        Mismatches:     6
Query Match:            19.85%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF117279 (1-346)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTTATGCTTTGCATACATGGCTCACCTGTGAACTCCTACACTAATACACCTTACACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCTCTTGGCCTGCTCGATTTTGCGCTTGAGCTTGAGTTTCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||||    |||||||||    ||||||||||||||||
Db        121 ACAAACACGCGCGTCTCTCGTTATTCGAGCAGTGCGCGCCATAAACTGCGCCGAGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGGTACTGCTGAATTGACTACTACTGCTGCTACACGATTTATGAAGGATCTTCATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACAGGGACTAATGGCGTAGGTGAGGTTGGTCGCGGGATAGCGCTTACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSer 279
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACACTTCTCGGCGGTCTCCCGACAGAATTGATTTCGTCG 345
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RESULT 438
AY596309
LOCUS AY596309 348 bp RNA linear VRL 09-MAY-2004
DEFINITION Swine hepatitis E virus strain swCH70 capsid protein gene, partial cds.
ACCESSION AY596309
VERSION AY596309.1 GI:46981703
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Detection and analysis of partial sequences of swine hepatitis E virus in Xinjiang
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Direct Submission
JOURNAL Submitted (09-APR-2004) College of Animal Medicine, Nanjing Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu 210095, P. R. China
FEATURES Location/Qualifiers
source 1. .348
/organism="Swine hepatitis E virus"
/mol_type="genomic RNA"
/strain="swCH70"
/db_xref="taxon:63421"
CDS <1. .>348
/note="ORF2"
/codon_start=1
/product="capsid protein"
/protein_id="AAT07938.1"
/db_xref="GI:46981704"
/translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
TLLGGLPTELISSA"

Alignment Scores:

Pred. No.:	274	Length:	348
Score:	109.00	Matches:	109
Percent Similarity:	93.97%	Conservative:	0
Best Local Similarity:	93.97%	Mismatches:	7
Query Match:	19.85%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AY596309 (1-348)

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Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTTATGCTCTGCATACATGGCTCGCCTGTGAACTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||    |||||||||    ||||||||||||
Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGCAGCGCACGTCATAAATTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGTACTGCAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGATACGTTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348
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RESULT 439
AY596315
LOCUS AY596315 348 bp RNA linear VRL 09-MAY-2004
DEFINITION Swine hepatitis E virus strain swCH24 capsid protein gene, partial cds.
ACCESSION AY596315
VERSION AY596315.1 GI:46981715
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Detection and analysis of partial sequences of swine hepatitis E virus in Xinjiang
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Direct Submission
JOURNAL Submitted (09-APR-2004) College of Animal Medicine, Nanjing Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu 210095, P. R. China
FEATURES Location/Qualifiers
source 1. .348
/organism="Swine hepatitis E virus"
/mol_type="genomic RNA"
/strain="swCH24"
/db_xref="taxon:63421"
CDS <1. .>348
/note="ORF2"
/codon_start=1
/product="capsid protein"
/protein_id="AAT07944.1"
/db_xref="GI:46981716"
/translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
TLLGGLPTELISSA"

Alignment Scores:

Pred. No.:	274	Length:	348
Score:	109.00	Matches:	109
Percent Similarity:	93.97%	Conservative:	0
Best Local Similarity:	93.97%	Mismatches:	7
Query Match:	19.85%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AY596315 (1-348)

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Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCATGCTCTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||    |||||||||    ||||||||||||
Db        121 ACTAATACGCGCGTTTCTCGCTATTCGAGTAGCGCACGTCATAAACTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGTACTGCAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGATACGCTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348
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RESULT 440
AY621098
LOCUS       AY621098                348 bp    RNA     linear   VRL 27-JUN-2004
DEFINITION  Swine hepatitis E virus isolate swCH112 capsid protein gene,
            partial cds.
ACCESSION   AY621098
VERSION     AY621098.1  GI:49036118
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="swCH112"
                     /isolation_source="pig feces"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT48732.1"
                     /db_xref="GI:49036119"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              274           Length:         348
Score:                  109.00        Matches:        109
Percent Similarity:     93.97%        Conservative:   0
Best Local Similarity:  93.97%        Mismatches:     7
Query Match:            19.85%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AY621098 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCATGTTTTGCATACATGGCTCACCTGTGAATTCTTACACTAATACACCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGCCTACTTGATTTCGCACTTGAGCTTGAGTTCCGTAATTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||||   |||||||||   ||||||||||||||||
Db        121 ACTAATACGCGTGTTTCTCGTTACTCGAGTAGCGCGCGACACAAATTGCGCCGAGGGGCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGTACTGCTGAGCTTACTACCACTGCTGCCACACGTTTTATGAAAGACCTTCACTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACGGGAACTAATGGTGTTGGCGAGGTCGGTCGTGGTATAGCGTTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCCGACACGCTTCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 441
AY621099
LOCUS       AY621099                348 bp    RNA     linear   VRL 27-JUN-2004
DEFINITION  Swine hepatitis E virus isolate swCH111 capsid protein gene,
            partial cds.
ACCESSION   AY621099
VERSION     AY621099.1  GI:49036120
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="swCH111"
                     /isolation_source="pig feces"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT48733.1"
                     /db_xref="GI:49036121"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              274           Length:         348
Score:                  109.00        Matches:        109
Percent Similarity:     93.97%        Conservative:   0
Best Local Similarity:  93.97%        Mismatches:     7
Query Match:            19.85%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AY621099 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCATGTTTTGCATACATGGCTCACCTGTGAATTCTTACACTAATACACCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGCCTACTTGATTTCGCACTTGAGCTTGAGTTCCGTAATTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||||   |||||||||   ||||||||||||||||
Db        121 ACTAATACGCGTGTTTCTCGTTACTCGAGTAGCGCGCGACACAAATTGCGCCGAGGGGCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGTACTGCTGAGCTTACTACCACTGCTGCCACACGTTTTATGAAAGACCTTCACTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACGGGAACTAATGGTGTTGGCGAGGTCGGTCGTGGTATAGCGTTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCCGACACGCTTCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 442
HEE344172
LOCUS       HEE344172                348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 292.
ACCESSION   AJ344172
VERSION     AJ344172.1  GI:15282369
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="mRNA"
                     /isolate="292"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51491.1"
                     /db_xref="GI:15282370"
                     /db_xref="GOA:Q91EC9"
                     /db_xref="UniProt/TrEMBL:Q91EC9"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAN
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              274             Length:         348
Score:                  109.00          Matches:        109
Percent Similarity:     93.97%          Conservative:   0
Best Local Similarity:  93.97%          Mismatches:     7
Query Match:            19.85%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x HEE344172 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTATGCTTTGCATACATGGCTCACCTGTGAACTCCTATACCAATACACCTTATACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db         61 GCCCTTGGCCTGCTCGATTTTGCGCTTGAGCTTGAGTTTCGTAATTTGACACCCGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||  |||||||||  ||||||||||||||||||
Db        121 ACAAACACGCGCGTTTCTCGTTATTCGAGCAGTGCGCGCCACAAACTGCGCCGGGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        181 GACGGCACTGCTGAGCTAACTACTACTGCTGCCACACGGTTTATGAAGGATCTTCATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||  ||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        241 ACAGGGACTAATGGTGTTGGTGAGGTCGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||  ||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTAACACACTTCTCGGCGGGCTTCCGACAGAATTGATTTCGTCGGCT 348

RESULT 443
HEE344179
LOCUS       HEE344179                348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 241.
ACCESSION   AJ344179
VERSION     AJ344179.1  GI:15282383
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="mRNA"
                     /isolate="241"
                     /db_xref="taxon:12461"
     CDS             <1. .>345
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51498.1"
                     /db_xref="GI:15282384"
                     /db_xref="GOA:Q91EC2"
                     /db_xref="UniProt/TrEMBL:Q91EC2"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                     TLLGGLPTELISS"

Alignment Scores:
Pred. No.:              274             Length:         348
Score:                  109.00          Matches:        109
Percent Similarity:     93.97%          Conservative:   0
Best Local Similarity:  93.97%          Mismatches:     7
Query Match:            19.85%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x HEE344179 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGTTTTGCATACATGGCTCACCTGTAAACTCCTACACTAATACACCTTACACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db         61 GCTCTTGGCCTGCTCGACTTTGCGCTTGAGCTTGAGTTTCGTAATTTGACACCTGGCAAC 120
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Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   |||||||||||||||
Db        121 ACAAACACGCGCGTCTCTCGCTATTCGAGCAGTGCGCGCCATAAACTGCGCCGAGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGGCACTGCTGAGCTAACCACTACTGCTGCCACACGGTTTATGAAAGATCTTCATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACAGGGACCAACGGTGTTGGTGAGGTCGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACACTTCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 444
HEE344180
LOCUS       HEE344180               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 255.
ACCESSION   AJ344180
VERSION     AJ344180.1  GI:15282385
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="mRNA"
                     /isolate="255"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51499.1"
                     /db_xref="GI:15282386"
                     /db_xref="GOA:Q91EC1"
                     /db_xref="UniProt/TrEMBL:Q91EC1"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              274           Length:        348
Score:                  109.00        Matches:       109
Percent Similarity:     93.97%        Conservative:  0
Best Local Similarity:  93.97%        Mismatches:    7
Query Match:            19.85%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x HEE344180 (1-348)
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Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTATGTTTTGCATACATGGCTCACCTGTAAACTCCTACACTAATACACCTTACACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db         61 GCTCTTGGCCTGCTCGACTTTGCGCTTGAGCTTGAGTTTCGTAATTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   |||||||||||||||
Db        121 ACAAACACGCGCGTCTCTCGCTATTCGAGCAGTGCGCGCCATAAACTGCGCCGAGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGGCACTGCTGAGCTAACCACTACTGCTGCCACACGGTTTATGAAAGATCTTCATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACAGGGACCAACGGTGTTGGTGAGGTTGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACACTTCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 445
HEE344183
LOCUS       HEE344183               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 277.
ACCESSION   AJ344183
VERSION     AJ344183.1  GI:15282391
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="mRNA"
                     /isolate="277"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51502.1"
                     /db_xref="GI:15282392"
                     /db_xref="GOA:Q91EB8"
                     /db_xref="UniProt/TrEMBL:Q91EB8"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              274           Length:        348
Score:                  109.00        Matches:       109
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Percent Similarity:     93.97%          Conservative:  0
Best Local Similarity:  93.97%          Mismatches:    7
Query Match:            19.85%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-16 (1-549) x HEE344183 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTATGTTTTGCATACATGGCTCACCTGTGAACTCCTATACCAATACACCTTATACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTTGGCCTGCTCGATTTTGCGCTTGAGCTTGAGTTTCGTAATTTGACACCCGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||  ||||||||  ||||||||||||||||||
Db        121 ACAAACACGCGCGTTTCTCGTTATTCGAGCAGTGCGCGCCACAAACTGCGCCGGGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGGCACTGCTGAGCTAACTACTACTGCTGCCACACGGTTTATGAAGGATCTTCATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||  ||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        241 ACAGGGACTAATGGTGTTGGTGAGGTCGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGACACACTTCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348

RESULT 446
HEE344184
LOCUS       HEE344184               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 202.
ACCESSION   AJ344184
VERSION     AJ344184.1  GI:15282393
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="mRNA"
                     /isolate="202"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51503.1"
                     /db_xref="GI:15282394"
                     /db_xref="GOA:Q91EB7"
                     /db_xref="UniProt/TrEMBL:Q91EB7"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              274             Length:        348
Score:                  109.00          Matches:       109
Percent Similarity:     93.97%          Conservative:  0
Best Local Similarity:  93.97%          Mismatches:    7
Query Match:            19.85%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-16 (1-549) x HEE344184 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTATGCTTTGCATACATGGCTCACCTGTGAATTCCTACACTAATACACCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGCTTACTTGATTTTGCACTCGAGCTCGAGTTCCGCAACTTAACACCTGGCAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||  ||||||||  ||||||||||||||||||
Db        121 ACTAACACGCGCGTTTCCCGCTATTCGAGTAGCGCGCGTCACAAATTGCGCCGAGGGCCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGCACTGCTGAGTTGACTACTACTGCTGCCACACGCTTTATGAAAGACCTCCATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||  ||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        241 ACGGGGACCAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACTCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGACACGCTTCTCGGTGGGCTTCCGACAGAATTGATTTCGTCGGCT 348

RESULT 447
HEE344192
LOCUS       HEE344192               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 210.
ACCESSION   AJ344192
VERSION     AJ344192.1  GI:15282409
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
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                     /db_xref="taxon:12461"
     CDS             <1. .>348
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                     /note="ORF2"
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                     /product="capsid protein"
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                     /db_xref="GI:15282410"
                     /db_xref="GOA:Q91EA9"
                     /db_xref="UniProt/TrEMBL:Q91EA9"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              274           Length:        348
Score:                  109.00        Matches:       109
Percent Similarity:     93.97%        Conservative:  0
Best Local Similarity:  93.97%        Mismatches:    7
Query Match:            19.85%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x HEE344192 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTTATGCTTTGCATACATGGCTCACCTGTAAATTCCTATACTAATACACCTTACACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGTTTGCTTGACTTTGCACTCGAACTCGAGTTTCGCAATTTGACACCTGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
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Db        121 ACGAACACGCGTGTCTCCCGTTATTCGAGTAGCGCGCGTCACAAGTTGCGCCGAGGACCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGGTACAGCGGAGCTAACTACTACTGCTGCTACACGTTTTATGAAAGACCTTCATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACTGGGACTAATGGTGTTGGTGAGGTTGGTCGTGGTATAGCACTGACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGCTTCTTGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 448
HEE344193
LOCUS       HEE344193               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 266.
ACCESSION   AJ344193
VERSION     AJ344193.1  GI:15282411
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="mRNA"
                     /isolate="266"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
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                     /db_xref="GI:15282412"
                     /db_xref="GOA:Q91EA8"
                     /db_xref="UniProt/TrEMBL:Q91EA8"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              274           Length:        348
Score:                  109.00        Matches:       109
Percent Similarity:     93.97%        Conservative:  0
Best Local Similarity:  93.97%        Mismatches:    7
Query Match:            19.85%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x HEE344193 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGTTTTGCATACATGGCTCACCTGTAAACTCCTACACTAATACACCTTACACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCTCTTGGCCTGCTCGACTTTGCGCTTGAGCTTGAGTTTCGTAATTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||||   |||||||||   ||||||||||||||||
Db        121 ACAAACACGCGCGTCTCTCGCTATTCGAGCAGTGCGCGCCATAAACTGCGCCGAGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGGCACTGCTGAGCTAACCACTACTGCTGCCACACGGTTTATGAAAGATCTTCATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACAGGGACCAACGGTGTTGGTGAGGTCGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGATACACTTCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 449
HEE344194
LOCUS       HEE344194               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 287.
ACCESSION   AJ344194
VERSION     AJ344194.1  GI:15282413
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
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REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
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                     /virion
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                     /db_xref="taxon:12461"
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                     /note="ORF2"
                     /codon_start=1
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Alignment Scores:
Pred. No.:              274             Length:         348
Score:                  109.00          Matches:        109
Percent Similarity:     93.97%          Conservative:   0
Best Local Similarity:  93.97%          Mismatches:     7
Query Match:            19.85%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x HEE344194 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGTTTTGCATACATGGCTCACCTGTAAACTCCTACACTAATACACCTTACACTGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCTCTTGGCCTGCTCGACTTTGCGCTTGAGCTTGAGTTTCGTAATTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||||||
Db        121 ACAAACACGCGCGTCTCTCGCTATTCGAGCAGTGCGCGCCATAAACTGCGCCGAGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGGCACTGCTGAGCTAACCACTACTGCTGCCACACGGTTTATGAAAGATCTTCATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACAGGGACCAACGGTGTTGGTGAGGTTGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACACTTCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 450
AF117276
LOCUS       AF117276                346 bp    mRNA    linear   VRL 12-SEP-2000
DEFINITION  Hepatitis E virus strain TW 2494E nucleocapsid protein mRNA,
            partial cds.
ACCESSION   AF117276
VERSION     AF117276.1  GI:10086228
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 346)
  AUTHORS   Wu,J.C., Chen,C.M., Chiang,T.Y., Sheen,I.J., Chen,J.Y., Tsai,W.H.,
            Huang,Y.H. and Lee,S.D.
  TITLE     Clinical and epidemiological implications of swine hepatitis E
            virus infection
  JOURNAL   J. Med. Virol. 60 (2), 166-171 (2000)
  MEDLINE   20062925
   PUBMED   10596016
REFERENCE   2  (bases 1 to 346)
  AUTHORS   Wu,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-DEC-1998) Division of Gastroenterology, Department of
            Medicine, Graduate Institute of Clinical Medicine, Veterans General
            Hospital-Taipei, National Yang-Ming University School of Medicine,
            Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .346
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                     /mol_type="mRNA"
                     /strain="TW2494E"
                     /db_xref="taxon:12461"
                     /country="Taiwan"
                     /note="isolated from a patient with acute hepatitis"
     CDS             <1. .>346
                     /note="ORF2"
                     /codon_start=1
                     /product="nucleocapsid protein"
                     /protein_id="AAG12449.1"
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                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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Alignment Scores:
Pred. No.:              277             Length:         346
Score:                  108.00          Matches:        108
Percent Similarity:     93.91%          Conservative:   0
Best Local Similarity:  93.91%          Mismatches:     7
Query Match:            19.67%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF117276 (1-346)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
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Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCTCTCGGCCTGCTCGACTTCGCGCTTGAGCTTGAGTTTCGTAATTTGACACCTGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||||||
Db        121 ACAAACACGCGCGTTTCTCGTTATTCGAGCAGTGCACGCCACAAATTGCGCCGAGGGGCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGGCACCGCTGAGCTAACTACTACTGCTGCTACACGGTTTATGAAGGATCTTCATTCT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACAGGGACTAATGGTGTTGGTGAGGTTGGCCGTGGGATAGCGCTTACCTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSer 279
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACACTTCTCGGCGGGCTCCCGACAGAATTGATTTCGTCG 345

RESULT 451
AF117277
LOCUS       AF117277                346 bp    mRNA    linear   VRL 12-SEP-2000
DEFINITION  Hepatitis E virus strain TW5483E nucleocapsid protein mRNA, partial
            cds.
ACCESSION   AF117277
VERSION     AF117277.1  GI:10086230
KEYWORDS    .
```

```
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 346)
  AUTHORS   Wu,J.C., Chen,C.M., Chiang,T.Y., Sheen,I.J., Chen,J.Y., Tsai,W.H.,
            Huang,Y.H. and Lee,S.D.
  TITLE     Clinical and epidemiological implications of swine hepatitis E
            virus infection
  JOURNAL   J. Med. Virol. 60 (2), 166-171 (2000)
  MEDLINE   20062925
   PUBMED   10596016
REFERENCE   2  (bases 1 to 346)
  AUTHORS   Wu,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-DEC-1998) Division of Gastroenterology, Department of
            Medicine, Graduate Institute of Clinical Medicine, Veterans General
            Hospital-Taipei, National Yang-Ming University School of Medicine,
            Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .346
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="TW5483E"
                     /db_xref="taxon:12461"
                     /country="Taiwan"
                     /note="isolated from a patient with acute hepatitis"
     CDS             <1. .>346
                     /note="ORF2"
                     /codon_start=1
                     /product="nucleocapsid protein"
                     /protein_id="AAG12450.1"
                     /db_xref="GI:10086231"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISS"

Alignment Scores:
Pred. No.:              277          Length:         346
Score:                  108.00       Matches:        108
Percent Similarity:     93.91%       Conservative:   0
Best Local Similarity:  93.91%       Mismatches:     7
Query Match:            19.67%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AF117277 (1-346)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTATGCTTTGCATACATGGCTCACCTGTAAATTCCTATACTAACACACCCTACACTGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGTCTGCTCGATTTCGCACTCGAGCTCGAGTTTCGTAATTTAACACCTGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||||    |||||||||   ||||||||||||
Db        121 ACGAACACGCGTGTCTCCCGTTATTCGAGTAGTGCGCGTCATAAGCTACGCCGAGGGCCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGCACAGCAGAACTAACCACCACTGCTGCGACACGTTTTATGAAAGATTTACATTTC 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACCGGGACTAATGGTGTTGGTGAGGTTGGTCGTGGTATAGCACTAACCCTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSer 279
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGCTTCTCGGCGGGCTTCCGACAGAATTGATTTCGTCG 345

RESULT 452
AY596308
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LOCUS       AY596308                348 bp    RNA     linear   VRL 09-MAY-2004
DEFINITION  Swine hepatitis E virus strain swCH72 capsid protein gene, partial
            cds.
ACCESSION   AY596308
VERSION     AY596308.1  GI:46981701
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-APR-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="swCH72"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT07937.1"
                     /db_xref="GI:46981702"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              277          Length:         348
Score:                  108.00       Matches:        108
Percent Similarity:     93.10%       Conservative:   0
Best Local Similarity:  93.10%       Mismatches:     8
Query Match:            19.67%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AY596308 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCATGTTCTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||||    |||||||||   ||||||||||||
Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGTAGCGCACGTCATAAATTGCGCCGTGGGCCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGTACTGCAGAACTGACTACTACTGCCGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGTTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348

RESULT 453
AY596311
```

```
LOCUS       AY596311                348 bp    RNA     linear   VRL 09-MAY-2004
DEFINITION  Swine hepatitis E virus strain swCH62 capsid protein gene, partial
            cds.
ACCESSION   AY596311
VERSION     AY596311.1  GI:46981707
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-APR-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="swCH62"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT07940.1"
                     /db_xref="GI:46981708"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              277             Length:         348
Score:                  108.00          Matches:        108
Percent Similarity:     93.10%          Conservative:   0
Best Local Similarity:  93.10%          Mismatches:     8
Query Match:            19.67%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AY596311 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTATGTTTTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||||
Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGCAGCGCACGTCATAAATTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGTACTGCAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGTTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348

RESULT 454
AY596312
```

```
LOCUS       AY596312                348 bp    RNA     linear   VRL 09-MAY-2004
DEFINITION  Swine hepatitis E virus strain swCH57 capsid protein gene, partial
            cds.
ACCESSION   AY596312
VERSION     AY596312.1  GI:46981709
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-APR-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="swCH57"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT07941.1"
                     /db_xref="GI:46981710"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              277             Length:         348
Score:                  108.00          Matches:        108
Percent Similarity:     93.10%          Conservative:   0
Best Local Similarity:  93.10%          Mismatches:     8
Query Match:            19.67%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AY596312 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCATGTTTTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||||
Db        121 ACTAATACGCGCGTTTCCCGCTATTCGAGTAGCGCACGTCATAAGCTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGTACTGCAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGCTGCTCGGCGGGCTTCCGACAGAATTGATTTCGTCGGCT 348

RESULT 455
AY596313
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```
LOCUS       AY596313                348 bp    RNA     linear   VRL 09-MAY-2004
DEFINITION  Swine hepatitis E virus strain swCH28 capsid protein gene, partial
            cds.
ACCESSION   AY596313
VERSION     AY596313.1  GI:46981711
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-APR-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="swCH28"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT07942.1"
                     /db_xref="GI:46981712"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              277           Length:         348
Score:                  108.00        Matches:        108
Percent Similarity:     93.10%        Conservative:   0
Best Local Similarity:  93.10%        Mismatches:     8
Query Match:            19.67%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AY596313 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCATGTTTTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||    |||||||||   ||||||||||||
Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGCAGCGCACGTCATAAATTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGTACTGCAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGTTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348

RESULT 456
AY596317
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LOCUS       AY596317                348 bp    RNA     linear   VRL 09-MAY-2004
DEFINITION  Swine hepatitis E virus strain swCH22 capsid protein gene, partial
            cds.
ACCESSION   AY596317
VERSION     AY596317.1  GI:46981719
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-APR-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="swCH22"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT07946.1"
                     /db_xref="GI:46981720"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              277           Length:         348
Score:                  108.00        Matches:        108
Percent Similarity:     93.10%        Conservative:   0
Best Local Similarity:  93.10%        Mismatches:     8
Query Match:            19.67%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AY596317 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTATGTTTTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||    |||||||||   ||||||||||||
Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGCAGCGCACGTCATAAATTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGTACTGCAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGTTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348

RESULT 457
AY596318
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```
LOCUS       AY596318                348 bp    RNA     linear   VRL 09-MAY-2004
DEFINITION  Swine hepatitis E virus strain swCH15 capsid protein gene, partial
            cds.
ACCESSION   AY596318
VERSION     AY596318.1  GI:46981721
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-APR-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="swCH15"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT07947.1"
                     /db_xref="GI:46981722"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              277             Length:         348
Score:                  108.00          Matches:        108
Percent Similarity:     93.10%          Conservative:   0
Best Local Similarity:  93.10%          Mismatches:     8
Query Match:            19.67%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AY596318 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTATGTTTTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||     |||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGCAGCGCACGTCATAAATTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGTACTGCAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGTTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCA 348

RESULT 458
AY596319
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LOCUS       AY596319                348 bp    RNA     linear   VRL 09-MAY-2004
DEFINITION  Swine hepatitis E virus strain swCH12 capsid protein gene, partial
            cds.
ACCESSION   AY596319
VERSION     AY596319.1  GI:46981723
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-APR-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="swCH12"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT07948.1"
                     /db_xref="GI:46981724"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSTRHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              277             Length:         348
Score:                  108.00          Matches:        108
Percent Similarity:     93.10%          Conservative:   0
Best Local Similarity:  93.10%          Mismatches:     8
Query Match:            19.67%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AY596319 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTATGCTTTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||     |||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGCAGCACACGTCATAAATTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGTACTGCGGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGTTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348

RESULT 459
AY596320
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LOCUS       AY596320                348 bp    RNA     linear   VRL 09-MAY-2004
DEFINITION  Swine hepatitis E virus strain swCH11 capsid protein gene, partial
            cds.
ACCESSION   AY596320
VERSION     AY596320.1  GI:46981725
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-APR-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="swCH11"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT07949.1"
                     /db_xref="GI:46981726"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              277           Length:         348
Score:                  108.00        Matches:        108
Percent Similarity:     93.10%        Conservative:   0
Best Local Similarity:  93.10%        Mismatches:     8
Query Match:            19.67%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AY596320 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTATGTTTTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGCAGCGCACGTCATAAACTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGTACTGCAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACGGGGACTAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACCTTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGCTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348

RESULT 460
AY621096
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LOCUS       AY621096                348 bp    RNA     linear   VRL 27-JUN-2004
DEFINITION  Swine hepatitis E virus isolate swCH119 capsid protein gene,
            partial cds.
ACCESSION   AY621096
VERSION     AY621096.1  GI:49036114
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="swCH119"
                     /isolation_source="pig feces"
                     /db_xref="taxon:63421"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT48730.1"
                     /db_xref="GI:49036115"
                     /translation="VMFCIHGSPVNSYTNTSYTGALGLLDFALELEFRNLTPGNTNTR
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              277           Length:         348
Score:                  108.00        Matches:        108
Percent Similarity:     93.10%        Conservative:   0
Best Local Similarity:  93.10%        Mismatches:     8
Query Match:            19.67%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AY621096 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||||||||||||||||||||||||   |||||||||
Db          1 GTTATGTTTTGCATACATGGCTCACCTGTGAATTCTTACACTAATACATCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGCCTACTTGATTTCGCACTTGAGCTTGAGTTCCGTAACTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||||
Db        121 ACTAATACGCGTGTTTCTCGTTACTCGAGTAGCGCGCGACACAAATTGCGCCGAGGGGCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGTACTGCTGAGCTTACTACCACTGCTGCCACACGTTTTATGAAAGACCTTCACTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACGGGAACTAATGGTGTTGGCGAGGTCGGTCGTGGTATAGCGTTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCCGACACGCTTCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 461
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HEE344182
LOCUS       HEE344182                348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 1,
            isolate 152.
ACCESSION   AJ344182
VERSION     AJ344182.1  GI:15282389
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
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                     /mol_type="mRNA"
                     /isolate="152"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51501.1"
                     /db_xref="GI:15282390"
                     /db_xref="GOA:Q91EB9"
                     /db_xref="UniProt/TrEMBL:Q91EB9"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFASTNGVGEIGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              277             Length:         348
Score:                  108.00          Matches:        108
Percent Similarity:     93.10%          Conservative:   0
Best Local Similarity:  93.10%          Mismatches:     8
Query Match:            19.67%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x HEE344182 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTTATGCTTTGCATACATGGCTCACCCGTAAATTCTTACACTAATACACCCTACACCGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGGCTGTTGGATTTTGCCCTTGAACTTGAGTTCCGCAACCTCACTCCCGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAATACTCGGGTCTCTCGTTACTCCAGCACTGCTCGCCACCGTCTTCGCCGCGGTGCA 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db        181 GATGGGACCGCCGAGCTCACCACCACGGCTGCCACCCGCTTTATGAAGGATCTCTATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
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Db        241 GCTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGACACTCTGCTTGGCGGCCTACCGACAGAATTAATTTCGTCGGCT 348

RESULT 462
HEE344185
LOCUS       HEE344185                348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 253.
ACCESSION   AJ344185
VERSION     AJ344185.1  GI:15282395
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="mRNA"
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                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51504.1"
                     /db_xref="GI:15282396"
                     /db_xref="GOA:Q91EB6"
                     /db_xref="UniProt/TrEMBL:Q91EB6"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              277             Length:         348
Score:                  108.00          Matches:        108
Percent Similarity:     93.10%          Conservative:   0
Best Local Similarity:  93.10%          Mismatches:     8
Query Match:            19.67%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x HEE344185 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGTTTTGCATACATGGCTCACCTGTGAATTCCTACACTAATACACCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGCTTACTTGATTTTGCACTCGAGCTCGAGTTCCGCAACTTAACACCTGGCAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACTAACACGCGCGTTTCCCGCTATTCGAGTAGCGCGCGTCACAAATTGCGCCGAGGGCCT 180
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Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGTACTGCTGAGTTGACTACTACTGCTGCCACACGCTTTATGAAAGACCTCCATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACGGGGACCAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACTCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGACACGCTTCTCGGTGGGCTTCCGACAGAATTAATTTCGTCGGCT 348

RESULT 463
HEE344191
LOCUS       HEE344191                348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 194.
ACCESSION   AJ344191
VERSION     AJ344191.1  GI:15282407
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
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                     /db_xref="GI:15282408"
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                     /db_xref="UniProt/TrEMBL:Q91EB0"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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Alignment Scores:
Pred. No.:              277           Length:         348
Score:                  108.00        Matches:        108
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Best Local Similarity:  93.10%        Mismatches:     8
Query Match:            19.67%        Indels:         0
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US-09-769-066-16 (1-549) x HEE344191 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGTTTTGCATACATGGCTCACCTGTGAATTCCTACACTAATACACCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
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Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
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Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
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Db        181 GATGGTACTGCTGAGTTGACTACTACTGCTGCCACACGCTTTATGAAAGACCTCCATTTT 240

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Db        241 ACGGGGACCAATGGTGTTGGTGAGGTCGGTCGTGGTATAGCGTTAACTCTGTTTAATCTT 300

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RESULT 464
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LOCUS       AF117280                 346 bp    mRNA    linear   VRL 12-SEP-2000
DEFINITION  Swine hepatitis E virus strain TW32SW nucleocapsid protein mRNA,
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ACCESSION   AF117280
VERSION     AF117280.1  GI:10086236
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 346)
  AUTHORS   Wu,J.C., Chen,C.M., Chiang,T.Y., Sheen,I.J., Chen,J.Y., Tsai,W.H.,
            Huang,Y.H. and Lee,S.D.
  TITLE     Clinical and epidemiological implications of swine hepatitis E
            virus infection
  JOURNAL   J. Med. Virol. 60 (2), 166-171 (2000)
  MEDLINE   20062925
   PUBMED   10596016
REFERENCE   2  (bases 1 to 346)
  AUTHORS   Wu,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-DEC-1998) Division of Gastroenterology, Department of
            Medicine, Graduate Institute of Clinical Medicine, Veterans General
            Hospital-Taipei, National Yang-Ming University School of Medicine,
            Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
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                     /db_xref="GI:10086237"
                     /translation="VMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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Alignment Scores:
Pred. No.:              281           Length:         346
Score:                  107.00        Matches:        107
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Best Local Similarity:  93.04%        Mismatches:     8
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DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF117280 (1-346)
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Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
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Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
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Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSer 279
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Db        301 GCTGATACGCTTCTCGGCGGGCTTCCGACAGAATTGATTTCGTCG 345
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RESULT 465
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LOCUS AF117281 346 bp mRNA linear VRL 12-SEP-2000
DEFINITION Swine hepatitis E virus strain TW74SW nucleocapsid protein mRNA, partial cds.
ACCESSION AF117281
VERSION AF117281.1 GI:10086238
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 346)
AUTHORS Wu,J.C., Chen,C.M., Chiang,T.Y., Sheen,I.J., Chen,J.Y., Tsai,W.H., Huang,Y.H. and Lee,S.D.
TITLE Clinical and epidemiological implications of swine hepatitis E virus infection
JOURNAL J. Med. Virol. 60 (2), 166-171 (2000)
MEDLINE 20062925
PUBMED 10596016
REFERENCE 2 (bases 1 to 346)
AUTHORS Wu,J.C.
TITLE Direct Submission
JOURNAL Submitted (31-DEC-1998) Division of Gastroenterology, Department of Medicine, Graduate Institute of Clinical Medicine, Veterans General Hospital-Taipei, National Yang-Ming University School of Medicine, Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES Location/Qualifiers
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Alignment Scores:
Pred. No.: 281 Length: 346
Score: 107.00 Matches: 107
Percent Similarity: 93.04% Conservative: 0
Best Local Similarity: 93.04% Mismatches: 8
Query Match: 19.49% Indels: 0
DB: 1 Gaps: 0

US-09-769-066-16 (1-549) x AF117281 (1-346)

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Db          1 GTAATGCTTTGCATTCACGGGTCACCTGTGAATTCTTACACTAACACACCCTACACTGGT 60

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Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
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Db        121 ACGAACACGCGTGTCTCCCGTTATTCGAGCAGCGCGCGTCATAAGCTACGCCGAGGGCCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
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Db        301 GCTGATACGCCTCTCGGTGGGCTCCCGACAGAATTGATTTCGTCG 345
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RESULT 466
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LOCUS AY596310 348 bp RNA linear VRL 09-MAY-2004
DEFINITION Swine hepatitis E virus strain swCH65 capsid protein gene, partial cds.
ACCESSION AY596310
VERSION AY596310.1 GI:46981705
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Detection and analysis of partial sequences of swine hepatitis E virus in Xinjiang
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 348)
AUTHORS Ma,X. and Lu,C.P.
TITLE Direct Submission
JOURNAL Submitted (09-APR-2004) College of Animal Medicine, Nanjing Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu 210095, P. R. China
FEATURES Location/Qualifiers
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TLLGGLPTELISSA"

Alignment Scores:
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Score: 107.00 Matches: 107
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US-09-769-066-16 (1-549) x AY596310 (1-348)

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Db          1 GTTATGTTTTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
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Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
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Db        301 GCTGATACGTTGCTCGGCGGGCTTCCGACAGAATTAATTTCGTCGGCT 348

RESULT 467
AY596314
LOCUS       AY596314                348 bp    RNA     linear   VRL 09-MAY-2004
DEFINITION  Swine hepatitis E virus strain swCH25 capsid protein gene, partial
            cds.
ACCESSION   AY596314
VERSION     AY596314.1  GI:46981713
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-APR-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .348
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              281           Length:        348
Score:                  107.00        Matches:       107
Percent Similarity:     92.24%        Conservative:  0
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Best Local Similarity:  92.24%        Mismatches:    9
Query Match:            19.49%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AY596314 (1-348)

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Db          1 GTCATGTTTTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACGCCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
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Db         61 GCCCTCGGCCTACTCGACTTCGCACTTGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
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Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
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RESULT 468
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LOCUS       AY596316                348 bp    RNA     linear   VRL 09-MAY-2004
DEFINITION  Swine hepatitis E virus strain swCH23 capsid protein gene, partial
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ACCESSION   AY596316
VERSION     AY596316.1  GI:46981717
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-APR-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
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                     TLLGGLPTELISPA"

Alignment Scores:
Pred. No.:              281           Length:        348
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Percent Similarity:     92.24%        Conservative:  0
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Best Local Similarity:  92.24%          Mismatches:     9
Query Match:            19.49%          Indels:         0
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US-09-769-066-16 (1-549) x AY596316 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTTATGTTCTGCATACATGGCTCGCCTGTGAATTCCTACACTAATACACCCTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGCCTACTCGACTTCGCACTCGAGCTCGAGTTCCGTAATTTGACACCTGGTAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||||    |||||||||   ||||||||||||
Db        121 ACTAACACGCGCGTTTCTCGCTATTCGAGCAGCGCACGTCATAAATTGCGCCGTGGGCCC 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
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Db        181 GATGGTACTGCAGAACTGACTACTACTGCTGCCACACGTTTTATGAAAGACCTCCACTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
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Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGATACGTTGCTCGGCGGGCTTCCGACAGAATTAATTTCGCCGGCT 348

RESULT 469
HEE344173
LOCUS       HEE344173               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 1,
            isolate 185.
ACCESSION   AJ344173
VERSION     AJ344173.1  GI:15282371
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              281             Length:         348
Score:                  107.00          Matches:        107
Percent Similarity:     92.24%          Conservative:   0
Best Local Similarity:  92.24%          Mismatches:     9
Query Match:            19.49%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x HEE344173 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCATGTTTTGCATACATGGCTCACCCGTAAATTCTTACACTAATACACCCTACACCGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGGCTGTTGGATTTTGCCCTTGAACTTGAGTTCCGCAACCTCACTCCCGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAATACTCGGGTCTCTCGTTACTCCAGCACTGCTCGCCACCGTCTTCGCCGCGGTGCA 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGGACCGCCGAGCTCACCACCACGGCTGCCACCCGCTTTATGAAGGATCTCTATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              |||||||||||||||   ||||||||||||||||||||||   ||||||
Db        241 GCTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGACACTCTGCTTGGCGGCCTACCGACAGAATTGATTTCGTCGGCT 348

RESULT 470
HEE344175
LOCUS       HEE344175               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 1,
            isolate 226.
ACCESSION   AJ344175
VERSION     AJ344175.1  GI:15282375
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="mRNA"
                     /isolate="226"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
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                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51494.1"
                     /db_xref="GI:15282376"
                     /db_xref="GOA:Q91EC6"
                     /db_xref="UniProt/TrEMBL:Q91EC6"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              281           Length:        348
Score:                  107.00        Matches:       107
Percent Similarity:     92.24%        Conservative:  0
Best Local Similarity:  92.24%        Mismatches:    9
Query Match:            19.49%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x HEE344175 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTATGTTCTGCATACATGGCTCACCCGTAAATTCTTACACTAATACACCCTACACCGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGGCTGTTGGATTTTGCCCTTGAACTTGAGTTCCGCAACCTCACTCCCGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAATACTCGGGTCTCTCGTTACTCCAGCACTGCTCGCCACCGTCTTCGCCGCGGTGCA 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGGACCGCCGAGCTCACCACCACGGCTGCCACCCGCTTTATGAAGGATCTCTATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
                  ||||||||||||||   ||||||||||||||||||||||||   ||||||
Db        241 GCTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGACACTCTGCTTGGCGGCCTACCGACAGAATTGATTTCGTCGGCT 348

RESULT 471
HEE344176
LOCUS       HEE344176               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 1,
            isolate 273.
ACCESSION   AJ344176
VERSION     AJ344176.1  GI:15282377
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="mRNA"
                     /isolate="273"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51495.1"
                     /db_xref="GI:15282378"
                     /db_xref="GOA:Q91EC5"
                     /db_xref="UniProt/TrEMBL:Q91EC5"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFASTNGVGEIGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              281           Length:        348
Score:                  107.00        Matches:       107
Percent Similarity:     92.24%        Conservative:  0
Best Local Similarity:  92.24%        Mismatches:    9
Query Match:            19.49%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x HEE344176 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCATGTTCTGCATACATGGCTCACCCGTAAATTCTTACACTAATACACCCTACACCGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGGCTGTTGGATTTTGCCCTTGAACTTGAGTTCCGCAACCTCACTCCCGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAATACTCGGGTCTCTCGTTACTCCAGCACTGCTCGCCACCGTCTTCGCCGCGGTGCA 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGGACCGCCGAGCTCACCACCACGGCTGCCACCCGCTTTATGAAGGATCTCTATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
                  ||||||||||||||   ||||||||||||||||||||||||   ||||||
Db        241 GCTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGACACTCTGCTTGGCGGCCTACCGACAGAATTGATTTCGTCGGCT 348

RESULT 472
HEE344177
LOCUS       HEE344177               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 297.
ACCESSION   AJ344177
VERSION     AJ344177.1  GI:15282379
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
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  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
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                     /isolate="297"
                     /db_xref="taxon:12461"
     CDS             <1. .>348
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                     /product="capsid protein"
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                     /db_xref="GI:15282380"
                     /db_xref="GOA:Q91EC4"
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:                281             Length:         348
Score:                    107.00          Matches:        107
Percent Similarity:       92.24%          Conservative:   0
Best Local Similarity:    92.24%          Mismatches:     9
Query Match:              19.49%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x HEE344177 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGTTTTGCATACATGGCTCACCTGTAAATTCCTATACTAATACACCTTACACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              |||||||||   ||||||||||||||||||||||||||||||||||||||       |||
Db         61 GCCCTCGGTTCGCTTGACTTTGCACTCGAACTCGAGTTTCGCAATTTGACACCTGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db        121 ACGAACACGCGTGTCTCCCGTTATTCGAGTAGCGCGCGTCACAAGTTGCGCCGAGGACCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGGTACAGCGGAGCTAACTACTACTGCTGCTACACGTTTTATGAAAGACCTTCATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||||||||||   ||||||
Db        241 ACTGGGACTAATGGTGTTGGTGAGGTTGGTCGTGGTATAGCACTGACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGATACGCTTCTTGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 473
HEE344181
LOCUS       HEE344181               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 108.
ACCESSION   AJ344181
VERSION     AJ344181.1  GI:15282387
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
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                     /db_xref="taxon:12461"
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                     /note="ORF2"
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                     /db_xref="GI:15282388"
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                     /db_xref="UniProt/TrEMBL:Q91EC0"
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:                281             Length:         348
Score:                    107.00          Matches:        107
Percent Similarity:       92.24%          Conservative:   0
Best Local Similarity:    92.24%          Mismatches:     9
Query Match:              19.49%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x HEE344181 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGTTTTGCATACATGGCTCACCTGTGAATTCTTACACTAATACACCCTATACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              |||||||||||||||||||||||||||||||||||||||||||||||||||||       |||
Db         61 GCCCTCGGCTTACTTGATTTTGCGCTCGAGCTCGAGTTCCGCAATTTAACACCTGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
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Db        121 ACTAACACGCGCGTTTCTCGCTACTCGAGTAGCGCGCGTCACAAATTGCGCCGAGGGCCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGCACTGCTGAGTTGACTACTACTGCCGCCACACGCTTTATGAAAGACCTTCATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||   ||||||||||||||||||   ||||||
Db        241 ACAGGGACTAATGGTGTTGGTGAAGTCGGTCATGGTATAGCGTTAACTTTGTTTAACCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGACACGCTTCTCGGTGGGCTTCCGACAGAATTGATTTCGTCGGCT 348

RESULT 474
HEE344186
LOCUS       HEE344186               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 254.
ACCESSION   AJ344186
VERSION     AJ344186.1  GI:15282397
KEYWORDS    capsid protein; ORF2.
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SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
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                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
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                     /product="capsid protein"
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                     /db_xref="GI:15282398"
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              281             Length:         348
Score:                  107.00          Matches:        107
Percent Similarity:     92.24%          Conservative:   0
Best Local Similarity:  92.24%          Mismatches:     9
Query Match:            19.49%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x HEE344186 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTTATGTTTTGCATACATGGCTCACCTGTAAATTCCTATACTAATACACCTTACACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGTTTGCTTGACTTTGCACTCGAACTCGAGTTTCGCAATTTGACACCTGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||||    |||||||||   ||||||||||||
Db        121 ACGAACACGCGTGTCTCCCGTTATTCGAGTAGCGCGCGTCACAAGTTGCGCCGAGGACCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGGTACAGCGGAGCTAACTACTACTGCTGCTACACGTTTTATGAAAGACCTTCATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||   ||||||||||||||||||||||||||||||   |||||||||   ||||||
Db        241 ACTGGGACTAATGGTGTTGGTGAGGTTGGTCGTGGTATAGTACTGACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGATACGCTTCTTGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 475
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HEE344188
LOCUS       HEE344188               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 4,
            isolate 181.
ACCESSION   AJ344188
VERSION     AJ344188.1  GI:15282401
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
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                     /db_xref="taxon:12461"
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              281             Length:         348
Score:                  107.00          Matches:        107
Percent Similarity:     92.24%          Conservative:   0
Best Local Similarity:  92.24%          Mismatches:     9
Query Match:            19.49%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x HEE344188 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTATGTTTTGCATACATGGCTCACCTGTAAATTCCTATACTAATACACCTTACACTGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGTTTGCTTGACTTTGCACTCGAACTCGAGTTTCGCAATTTGACACCTGGTAAT 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              |||||||||||||||||||||||||||||    |||||||||   ||||||||||||
Db        121 ACGAACACGCGTGTCTCCCGTTATTCGAGTAGCGCGCGTCACAAGTTGCGCCGAGGACCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db        181 GACGGTACAGCGGAGCTAACTACTACTGCTGCTACACGTTTTATGGAAGACCTTCATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
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Db        241 ACTGGGACTAATGGTGTTGGTGAGGTTGGTCGTGGTATAGCACTGACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGATACGCTTCTTGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 348

RESULT 476
HEE344189
LOCUS       HEE344189               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 1,
            isolate 153.
ACCESSION   AJ344189
VERSION     AJ344189.1  GI:15282403
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
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                     /db_xref="taxon:12461"
     CDS             <1. .>348
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="CAC51508.1"
                     /db_xref="GI:15282404"
                     /db_xref="GOA:Q91EB2"
                     /db_xref="UniProt/TrEMBL:Q91EB2"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              281           Length:         348
Score:                  107.00        Matches:        107
Percent Similarity:     92.24%        Conservative:   0
Best Local Similarity:  92.24%        Mismatches:     9
Query Match:            19.49%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x HEE344189 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCATGTTTTGCATACATGGCTCACCCGTAAATTCTTACACTAATACACCCTACACCGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGGCTGTTGGATTTTGCCCTTGAACTTGAGTTCCGCAACCTCACTCCCGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAATACTCGGGTCTCTCGTTACTCCAGCACTGCTCGCCACCGTCTTCGCCGCGGTGCA 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
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Db        181 GATGGGACCGCCGAGCTCACCACCACGGCTGCCACCCGCTTTATGAAGGATCTCTATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||||||||||||   ||||||||||||||||||||||   ||||||
Db        241 GCTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGACACTCTGCTTGGCGGCCTACCGACAGAATTGATTTCGTCGGCT 348

RESULT 477
HEE344190
LOCUS       HEE344190               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 1,
            isolate 219.
ACCESSION   AJ344190
VERSION     AJ344190.1  GI:15282405
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus"
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                     /db_xref="taxon:12461"
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                     /note="ORF2"
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                     /product="capsid protein"
                     /protein_id="CAC51509.1"
                     /db_xref="GI:15282406"
                     /db_xref="GOA:Q91EB1"
                     /db_xref="UniProt/TrEMBL:Q91EB1"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFASTNGVGEIGRGIALTLFNLAD
                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              281           Length:         348
Score:                  107.00        Matches:        107
Percent Similarity:     92.24%        Conservative:   0
Best Local Similarity:  92.24%        Mismatches:     9
Query Match:            19.49%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x HEE344190 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCATGTTCTGCATACATGGCTCACCCGTAAATTCTTACACTAATACACCCTACACCGGC 60
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Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db         61 GCCCTCGGGCTGTTGGATTTTGCCCTTGAACTTGAGTTCCGCAACCTCACTCCCGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAATACTCGGGTCTCTCGTTACTCCAGCACTGCTCGCCACCGTCTTCGCCGCGGTGCA 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGGACCGCCGAGCTCACCACCACGGCTGCCACCCGCTTTATGAAGGATCTCTATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
                  ||||||||||||||||   ||||||||||||||||||||||   ||||||
Db        241 GCTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGACACTCTGCTTGGCGGCCTACCGACAGAATTAATTTCGTCGGCT 348

RESULT 478
HEE344174
LOCUS       HEE344174               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 1,
            isolate 218.
ACCESSION   AJ344174
VERSION     AJ344174.1  GI:15282373
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
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                     /db_xref="taxon:12461"
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                     /note="ORF2"
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                     /db_xref="GI:15282374"
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                     /db_xref="UniProt/TrEMBL:Q91EC7"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
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                     TLLGGLPTELISSA"

Alignment Scores:
Pred. No.:              285          Length:         348
Score:                  106.00       Matches:        106
Percent Similarity:     91.38%       Conservative:   0
Best Local Similarity:  91.38%       Mismatches:     10
Query Match:            19.31%       Indels:         0
DB:                     1            Gaps:           0
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US-09-769-066-16 (1-549) x HEE344174 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGTTTTGCATACATGGCTCACCCGTAAATTCTTACACTAATACACCCTACACCGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db         61 GCCCTCGGGCTGTTGGATTTTGCCCTTGAACTTGAGTTCCGCAACCTCACTCCCGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
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Db        121 ACCAATACTCGGGTCTCTCGTTACTCCAGCACTGCTCGCCACCGTCTTCGCCGCGGTGCA 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        181 GATGGGACCGCCGAGCTCACCACCACGGCTGCCACCCGCTTTATGGAGGATCTCTATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
                  ||||||||||||||||   ||||||||||||||||||||||   ||||||   |||
Db        241 GCTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGACACTCTGCTTGGCGGCCTACCGACAGAATTGATTTCGTCGGCT 348

RESULT 479
HEE344178
LOCUS       HEE344178               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 1,
            isolate 170.
ACCESSION   AJ344178
VERSION     AJ344178.1  GI:15282381
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
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     CDS             <1. .>348
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Alignment Scores:
Pred. No.:              285             Length:         348
Score:                  106.00          Matches:        106
Percent Similarity:     91.38%          Conservative:   0
Best Local Similarity:  91.38%          Mismatches:     10
Query Match:            19.31%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x HEE344178 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGTTTTGCATACATGGCTCACCCGTAAATTCTTACACTAATACACCCTACACCGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGGCTGTTGGATTTTGCCCTTGAACTTGAGTTCCGCAACCTCACTCCCGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAATACTCGGGTCTCTCGTTACTCCAGCACTGCTCGCCACCGTCTTCGCCGCGGTGCA 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||    |||
Db        181 GATGGGACCGCCGAGCCCACCACCACGGCTGCCACCCGCTTTATGAAGGATCTCTATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||||||||||||  ||||||||||||||||||||||||  ||||||
Db        241 GCTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGACACTCTGCTTGGCGGCCTACCGACAGAATTAATTTCGTCGGCT 348

RESULT 480
HEE344187
LOCUS       HEE344187               348 bp    mRNA    linear   VRL 14-DEC-2001
DEFINITION  Hepatitis E virus partial mRNA for capsid protein, genotype 1,
            isolate 290.
ACCESSION   AJ344187
VERSION     AJ344187.1  GI:15282399
KEYWORDS    capsid protein; ORF2.
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Li,Z., Gu,W., Lan,H., Hao,W., Ling,R., Li,H. and
            Harrison,T.J.
  TITLE     Detection of sporadic cases of hepatitis E virus (HEV) infection in
            China using immunoassays based on recombinant open reading frame 2
            and 3 polypeptides from HEV genotype 4
  JOURNAL   J. Clin. Microbiol. 39 (12), 4370-4379 (2001)
  MEDLINE   21646397
   PUBMED   11724847
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2001) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Hepatitis E virus"
                     /virion
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     CDS             <1. .>348
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                     /codon_start=1
                     /product="capsid protein"
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                     /db_xref="GI:15282400"
                     /db_xref="GOA:Q91EB4"
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Alignment Scores:
Pred. No.:              285             Length:         348
Score:                  106.00          Matches:        106
Percent Similarity:     91.38%          Conservative:   0
Best Local Similarity:  91.38%          Mismatches:     10
Query Match:            19.31%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x HEE344187 (1-348)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
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Db          1 GTCATGTTTTGCATACATGGCTCACCCGTAAATTCTTACACTAATACACCCTACACCGGC 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGGCTGTTGGATTTTGCCCTTGAACTTGAGTTCCGCAACCTCACTCCCGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAATACTCGGGTCTCTCGTTACTCCAGCACTGCTCGCCACCGTCTTCGCCGCGGTGCA 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db        181 GATGGGACCGCCGAGCTCACCACCACGGCTGCCACCCGCTTTATGAAGGATCTCTATTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
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Db        241 GCTAGTACTAATGGTGTCGATGAGATCGGCCGCGGGATAGCCCTAACCCTGTTTAATCTT 300

Qy        265 AlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
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Db        301 GCTGACACTCTGCTTGGCGGCCTACCGACAGAATTAATTTCGTCGGCT 348

RESULT 481
AF446094
LOCUS       AF446094                318 bp    RNA     linear   VRL 02-JAN-2003
DEFINITION  Hepatitis E virus isolate BULDH2K structural protein 2 gene,
            partial cds.
ACCESSION   AF446094
VERSION     AF446094.1  GI:27462556
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 318)
  AUTHORS   Chobe,L.P., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Hepatitis E Outbreaks in Maharashtra (1999-2000), India:
            Phylogenetic Analysis of Currently Prevalent HEV Isolates
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 318)
  AUTHORS   Chobe,L.P., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-NOV-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
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                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPT
                     ELIS"

Alignment Scores:
Pred. No.:                310             Length:         318
Score:                    99.00           Matches:        99
Percent Similarity:       93.40%          Conservative:   0
Best Local Similarity:    93.40%          Mismatches:     7
Query Match:              18.03%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF446094 (1-318)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGTTGCTGGACTTTGCC 60

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         61 CTTGAGCTTGAGTTTCGTAACCTTACCCCCGGTAACACTAATACGCGGGTTTCCCGTTAT 120

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCAGCACTGCCCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACC 180

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACGGCTGCTACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAG 240

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 300

Qy        273 ProThrGluLeuIleSer 278
              ||||||||||||||||||
Db        301 CCGACAGAATTGATTTCG 318

RESULT 482
AF446095
LOCUS       AF446095                317 bp    RNA     linear   VRL 02-JAN-2003
DEFINITION  Hepatitis E virus isolate NANDED99 structural protein 2 gene,
            partial cds.
ACCESSION   AF446095
VERSION     AF446095.1  GI:27462558
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 317)
  AUTHORS   Chobe,L.P., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Hepatitis E Outbreaks in Maharashtra (1999-2000), India:
            Phylogenetic Analysis of Currently Prevalent HEV Isolates
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 317)
  AUTHORS   Chobe,L.P., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-NOV-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .317
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NANDED99"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>317
                     /note="ORF2"
                     /codon_start=1
                     /product="structural protein 2"
                     /protein_id="AAO15475.1"
                     /db_xref="GI:27462559"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPT
                     ELIS"

Alignment Scores:
Pred. No.:                314             Length:         317
Score:                    98.00           Matches:        98
Percent Similarity:       93.33%          Conservative:   0
Best Local Similarity:    93.33%          Mismatches:     7
Query Match:              17.85%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF446095 (1-317)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCC 60

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         61 CTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTTTCCCGTTAT 120

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCAGCACTGCCCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACC 180

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACGGCTGCTACCCGCTTCATGAAGGACCTCTATTTTACTAGTACCAATGGTGTTGGTGAG 240

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCGGCCGCGGGATAGCCCTTACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 300

Qy        273 ProThrGluLeuIle 277
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Db        301 CCGACAGAATTGATT 315

RESULT 483
AF446093
LOCUS       AF446093                312 bp    RNA     linear   VRL 02-JAN-2003
DEFINITION  Hepatitis E virus isolate AMRAV99 structural protein 2 gene,
            partial cds.
ACCESSION   AF446093
VERSION     AF446093.1  GI:27462554
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 312)
  AUTHORS   Chobe,L.P., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Hepatitis E Outbreaks in Maharashtra (1999-2000), India:
            Phylogenetic Analysis of Currently Prevalent HEV Isolates
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 312)
  AUTHORS   Chobe,L.P., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-NOV-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .312
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="AMRAV99"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:12461"
                     /country="India"
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     CDS             <1. .>312
                     /note="ORF2"
                     /codon_start=2
                     /product="structural protein 2"
                     /protein_id="AAO15473.1"
                     /db_xref="GI:27462555"
                     /translation="NSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARH
                     RLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTEL
                     IS"

Alignment Scores:
Pred. No.:              322             Length:         312
Score:                  96.00           Matches:        96
Percent Similarity:     93.20%          Conservative:   0
Best Local Similarity:  93.20%          Mismatches:     7
Query Match:            17.49%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF446093 (1-312)

Qy        175 AsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGlu 194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 AATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTCGAG 61

Qy        195 LeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSer 214
              ||||||||||||||||||||      ||||||||||||||||||||||||||||||||||
Db         62 CTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTTTCCCGTTATTCCAGC 121

Qy        215 ThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAla 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACTGCCCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCT 181

Qy        235 AlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGly 254
              ||||||||||||||||||||||    ||||||      ||||||||||||||   |||
Db        182 GCTACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGC 241

Qy        255 ArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThr 274
              ||||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        242 CGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACA 301

Qy        275 GluLeuIle 277
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Db        302 GAATTGATT 310

RESULT 484
AF466660
LOCUS       AF466660                300 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-19248-3 capsid protein gene,
            partial cds.
ACCESSION   AF466660
VERSION     AF466660.1  GI:19919472
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-19248-3"
                     /db_xref="taxon:63421"
     CDS             <1. .>300
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM08292.1"
                     /db_xref="GI:19919473"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              325             Length:         300
Score:                  95.00           Matches:        95
Percent Similarity:     95.00%          Conservative:   0
Best Local Similarity:  95.00%          Mismatches:     5
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF466660 (1-300)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCTGTTAATTCCTATACTAATACACCTTACACTGGTGCATTGGGGCTTCTTGATTTTGCA 60

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||      ||||||||||||||||||||||||||||||
Db         61 TTAGAGCTTGAATTTAGAAATCTGACACCTGGGAACACTAACACCCGTGTTTCCAGGTAT 120

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACTAGCACAGCCCGCCATCGGCTGCGCCGCGGTGCTGACGGGACCGCTGAGCTCACTACC 180

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        181 ACAGCAGCCACACGTTTTATGAAGGATTTACATTTTACTGGCACGAACGGTGTCGGTGAG 240

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db        241 GTTGGTCGTGGTATCGCTCTGACATTGTTTAACCTTGCTGACACGCTTCTCGGTGGTTTA 300

RESULT 485
AF466661
LOCUS       AF466661                300 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-18934D1 capsid protein gene,
            partial cds.
ACCESSION   AF466661
VERSION     AF466661.1  GI:19919474
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .300
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                /organism="Swine hepatitis E virus"
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                /strain="01-18934D1"
                /db_xref="taxon:63421"
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                /product="capsid protein"
                /protein_id="AAM08293.1"
                /db_xref="GI:19919475"
                /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
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Alignment Scores:
Pred. No.:                325             Length:         300
Score:                    95.00           Matches:        95
Percent Similarity:       95.00%          Conservative:   0
Best Local Similarity:    95.00%          Mismatches:     5
Query Match:              17.30%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF466661 (1-300)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCTGTTAATTCCTATACCAATACACCTTACACTGGTGCACTGGGGCTTCTTGATTTTGCA 60

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         61 TTAGAGCTTGAATTTAGAAATTTGACACCTGGGAACACTAACACCCGTGTTTCTAGATAT 120

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACC 180

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACAGCAGCCACACGTTTCATGAAGGATTTGCATTTTACTGGCACGAACGGTGTTGGTGAG 240

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGGCCGTGGTATTGCTCTGACATTGTTTAATCTTGCTGACACGCTTCTTGGTGGTTTA 300

RESULT 486
AF466662
LOCUS       AF466662                 300 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-18934C1 capsid protein gene,
            partial cds.
ACCESSION   AF466662
VERSION     AF466662.1  GI:19919476
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-18934C1"
                     /db_xref="taxon:63421"
     CDS             <1. .>300
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM08294.1"
                     /db_xref="GI:19919477"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:                325             Length:         300
Score:                    95.00           Matches:        95
Percent Similarity:       95.00%          Conservative:   0
Best Local Similarity:    95.00%          Mismatches:     5
Query Match:              17.30%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF466662 (1-300)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCTGTTAATTCCTATACTAATACACCCTACACCGGTGCACTAGGGCTTCTTGATTTCGCA 60

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         61 TTAGAGCTTGAATTTAGAAACCTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTAT 120

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAGCACAGCTCGCCACCGGCTGCGCCGTGGTGCTGATGGGACCGCTGAGCTTACAACC 180

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACAGCAGCTACACGTTTCATGAAAGATCTGCATTTTACTGGCACGAATGGTGTTGGTGAG 240

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGGCCGTGGTATCGCTTTAACATTGTTTAATCTTGCTGATACGCTTCTCGGCGGTTTA 300

RESULT 487
AF466663
LOCUS       AF466663                 300 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-18356-1 capsid protein gene,
            partial cds.
ACCESSION   AF466663
VERSION     AF466663.1  GI:19919478
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .300
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                     /strain="01-18356-1"
                     /db_xref="taxon:63421"
     CDS             <1. .>300
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                     /protein_id="AAM08295.1"
                     /db_xref="GI:19919479"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:                325             Length:         300
Score:                    95.00           Matches:        95
Percent Similarity:       95.00%          Conservative:   0
Best Local Similarity:    95.00%          Mismatches:     5
Query Match:              17.30%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF466663 (1-300)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCTGTTAATTCCTACACTAATACACCTTATACTGGTGCATTGGGGCTTCTTGATTTTGCA 60

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              |||||||||||||||||||||||||||||      ||||||||||||||||||||||||||
Db         61 TTAGAACTTGAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTAC 120

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAGTACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACC 180

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACAGCAGCCACACGCTTCATGAAGGATTTGCATTTTACTGGCACGAACGGCGTTGGTGAG 240

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGGTCGCGGCATTGCCCTGACACTGTTTAATCTTGCTGATACGCTTCTTGGCGGTTTA 300

RESULT 488
AF466666
LOCUS       AF466666                300 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain UMC9A capsid protein gene, partial
            cds.
ACCESSION   AF466666
VERSION     AF466666.1  GI:19919484
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="UMC9A"
                     /db_xref="taxon:63421"
     CDS             <1. .>300
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM08298.1"
                     /db_xref="GI:19919485"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:                325             Length:         300
Score:                    95.00           Matches:        95
Percent Similarity:       95.00%          Conservative:   0
Best Local Similarity:    95.00%          Mismatches:     5
Query Match:              17.30%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF466666 (1-300)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCTGTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTTCTTGACTTTGCA 60

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              |||||||||||||||||||||||||||||      ||||||||||||||||||||||||||
Db         61 TTAGAACTTGAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTAT 120

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAGTACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGCACCGCTGAGCTTACTACT 180

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACGGCAGCCACACGCTTCATGAAGGACTTGCATTTTACTGGTACGAACGGTGTTGGTGAG 240

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGGCCGTGGTATCGCTCTGACACTGTTTAATCTCGCTGACACGCTTCTCGGTGGTTTA 300

RESULT 489
AF466667
LOCUS       AF466667                300 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain UMC7A capsid protein gene, partial
            cds.
ACCESSION   AF466667
VERSION     AF466667.1  GI:19919486
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="UMC7A"
                     /db_xref="taxon:63421"
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     CDS             <1. .>300
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM08299.1"
                     /db_xref="GI:19919487"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:                325           Length:         300
Score:                    95.00         Matches:        95
Percent Similarity:       95.00%        Conservative:   0
Best Local Similarity:    95.00%        Mismatches:     5
Query Match:              17.30%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-16 (1-549) x AF466667 (1-300)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCTGTCAATTCTTATACTAATACACCTTACACGGGTGCACTGGGGCTTCTTGATTTTGCA 60

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         61 TTAGAACTTGAATTTAGAAATTTAACACCTGGGAACACTAACACCCGTGTTTCCCGGTAT 120

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAGTACAGCCCGCCACCGGCTGCGTCGCGGTGCTGATGGCACCGCTGAGCTTACTACC 180

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACGGCAGCCACACGTTTCATGAAGGACCTGCATTTTACTGGTACGAACGGCGTCGGTGAG 240

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGGCCGTGGTATCGCTCTGACACTGTTTAATCTCGCTGACACGCTTCTCGGTGGTTTA 300

RESULT 490
AF466665
LOCUS       AF466665                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain UMC12B capsid protein gene, partial
            cds.
ACCESSION   AF466665
VERSION     AF466665.1  GI:19919482
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="UMC12B"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08297.1"
                     /db_xref="GI:19919483"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:                325           Length:         301
Score:                    95.00         Matches:        95
Percent Similarity:       95.00%        Conservative:   0
Best Local Similarity:    95.00%        Mismatches:     5
Query Match:              17.30%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-16 (1-549) x AF466665 (1-301)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CCTGTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTTCTTGACTTTGCA 61

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         62 TTAGAACTTGAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTAT 121

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACCAGTACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGCACCGCTGAGCTTACTACT 181

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 ACGGCAGCCACACGTTTTATGAAGGACTTGCATTTTACTGGTACGAACGGTGTTGGTGAG 241

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GTGGGCCGTGGTATCGCTCTGACACTGTTTAATCTTGCTGACACGCTTCTTGGTGGTTTA 301

RESULT 491
AF466668
LOCUS       AF466668                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-161371-1 capsid protein gene,
            partial cds.
ACCESSION   AF466668
VERSION     AF466668.1  GI:19919488
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-161371-1"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
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                     /product="capsid protein"
                     /protein_id="AAM08300.1"
                     /db_xref="GI:19919489"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:                325             Length:         301
Score:                    95.00           Matches:        95
Percent Similarity:       95.00%          Conservative:   0
Best Local Similarity:    95.00%          Mismatches:     5
Query Match:              17.30%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF466668 (1-301)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CCTGTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTTCTTGATTTCGCA 61

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         62 TTAGAGCTTGAATTTAGAAACTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTAT 121

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACCAGCACAGCCCGTCACCGGCTGCGCCGTGGTGCTGATGGGACCGCTGAGCTCACCACC 181

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 ACAGCAGCCACACGTTTCATGAAGGACTTGCATTTTACTGGCACGAACGGCGTCGGTGAG 241

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GTGGGTCGTGGTATCGCTCTAACACTGTTCAATCTCGCTGATACGCTTCTCGGTGGTTTA 301

RESULT 492
AF466669
LOCUS       AF466669                 301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-16138-2 capsid protein gene,
            partial cds.
ACCESSION   AF466669
VERSION     AF466669.1  GI:19919490
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
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                     /strain="01-16138-2"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08301.1"
                     /db_xref="GI:19919491"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:                325             Length:         301
Score:                    95.00           Matches:        95
Percent Similarity:       95.00%          Conservative:   0
Best Local Similarity:    95.00%          Mismatches:     5
Query Match:              17.30%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF466669 (1-301)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          2 CCTGTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTTCTTGATTTCGCA 61

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         62 TTAGAGCTTGAATTTAGAAACTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTAT 121

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACCAGCACAGCCCGTCACCGGCTGCGCCGTGGTGCTGATGGGACCGCTGAGCTCACCACC 181

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 ACAGCAGCCACACGTTTCATGAAGGACTTGCATTTTACTGGCACGAACGGCGTCGGTGAG 241

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GTGGGTCGTGGTATCGCTCTAACACTGTTCAATCTCGCTGATACGCTTCTCGGTGGTTTA 301

RESULT 493
AF466670
LOCUS       AF466670                 301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-16138-3 capsid protein gene,
            partial cds.
ACCESSION   AF466670
VERSION     AF466670.1  GI:19919492
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-16138-3"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08302.1"
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                /db_xref="GI:19919493"
                /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
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Alignment Scores:
Pred. No.:              325             Length:         301
Score:                  95.00           Matches:        95
Percent Similarity:     95.00%          Conservative:   0
Best Local Similarity:  95.00%          Mismatches:     5
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF466670 (1-301)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CCTGTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTTCTTGATTTCGCA 61

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||      ||||||||||||||||||||||||||
Db         62 TTAGAGCTTGAATTTAGAAACTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTAT 121

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACCAGCACAGCCCGTCACCGGCTGCGCCGTGGTGCTGATGGGACCGCTGAGCTCACCACC 181

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||
Db        182 ACAGCAGCCACACGTTTCATGAAGGACTTGCATTTTACTGGCACGAACGGCGTCGGTGAG 241

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        242 GTGGGTCGTGGTATCGCTCTAACACTGTTCAATCTCGCTGATACGCTTCTCGGTGGTTTA 301

RESULT 494
AF466671
LOCUS       AF466671                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-16139-2 capsid protein gene,
            partial cds.
ACCESSION   AF466671
VERSION     AF466671.1  GI:19919494
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-16139-2"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08303.1"
                     /db_xref="GI:19919495"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              325             Length:         301
Score:                  95.00           Matches:        95
Percent Similarity:     95.00%          Conservative:   0
Best Local Similarity:  95.00%          Mismatches:     5
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF466671 (1-301)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CCTGTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTTCTTGATTTCGCA 61

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||      ||||||||||||||||||||||||||
Db         62 TTAGAGCTTGAATTTAGAAACTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTAT 121

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACCAGCACAGCCCGTCACCGGCTGCGCCGTGGTGCTGATGGGACCGCTGAGCTCACCACC 181

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||
Db        182 ACAGCAGCCACACGTTTCATGAAGGACTTGCATTTTACTGGCACGAACGGCGTCGGTGAG 241

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        242 GTGGGTCGTGGTATCGCTCTAACACTGTTCAATCTCGCTGATACGCTTCTCGGTGGTTTA 301

RESULT 495
AF466672
LOCUS       AF466672                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-16140-3 capsid protein gene,
            partial cds.
ACCESSION   AF466672
VERSION     AF466672.1  GI:19919496
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-16140-3"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08304.1"
                     /db_xref="GI:19919497"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
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RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:

Pred. No.:	325	Length:	301
Score:	95.00	Matches:	95
Percent Similarity:	95.00%	Conservative:	0
Best Local Similarity:	95.00%	Mismatches:	5
Query Match:	17.30%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AF466672 (1-301)

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Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CCTGTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTTCTTGATTTCGCA 61

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db         62 TTAGAGCTTGAATTTAGAAACTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTAT 121

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACCAGCACAGCCCGTCACCGGCTGCGCCGTGGTGCTGATGGGACCGCTGAGCTCACCACC 181

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        182 ACAGCAGCCACACGTTTCATGAAGGACTTGCATTTTACTGGCACCAACGGCGTCGGTGAG 241

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        242 GTGGGTCGCGGTATCGCTCTAACACTGTTCAATCTCGCTGATACGCTTCTCGGCGGTTTA 301
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RESULT 496
AF466673
LOCUS AF466673 301 bp RNA linear VRL 04-APR-2002
DEFINITION Swine hepatitis E virus strain 01-22171B1 capsid protein gene, partial cds.
ACCESSION AF466673
VERSION AF466673.1 GI:19919498
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 301)
AUTHORS Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G., Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
TITLE Detection by reverse transcription-PCR and genetic characterization of field isolates of swine hepatitis E virus from pigs in different geographic regions of the United States
JOURNAL J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
MEDLINE 21920873
PUBMED 11923352
REFERENCE 2 (bases 1 to 301)
AUTHORS Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S., Pierson,F., Toth,T. and Meng,X.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia Polytechnic Institute and State University, 1410 Prices Fork Road, Blacksburg, VA 24060, USA
FEATURES Location/Qualifiers
source 1. .301
/organism="Swine hepatitis E virus"
/mol_type="genomic RNA"
/strain="01-22171B1"
/db_xref="taxon:63421"
CDS <1. .>301
/codon_start=2
/product="capsid protein"
/protein_id="AAM08305.1"
/db_xref="GI:19919499"
/translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:

Pred. No.:	325	Length:	301
Score:	95.00	Matches:	95
Percent Similarity:	95.00%	Conservative:	0
Best Local Similarity:	95.00%	Mismatches:	5
Query Match:	17.30%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AF466673 (1-301)

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Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CCTGTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTCCTTGATTTCGCA 61

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db         62 TTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTAT 121

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACCAGCACAGCCCGTCACCGGCTGCGCCGTGGTGCTGATGGGACCGCTGAGCTCACCACC 181

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        182 ACAGCAGCCACACGTTTCATGAAGGACTTGCATTTTACTGGCACGAACGGCGTCGGTGAG 241

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        242 GTGGGTCGTGGTATCGCTCTAACACTGTTCAATCTCGCTGATACGCTTCTCGGTGGTTTA 301
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RESULT 497
AF466674
LOCUS AF466674 301 bp RNA linear VRL 04-APR-2002
DEFINITION Swine hepatitis E virus strain 01-19248-1 capsid protein gene, partial cds.
ACCESSION AF466674
VERSION AF466674.1 GI:19919500
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 301)
AUTHORS Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G., Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
TITLE Detection by reverse transcription-PCR and genetic characterization of field isolates of swine hepatitis E virus from pigs in different geographic regions of the United States
JOURNAL J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
MEDLINE 21920873
PUBMED 11923352
REFERENCE 2 (bases 1 to 301)
AUTHORS Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S., Pierson,F., Toth,T. and Meng,X.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia Polytechnic Institute and State University, 1410 Prices Fork Road, Blacksburg, VA 24060, USA
FEATURES Location/Qualifiers
source 1. .301
/organism="Swine hepatitis E virus"
/mol_type="genomic RNA"
/strain="01-19248-1"
/db_xref="taxon:63421"
CDS <1. .>301
/codon_start=2
/product="capsid protein"
/protein_id="AAM08306.1"
/db_xref="GI:19919501"
/translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

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Alignment Scores:
Pred. No.:              325           Length:         301
Score:                  95.00         Matches:        95
Percent Similarity:     95.00%        Conservative:   0
Best Local Similarity:  95.00%        Mismatches:     5
Query Match:            17.30%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF466674 (1-301)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CCTGTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTTCTTGATTTCGCA 61

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         62 TTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTAT 121

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACCAGCACAGCCCGTCACCGGCTGCGCCGTGGTGCTGATGGGACCGCTGAGCTCACCACC 181

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 ACAGCAGCCACACGTTTCATGAAGGACTTGCATTTTACTGGCACGAACGGCGTCGGTGAG 241

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GTGGGTCGTGGTATCGCTCTAACACTGTTCAATCTCGCTGATACGCTTCTCGGTGGTTTA 301

RESULT 498
AF466675
LOCUS       AF466675                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-16139-1 capsid protein gene,
            partial cds.
ACCESSION   AF466675
VERSION     AF466675.1  GI:19919502
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-16139-1"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08307.1"
                     /db_xref="GI:19919503"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              325           Length:         301
Score:                  95.00         Matches:        95
Percent Similarity:     95.00%        Conservative:   0
Best Local Similarity:  95.00%        Mismatches:     5
Query Match:            17.30%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF466675 (1-301)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CCTGTCAATTCTTATACTAATACACCTTACACTGGTGCACTAGGGCTTCTTGATTTTGCA 61

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         62 TTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTAT 121

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACCAGCACAGCCCGTCACCGGCTGCGCCGTGGTGCTGATGGGACCGCTGAGCTCACCACC 181

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
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Db        182 ACAGCAGCCACACGTTTCATGAAGGACTTGCATTTTACTGGCACGAACGGCGTCGGTGAG 241

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GTGGGTCGTGGTATCGCTCTAACACTGTTCAATCTCGCTGATACGCTTCTCGGTGGTTTA 301

RESULT 499
AF466677
LOCUS       AF466677                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-12116-2 capsid protein gene,
            partial cds.
ACCESSION   AF466677
VERSION     AF466677.1  GI:19919506
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-12116-2"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08309.1"
                     /db_xref="GI:19919507"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              325           Length:         301
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Score:                  95.00          Matches:        95
Percent Similarity:     95.00%         Conservative:   0
Best Local Similarity:  95.00%         Mismatches:     5
Query Match:            17.30%         Indels:         0
DB:                     1              Gaps:           0

US-09-769-066-16 (1-549) x AF466677 (1-301)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CCTGTTAATTCCTATACTAACACACCTTATACTGGTGCATTGGGGCTCCTTGATTTTGCA 61

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db         62 TTAGAGCTTGAATTCAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTAC 121

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACCAGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACC 181

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        182 ACAGCAGCCACACGTTTCATGAAGGACTTGCATTTCACCGGCACGAACGGCGTTGGTGAG 241

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        242 GTGGGTCGCGGTATAGCTCTAACACTGTTTAACCTTGCTGATACGCTTCTCGGTGGTTTA 301

RESULT 500
AF466678
LOCUS       AF466678                 301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain UMC13A capsid protein gene, partial
            cds.
ACCESSION   AF466678
VERSION     AF466678.1  GI:19919508
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="UMC13A"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08310.1"
                     /db_xref="GI:19919509"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              325            Length:         301
Score:                  95.00          Matches:        95
Percent Similarity:     95.00%         Conservative:   0
Best Local Similarity:  95.00%         Mismatches:     5
Query Match:            17.30%         Indels:         0
DB:                     1              Gaps:           0

US-09-769-066-16 (1-549) x AF466678 (1-301)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CCTGTTAATTCCTATACTAATACACCCTATACTGGTGCGCTGGGGCTTCTTGACTTTGCA 61

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db         62 CTAGAGCTTGAATTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTAT 121

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACCAGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACTGCTGAACTTACCACC 181

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        182 ACAGCAGCCACACGTTTCATGAAGGATCTGCACTTCACTGGCACGAACGGCGTTGGTGAG 241

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        242 GTGGGTCGTGGTATCGCCCTGACACTGTTCAATCTCGCTGATACGCTTCTCGGCGGTTTA 301

RESULT 501
AF466679
LOCUS       AF466679                 301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-22807-1 capsid protein gene,
            partial cds.
ACCESSION   AF466679
VERSION     AF466679.1  GI:19919510
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-22807-1"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08311.1"
                     /db_xref="GI:19919511"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              325            Length:         301
Score:                  95.00          Matches:        95
Percent Similarity:     95.00%         Conservative:   0
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Best Local Similarity:  95.00%          Mismatches:     5
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF466679 (1-301)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          2 CCTGTCAATTCTTATACTAATACACCTTACACCGGTGCACTGGGGCTTCTTGATTTTGCA 61

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         62 CTAGAGCTTGAGTTCAGGAATCTGACACCCGGGAACACCAACACCCGTGTCTCCCGGTAT 121

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACCAGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACC 181

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
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Db        182 ACAGCAGCCACACGTTTCATGAAGGACCTGCACTTCACTGGCACGAACGGAGTTGGTGAG 241

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GTGGGTCGTGGTATCGCCCTGACACTGTTCAATCTCGCTGACACGCTTCTCGGCGGTTTA 301

RESULT 502
AF466680
LOCUS       AF466680                 301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-22807-2 capsid protein gene,
            partial cds.
ACCESSION   AF466680
VERSION     AF466680.1  GI:19919512
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-22807-2"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08312.1"
                     /db_xref="GI:19919513"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              325             Length:         301
Score:                  95.00           Matches:        95
Percent Similarity:     95.00%          Conservative:   0
Best Local Similarity:  95.00%          Mismatches:     5
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF466680 (1-301)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          2 CCTGTCAATTCTTATACTAATACACCTTACACCGGTGCACTGGGGCTTCTTGATTTTGCA 61

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         62 CTAGAGCTTGAGTTCAGGAATCTGACACCCGGGAACACCAACACCCGTGTCTCCCGGTAT 121

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACCAGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACC 181

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
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Db        182 ACAGCAGCCACACGTTTCATGAAGGACCTGCACTTCACTGGCACGAACGGAGTTGGTGAG 241

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GTGGGTCGTGGTATCGCCCTGACACTGTTCAATCTCGCTGACACGCTTCTCGGCGGTTTA 301

RESULT 503
AF466681
LOCUS       AF466681                 301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-18934D2 capsid protein gene,
            partial cds.
ACCESSION   AF466681
VERSION     AF466681.1  GI:19919514
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-18934D2"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08313.1"
                     /db_xref="GI:19919515"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              325             Length:         301
Score:                  95.00           Matches:        95
Percent Similarity:     95.00%          Conservative:   0
Best Local Similarity:  95.00%          Mismatches:     5
Query Match:            17.30%          Indels:         0
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DB:                    1              Gaps:          0

US-09-769-066-16 (1-549) x AF466681 (1-301)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          2 CCTGTTAATTCCTATACTAATACACCTTATACTGGTGCACTGGGGCTTCTTGATTTTGCA 61

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CTAGAGCTTGAATTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTAT 121

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
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Db        122 ACCAGCACAGCCCGCCATCGGCTGCGCCGCGGTGCTGATGGGACTGCTGAGCTTACTACC 181

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
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Db        182 ACAGCAGCCACACGTTTCATGAAGGACCTGCATTTTACTGGCACGAACGGCGTTGGCGAG 241

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GTAGGTCGTGGTATCGCTCTCACACTGTTCAATCTTGCTGATACGCTTCTTGGCGGTTTA 301

RESULT 504
AF466682
LOCUS       AF466682                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-31692C1 capsid protein gene,
            partial cds.
ACCESSION   AF466682
VERSION     AF466682.1  GI:19919516
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-31692C1"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08314.1"
                     /db_xref="GI:19919517"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              325          Length:         301
Score:                  95.00        Matches:        95
Percent Similarity:     95.00%       Conservative:   0
Best Local Similarity:  95.00%       Mismatches:     5
Query Match:            17.30%       Indels:         0
DB:                     1            Gaps:           0
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US-09-769-066-16 (1-549) x AF466682 (1-301)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          2 CCTGTCAATTCTTACACTAATACACCTTACACTGGTGCACTGGGGCTTCTTGATTTCGCA 61

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACCAACACCCGTGTTTCCCGGTAC 121

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
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Db        122 ACCAGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACC 181

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 ACAGCAGCCACACGTTTCATGAAGGATTTACACTTCACTGGCACGAACGGCGTTGGTGAG 241

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
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Db        242 GTGGGTCGTGGTATCGCTCTGACACTGTTCAATCTTGCTGATACGCTTCTCGGTGGCTTA 301

RESULT 505
AF466683
LOCUS       AF466683                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-15555A capsid protein gene,
            partial cds.
ACCESSION   AF466683
VERSION     AF466683.1  GI:19919518
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-15555A"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08315.1"
                     /db_xref="GI:19919519"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              325          Length:         301
Score:                  95.00        Matches:        95
Percent Similarity:     95.00%       Conservative:   0
Best Local Similarity:  95.00%       Mismatches:     5
Query Match:            17.30%       Indels:         0
DB:                     1            Gaps:           0
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US-09-769-066-16 (1-549) x AF466683 (1-301)

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Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          2 CCTGTTAATTCTTATACTAATACACCTTACACTGGTGCACTGGGGCTCCTTGACTTCGCA 61

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              |||||||||||||||||||||||||||||      ||||||||||||||||||||||||||
Db         62 CTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACTAACACCCGCGTTTCCCGGTAT 121

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
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Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
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Db        182 ACAGCAGCCACACGTTTCATGAAGGATTTGCATTTCACTGGCACGAACGGTGTTGGTGAG 241

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GTGGGCCGTGGTATCGCCCTGACACTATTTAATCTCGCTGATACGCTTCTCGGTGGCTTA 301
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RESULT 506
AF466684
LOCUS AF466684 301 bp RNA linear VRL 04-APR-2002
DEFINITION Swine hepatitis E virus strain 01-15025-3 capsid protein gene, partial cds.
ACCESSION AF466684
VERSION AF466684.1 GI:19919520
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 301)
AUTHORS Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G., Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
TITLE Detection by reverse transcription-PCR and genetic characterization of field isolates of swine hepatitis E virus from pigs in different geographic regions of the United States
JOURNAL J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
MEDLINE 21920873
PUBMED 11923352
REFERENCE 2 (bases 1 to 301)
AUTHORS Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S., Pierson,F., Toth,T. and Meng,X.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia Polytechnic Institute and State University, 1410 Prices Fork Road, Blacksburg, VA 24060, USA
FEATURES Location/Qualifiers
source 1. .301
/organism="Swine hepatitis E virus"
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/strain="01-15025-3"
/db_xref="taxon:63421"
CDS <1. .>301
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/product="capsid protein"
/protein_id="AAM08316.1"
/db_xref="GI:19919521"
/translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:

Pred. No.:	325	Length:	301
Score:	95.00	Matches:	95
Percent Similarity:	95.00%	Conservative:	0
Best Local Similarity:	95.00%	Mismatches:	5
Query Match:	17.30%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AF466684 (1-301)

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Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
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Db         62 TTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACTAACACCCGTGTTTCCCGGTAT 121

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACCAGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACC 181

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
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Db        182 ACAGCAGCCACACGCTTTATGAAGGATTTGCATTTCACCGGCACGAATGGTGTTGGCGAG 241

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
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Db        242 GTGGGTCGCGGTATCGCCCTGACACTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTA 301
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RESULT 507
AF466685
LOCUS AF466685 301 bp RNA linear VRL 04-APR-2002
DEFINITION Swine hepatitis E virus strain 01-14185-1 capsid protein gene, partial cds.
ACCESSION AF466685
VERSION AF466685.1 GI:19919522
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 301)
AUTHORS Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G., Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
TITLE Detection by reverse transcription-PCR and genetic characterization of field isolates of swine hepatitis E virus from pigs in different geographic regions of the United States
JOURNAL J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
MEDLINE 21920873
PUBMED 11923352
REFERENCE 2 (bases 1 to 301)
AUTHORS Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S., Pierson,F., Toth,T. and Meng,X.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia Polytechnic Institute and State University, 1410 Prices Fork Road, Blacksburg, VA 24060, USA
FEATURES Location/Qualifiers
source 1. .301
/organism="Swine hepatitis E virus"
/mol_type="genomic RNA"
/strain="01-14185-1"
/db_xref="taxon:63421"
CDS <1. .>301
/codon_start=2
/product="capsid protein"
/protein_id="AAM08317.1"
/db_xref="GI:19919523"
/translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:

Pred. No.:	325	Length:	301
Score:	95.00	Matches:	95
Percent Similarity:	95.00%	Conservative:	0
Best Local Similarity:	95.00%	Mismatches:	5
Query Match:	17.30%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AF466685 (1-301)

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Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          2 CCTGTTAATTCGTATACCAATACACCTTACACTGGTGCACTCGGGCTCCTTGATTTTGCA 61

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
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Db         62 CTAGAGCTTGAGTTTAGAAATCTAACACCCGGGAACACCAACACCCGTGTTTCCCGGTAC 121

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACCAGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACC 181

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 ACAGCAGCCACACGCTTTATGAAGGATTTACATTTCACCGGCACGAATGGTGTTGGCGAG 241

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
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Db        242 GTGGGTCGCGGTATCGCCCTGACACTGTTCAATCTTGCTGATACGCTTCTCGGTGGTTTA 301

RESULT 508
AF195061
LOCUS       AF195061                304 bp    RNA     linear   VRL 07-NOV-2000
DEFINITION  Hepatitis E virus strain VH1 putative capsid protein gene, partial
            cds.
ACCESSION   AF195061
VERSION     AF195061.1  GI:10802597
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Pina,S., Buti,M., Cotrina,M., Piella,J. and Girones,R.
  TITLE     HEV identified in serum from humans with acute hepatitis and in
            sewage of animal origin in Spain
  JOURNAL   J. Hepatol. 33 (5), 826-833 (2000)
  MEDLINE   20547280
   PUBMED   11097493
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Pina,S., Buti,M., Cotrina,M., Piella,J. and Girones,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-OCT-1999) Microbiology, Fac. Biologia, Diagonal Ave.
            645, Barcelona 08020, Spain
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="VH1"
                     /db_xref="taxon:12461"
                     /note="isolated from serum of an acute hepatitis patient"
     CDS             <1. .>304
                     /note="ORF2"
                     /codon_start=3
                     /product="putative capsid protein"
                     /protein_id="AAG23523.1"
                     /db_xref="GI:10802598"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              325             Length:         304
Score:                  95.00           Matches:        95
Percent Similarity:     95.00%          Conservative:   0
Best Local Similarity:  95.00%          Mismatches:     5
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF195061 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          3 CCTGTTAATTCCTATACCAACACGCCCTATACCGGGGCGCTGGGGCTCCTCGACTTTGCA 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
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Db         63 CTTGAGCTTGAATTTAGAAATTTGACCCCCGGGAACACTAACACCCGAGTGTCCCGTTAC 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACTAGCACAGCCCGACACCGTTTGCGCCGTGGTGCCGATGGTACTGCCGAGCTTACAACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 ACTGCAGCCACACGTTTTATGAAGGACTTGCATTTCACCGGGACAAATGGTGTTGGCGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GTGGGCCGTGGTATAGCTTTAACGCTATTTAATCTTGCTGATACACTTCTCGGCGGGCTG 302

RESULT 509
AF195062
LOCUS       AF195062                304 bp    RNA     linear   VRL 07-NOV-2000
DEFINITION  Hepatitis E virus strain VH2 putative capsid protein gene, partial
            cds.
ACCESSION   AF195062
VERSION     AF195062.1  GI:10802599
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Pina,S., Buti,M., Cotrina,M., Piella,J. and Girones,R.
  TITLE     HEV identified in serum from humans with acute hepatitis and in
            sewage of animal origin in Spain
  JOURNAL   J. Hepatol. 33 (5), 826-833 (2000)
  MEDLINE   20547280
   PUBMED   11097493
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Pina,S., Buti,M., Cotrina,M., Piella,J. and Girones,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-OCT-1999) Microbiology, Fac. Biologia, Diagonal Ave.
            645, Barcelona 08020, Spain
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="VH2"
                     /db_xref="taxon:12461"
                     /note="isolated from serum of an acute hepatitis patient"
     CDS             <1. .>304
                     /note="ORF2"
                     /codon_start=3
                     /product="putative capsid protein"
                     /protein_id="AAG23524.1"
                     /db_xref="GI:10802600"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
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Alignment Scores:
Pred. No.:              325             Length:         304
Score:                  95.00           Matches:        95
Percent Similarity:     95.00%          Conservative:   0
Best Local Similarity:  95.00%          Mismatches:     5
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF195062 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          3 CCTGTTAATTCCTACACCAACACGCCCTATACTGGGGCATTAGGGCTCCTCGACTTTGCA 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
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Db         63 CTCGAGCTTGAATTTAGAAATTTAACCCCTGGGAACACTAACACCCGTGTGTCCCGATAC 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACTAGTACAGCCCGGCACCGTTTGCGCCGTGGTGCCGATGGGACAGCCGAGCTTACAACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||
Db        183 ACTGCAGCCACACGTTTTATGAAGGACTTGCACTTCACTGGGACAAATGGTGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        243 GTGGGCCGTGGTATAGCCCTAACGCTATTTAATCTTGCTGATACACTTCTCGGCGGGCTG 302

RESULT 510
AF296165
LOCUS       AF296165                304 bp    RNA     linear   VRL 12-SEP-2001
DEFINITION  Hepatitis E virus strain TW12SW nucleocapsid protein gene, partial
            cds.
ACCESSION   AF296165
VERSION     AF296165.1  GI:15558953
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2000) Department of Medicine, Division of
            Gastroenterology, Taipei Veterans General Hospital, Institute of
            Clinical Medicine, National Yang-Ming University School of
            Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW12SW"
                     /db_xref="taxon:12461"
                     /note="from swine stool"
     CDS             <1. .>304
                     /codon_start=3
                     /product="nucleocapsid protein"
                     /protein_id="AAL02059.1"
                     /db_xref="GI:15558954"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
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Alignment Scores:
Pred. No.:              325           Length:         304
Score:                  95.00         Matches:        95
Percent Similarity:     95.00%        Conservative:   0
Best Local Similarity:  95.00%        Mismatches:     5
Query Match:            17.30%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF296165 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          3 CCTGTTAATTCCTATACTAACACACCTTATACTGGCGCACTTGGACTTCTTGATTTTGCG 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||      ||||||||||||||||||||||||||||||
Db         63 CTGGAGCTTGAATTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTTTCCCGATAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACTAGTACAGCCCGCCACCGGCTGCGCCGTGGTGCGGACGGGACTGCTGAGCTTACAACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||
Db        183 ACAGCAGCCACGCGCTTCATGAAAGACCTGCATTTTACAGGCACGAATGGGGTCGGCGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        243 GTGGGCCGCGGTATTGCTCTTACATTGTTCAATCTTGCTGACACTCTCCTTGGTGGGTTG 302

RESULT 511
AF296166
LOCUS       AF296166                304 bp    RNA     linear   VRL 12-SEP-2001
DEFINITION  Hepatitis E virus strain TW13SW nucleocapsid protein gene, partial
            cds.
ACCESSION   AF296166
VERSION     AF296166.1  GI:15558955
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2000) Department of Medicine, Division of
            Gastroenterology, Taipei Veterans General Hospital, Institute of
            Clinical Medicine, National Yang-Ming University School of
            Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW13SW"
                     /db_xref="taxon:12461"
                     /note="from swine stool"
     CDS             <1. .>304
                     /codon_start=3
                     /product="nucleocapsid protein"
                     /protein_id="AAL02060.1"
                     /db_xref="GI:15558956"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLL"

Alignment Scores:
Pred. No.:              325           Length:         304
Score:                  95.00         Matches:        95
Percent Similarity:     95.00%        Conservative:   0
Best Local Similarity:  95.00%        Mismatches:     5
Query Match:            17.30%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF296166 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          3 CCTGTTAATTCCTATACTAACACACCTTATACTGGCGCACTTGGACTTCTTGATTTTGCG 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||      ||||||||||||||||||||||||||||||
Db         63 CTGGAGCTTGAATTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTCTCCCGATAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
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Db        123 ACTAGTACAGCCCGCCACCGACTGCGCCGTGGTGCAGACGGGACTGCTGAGCTTACAACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||
Db        183 ACAGCAGCCACGCGCTTCATGAAAGACCTGCATTTTACAGGCACGAATGGGGTCGGCGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        243 GTGGGCCGCGGTATTGCTCTTACATTGTTCAATCTTGCTGACACTCTCCTTGGTGGGTTG 302

RESULT 511
AF296166
LOCUS       AF296166                304 bp    RNA     linear   VRL 12-SEP-2001
DEFINITION  Hepatitis E virus strain TW13SW nucleocapsid protein gene, partial
            cds.
ACCESSION   AF296166
VERSION     AF296166.1  GI:15558955
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2000) Department of Medicine, Division of
            Gastroenterology, Taipei Veterans General Hospital, Institute of
            Clinical Medicine, National Yang-Ming University School of
            Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
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                     /mol_type="genomic RNA"
                     /strain="TW13SW"
                     /db_xref="taxon:12461"
                     /note="from swine stool"
     CDS             <1. .>304
                     /codon_start=3
                     /product="nucleocapsid protein"
                     /protein_id="AAL02060.1"
                     /db_xref="GI:15558956"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLL"

Alignment Scores:
Pred. No.:              325           Length:         304
Score:                  95.00         Matches:        95
Percent Similarity:     95.00%        Conservative:   0
Best Local Similarity:  95.00%        Mismatches:     5
Query Match:            17.30%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF296166 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          3 CCTGTTAATTCCTATACTAACACACCTTATACTGGCGCACTTGGACTTCTTGATTTTGCG 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||      ||||||||||||||||||||||||||||||
Db         63 CTGGAGCTTGAATTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTCTCCCGATAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACTAGTACAGCCCGCCACCGACTGCGCCGTGGTGCAGACGGGACTGCTGAGCTTACAACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||
Db        183 ACAGCAGCCACGCGCTTCATGAAAGACCTGCATTTTACAGGCACGAATGGGGTCGGCGAG 242
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Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
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Db        243 GTGGGCCGCGGTATTGCTCTTACATTGTTCAATCTTGCTGACACTCTCCTTGGTGGGTTG 302

RESULT 512
AY032756
LOCUS       AY032756                304 bp ss-RNA     linear   VRL 01-FEB-2002
DEFINITION  Swine hepatitis E virus isolate NLSW68 structural protein gene,
            partial cds.
ACCESSION   AY032756
VERSION     AY032756.1  GI:18476127
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   van der Poel,W.H.M., Verschoor,F. and van de Heide,R.
  TITLE     Hepatitis E virus sequences in swine in the Netherlands are closely
            related to human hepatitis E virus sequences
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van de Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-APR-2001) MGB, RIVM, Antonie v. Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Nederland
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW68"
                     /db_xref="taxon:63421"
     CDS             <1. .>304
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAK53068.1"
                     /db_xref="GI:18476128"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              325             Length:         304
Score:                  95.00           Matches:        95
Percent Similarity:     95.00%          Conservative:   0
Best Local Similarity:  95.00%          Mismatches:     5
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AY032756 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTTAATTCTTACACCAATACTCCCTATACTGGGGCGCTCGGGCTTCTTGATTTTGCT 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db         63 TTAGAGCTTGAGTTTAGGAACCTTACACCCGGGAACACCAATACTCGTGTTTCCCGGTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACAAGTACAGCCCGCCATCGGCTGCGTCGTGGTGCTGATGGCACCGCCGAGCTTACCACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        183 ACAGCGGCCACGCGCTTCATGAAGGACCTGCACTTCACCGGTACGAATGGGGTCGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        243 GTGGGCCGTGGCATCGCCCTCACTCTCTTTAATCTTGCTGACACGCTTCTCGGTGGTTTG 302

RESULT 513
AY032757
LOCUS       AY032757                304 bp ss-RNA     linear   VRL 01-FEB-2002
DEFINITION  Swine hepatitis E virus isolate NLSW76 structural protein gene,
            partial cds.
ACCESSION   AY032757
VERSION     AY032757.1  GI:18476129
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   van der Poel,W.H.M., Verschoor,F. and van de Heide,R.
  TITLE     Hepatitis E virus sequences in swine in the Netherlands are closely
            related to human hepatitis E virus sequences
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van de Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-APR-2001) MGB, RIVM, Antonie v. Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Nederland
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW76"
                     /db_xref="taxon:63421"
     CDS             <1. .>304
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAK53069.1"
                     /db_xref="GI:18476130"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              325             Length:         304
Score:                  95.00           Matches:        95
Percent Similarity:     95.00%          Conservative:   0
Best Local Similarity:  95.00%          Mismatches:     5
Query Match:            17.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AY032757 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTTAATTCTTATACCAATACACCCTATACTGGGGCATTGGGGCTTCTTGACTTTGCT 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTAGAAATCTGACCCCTGGGAATACTAACACCCGTGTGTCCCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACTAGTACAGCCCGACACCGTTTGCGCCGTGGTGCCGACGGGACAGCCGAGCTTACAACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        183 ACTGCAGCTACACGTTTTATGAAGGACTTGCATTTTACCGGGACAAATGGTGTTGGCGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        243 GTGGGCCGTGGTATAGCCCTAACGCTATTTAATCTTGCTGATACACTTCTCGGCGGGCTG 302

RESULT 514
AY032758
LOCUS       AY032758                304 bp ss-RNA     linear   VRL 01-FEB-2002
DEFINITION  Swine hepatitis E virus isolate NLSW50 structural protein gene,
            partial cds.
ACCESSION   AY032758
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VERSION     AY032758.1  GI:18476131
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   van der Poel,W.H.M., Verschoor,F. and van de Heide,R.
  TITLE     Hepatitis E virus sequences in swine in the Netherlands are closely
            related to human hepatitis E virus sequences
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van de Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-APR-2001) MGB, RIVM, Antonie v. Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Nederland
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW50"
                     /db_xref="taxon:63421"
     CDS             <1. .>304
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAK53070.1"
                     /db_xref="GI:18476132"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              325           Length:         304
Score:                  95.00         Matches:        95
Percent Similarity:     95.00%        Conservative:   0
Best Local Similarity:  95.00%        Mismatches:     5
Query Match:            17.30%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AY032758 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTTAATTCTTATACCAATACACCCTATACTGGGGCATTGGGGCTTCTTGACTTTGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||      |||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTAGAAATCTGACCCCTGGCAATACTAACACCCGTGTGTCCCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACTAGCACAGCCCGACACCGTTTGCGCCGTGGTGCCGATGGGACAGCCGAGCTTACAACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        183 ACTGCAGCCACACGTTTTATGAAGGACTTGCATTTTACCGGGACAAATGGTGTTGGCGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||   |||||||||||||||||||||||||||||||
Db        243 GTGGGCCGTGGTATAGCCCTAACGCTATTTAATCTTGCTGATACACTTCTCGGCGGGCTG 302

RESULT 515
AY032759
LOCUS       AY032759                304 bp ss-RNA     linear   VRL 01-FEB-2002
DEFINITION  Swine hepatitis E virus isolate NLSW91 structural protein gene,
            partial cds.
ACCESSION   AY032759
VERSION     AY032759.1  GI:18476133
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   van der Poel,W.H.M., Verschoor,F. and van de Heide,R.
  TITLE     Hepatitis E virus sequences in swine in the Netherlands are closely
            related to human hepatitis E virus sequences
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   van der Poel,W.H.M., Verschoor,F., van de Heide,R. and de Roda
            Husman,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-APR-2001) MGB, RIVM, Antonie v. Leeuwenhoeklaan 9,
            Bilthoven, Utrecht 3720 BA, Nederland
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="NLSW91"
                     /db_xref="taxon:63421"
     CDS             <1. .>304
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein"
                     /protein_id="AAK53071.1"
                     /db_xref="GI:18476134"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              325           Length:         304
Score:                  95.00         Matches:        95
Percent Similarity:     95.00%        Conservative:   0
Best Local Similarity:  95.00%        Mismatches:     5
Query Match:            17.30%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AY032759 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTTAACTCCTATACCAATACGCCCTATACCGGGGCGCTGGGGCTTCTTGACTTCGCA 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||      |||||||||||||||||||||||||||||
Db         63 CTCGAGCTTGAATTTAGAAACTTGACCCCTGGGAACACCAACACCCGTGTGTCTCGCTAC 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACTAGCACAGCCCGACACCGTTTGCGTCGTGGCGCCGATGGGACAGCCGAGCTCACAACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        183 ACTGCAGCCACACGTTTTATGAAGGATCTGCATTTCACTGGGACAAATGGTGTTGGCGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||   |||||||||||||||||||||||||||||||
Db        243 GTAGGCCGTGGTATAGCCTTAACGCTATTTAATCTTGCTGATACACTTCTCGGCGGGCTG 302

RESULT 516
AY362357
LOCUS       AY362357                304 bp    RNA     linear   VRL 05-AUG-2004
DEFINITION  Hepatitis E virus isolate UK 8734 capsid protein gene, partial cds.
ACCESSION   AY362357
VERSION     AY362357.1  GI:38224519
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Banks,M., Bendall,R.P., Grierson,S.S., Heath,G.S., Mitchell,J. and
            Dalton,H.
  TITLE     United Kingdom acquired hepatitis E is due to porcine strain of
            hepatitis E virus
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  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Banks,M., Bendall,R.P., Grierson,S.S., Heath,G.S., Mitchell,J. and
            Dalton,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-AUG-2003) Department of Virology, Veterinary
            Laboratories Agency, Woodham Lane, New Haw, Addlestone, Surrey KT15
            3NB, United Kingdom
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="UK 8734"
                     /isolation_source="human serum"
                     /db_xref="taxon:12461"
                     /country="United Kingdom"
     CDS             <1. .>304
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAR14144.1"
                     /db_xref="GI:38224520"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:                325             Length:         304
Score:                    95.00           Matches:        95
Percent Similarity:       95.00%          Conservative:   0
Best Local Similarity:    95.00%          Mismatches:     5
Query Match:              17.30%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AY362357 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          3 CCTGTAAACTCTTATACTAATACGCCCTACACTGGAGCATTGGGCCTTCTTGACTTTGCA 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAATTTAGAAATTTGACCCCTGGGAACACTAACACCCGTGTCTCCCGGTAC 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACTAGCACGGCTCGTCACCGCTTACGCCGTGGCGCTGATGGAACTGCTGAGCTTACGACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
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Db        183 ACTGCGGCCACGCGTTTCATGAAGGACCTGCACTTCACTGGGACGAATGGCGTCGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GTGGGCCGTGGCATAGCCCTAACTTTATTTAACCTTGCTGACACACTTCTCGGCGGCTTG 302

RESULT 517
AF466659
LOCUS       AF466659                300 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-21160-1 capsid protein gene,
            partial cds.
ACCESSION   AF466659
VERSION     AF466659.1  GI:19919470
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-21160-1"
                     /db_xref="taxon:63421"
     CDS             <1. .>300
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM08291.1"
                     /db_xref="GI:19919471"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNIRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:                329             Length:         300
Score:                    94.00           Matches:        94
Percent Similarity:       94.00%          Conservative:   0
Best Local Similarity:    94.00%          Mismatches:     6
Query Match:              17.12%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF466659 (1-300)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCTGTTAATTCCTACACCAATACACCTTACACTGGTGCTCTGGGGCTTCTTGATTTTGCA 60

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||||
Db         61 TTAGAGCTTGAATTCAGAAATTTGACACCTGGGAACACCAACATCCGTGTTTCCAGGTAT 120

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACTACC 180

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACAGCAGCCACACGTTTTATGAAGGATTTGCATTTTACTGGCACGAATGGCGTTGGTGAG 240

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGGTCGTGGTATCGCTCTGACACTGTTTAACCTTGCTGATACGCTTCTCGGTGGTTTA 300

RESULT 518
AF466664
LOCUS       AF466664                300 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain UMC7B capsid protein gene, partial
            cds.
ACCESSION   AF466664
VERSION     AF466664.1  GI:19919480
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
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   PUBMED   11923352
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="UMC7B"
                     /db_xref="taxon:63421"
     CDS             <1. .>300
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM08296.1"
                     /db_xref="GI:19919481"
                     /translation="PVNSYTNTPYTAALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:                329             Length:         300
Score:                    94.00           Matches:        94
Percent Similarity:       94.00%          Conservative:   0
Best Local Similarity:    94.00%          Mismatches:     6
Query Match:              17.12%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF466664 (1-300)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||  |||||||||||||||||||||||||
Db          1 CCTGTTAATTCCTATACTAATACACCTTACACTGCTGCACTGGGGCTCCTTGATTTTGCA 60

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||||      ||||||||||||||||||||||||||
Db         61 TTAGAGCTTGAGTTTAGAAATTTGACACCCGGGAACACTAATACCCGTGTTTCCCGGTAT 120

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCAGCACAGCCCGCCACCGGCTGCGTCGCGGTGCTGATGGGACCGCTGAACTTACAACC 180

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACAGCAGCCACACGTTTCATGAAGGATCTGCATTTTACTGGTACGAACGGCGTTGGTGAG 240

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        241 GTGGGTCGTGGTATCGCTCTGACACTGTTTAATCTTGCTGATACGCTTCTTGGTGGTTTA 300

RESULT 519
AF466676
LOCUS       AF466676                301 bp    RNA     linear   VRL 04-APR-2002
DEFINITION  Swine hepatitis E virus strain 01-9913 capsid protein gene, partial
            cds.
ACCESSION   AF466676
VERSION     AF466676.1  GI:19919504
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Huang,F.F., Haqshenas,G., Guenette,D.K., Halbur,P.G.,
            Schommer,S.K., Pierson,F.W., Toth,T.E. and Meng,X.J.
  TITLE     Detection by reverse transcription-PCR and genetic characterization
            of field isolates of swine hepatitis E virus from pigs in different
            geographic regions of the United States
  JOURNAL   J. Clin. Microbiol. 40 (4), 1326-1332 (2002)
  MEDLINE   21920873
   PUBMED   11923352

REFERENCE   2  (bases 1 to 301)
  AUTHORS   Huang,F., Haqshenas,G., Guenette,D., Halbur,P., Schommer,S.,
            Pierson,F., Toth,T. and Meng,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) College of Veterinary Medicine, Virginia
            Polytechnic Institute and State University, 1410 Prices Fork Road,
            Blacksburg, VA 24060, USA
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="01-9913"
                     /db_xref="taxon:63421"
     CDS             <1. .>301
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM08308.1"
                     /db_xref="GI:19919505"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTWFNLADTLLGGL"

Alignment Scores:
Pred. No.:                329             Length:         301
Score:                    94.00           Matches:        94
Percent Similarity:       94.00%          Conservative:   0
Best Local Similarity:    94.00%          Mismatches:     6
Query Match:              17.12%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF466676 (1-301)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          2 CCTGTTAACTCCTATACTAACACACCTTACACTGGTGCATTGGGGCTTCTTGATTTTGCA 61

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||||      ||||||||||||||||||||||||||
Db         62 TTAGAGCTTGAATTTAGAAATTTGACACCCGGGAACACTAACACCCGCGTTTCCCGGTAC 121

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACCAGCACAGCCCGCCACCGGCTGCGCCGCGGTGCTGATGGGACCGCTGAGCTTACCACC 181

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db        182 ACAGCAGCCACACGTTTCATGAAGGACTTGCATTTCACTGGCACGAATGGCGTTGGTGAG 241

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db        242 GTGGGTCGCGGTATAGCTCTAACATGGTTTAACCTTGCTGATACGCTTCTCGGTGGTTTA 301

RESULT 520
AF195063
LOCUS       AF195063                304 bp    RNA     linear   VRL 07-NOV-2000
DEFINITION  Hepatitis E virus strain E11 putative capsid protein gene, partial
            cds.
ACCESSION   AF195063
VERSION     AF195063.1  GI:10802601
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Pina,S., Buti,M., Cotrina,M., Piella,J. and Girones,R.
  TITLE     HEV identified in serum from humans with acute hepatitis and in
            sewage of animal origin in Spain
  JOURNAL   J. Hepatol. 33 (5), 826-833 (2000)
  MEDLINE   20547280
   PUBMED   11097493
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Pina,S., Buti,M., Cotrina,M., Piella,J. and Girones,R.
  TITLE     Direct Submission
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  JOURNAL   Submitted (14-OCT-1999) Microbiology, Fac. Biologia, Diagonal Ave.
            645, Barcelona 08020, Spain
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="E11"
                     /db_xref="taxon:12461"
                     /note="isolated from porcine slaughterhouse sewage"
     CDS             <1. .>304
                     /note="ORF2"
                     /codon_start=3
                     /product="putative capsid protein"
                     /protein_id="AAG23525.1"
                     /db_xref="GI:10802602"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYTSTA
                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGITLTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              329             Length:         304
Score:                  94.00           Matches:        94
Percent Similarity:     94.00%          Conservative:   0
Best Local Similarity:  94.00%          Mismatches:     6
Query Match:            17.12%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF195063 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTTAACTCTTATACCAACACGCCCTATACTGGGGCATTGGGGCTCCTCGACTTTGCA 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||||      ||||||||||||||||||||||||||
Db         63 CTCGAGCTCGAATTTAGAAATTTGACCCCTGGGAACACTAACACCCGTGTGTCCCGTTAC 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACTAGTACAGCCCGGCACCGCCTGCGTCGTGGTGCCGATGGGACAGCTGAGCTTACAACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 ACTGCAGCCACACGTTTTATGAAGGACTTGCATTTCACCGGGACAAATGGTGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GTGGGTCGTGGTATAACCCTAACGCTATTTAATCTTGCTGATACACTTCTCGGTGGGTTG 302

RESULT 521
AF296159
LOCUS       AF296159                304 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus strain TW1108E nucleocapsid protein gene, partial
            cds.
ACCESSION   AF296159
VERSION     AF296159.1  GI:22384853
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2000) Department of Medicine, Division of
            Gastroenterology, Taipei Veterans General Hospital, Institute of
            Clinical Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW1108E"
                     /db_xref="taxon:12461"
                     /note="from patient serum"
     CDS             <1. .>304
                     /codon_start=3
                     /product="nucleocapsid protein"
                     /protein_id="AAM96006.1"
                     /db_xref="GI:22384854"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              329             Length:         304
Score:                  94.00           Matches:        94
Percent Similarity:     94.00%          Conservative:   0
Best Local Similarity:  94.00%          Mismatches:     6
Query Match:            17.12%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF296159 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          3 CCTGTGAACTCCTATACCAATACACCTTATACTGGTGCCCTCGGCCTGCTCGACTTCGCG 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||||      ||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTCGTAATTTGACACCTGGTAATACAAACACGCGCGTTTCTCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||    ||||||||    ||||||||||||||||||||||||||||||||||||||||
Db        123 TCGAGCAGTGCACGCCACAAATTGCGCCGAGGGGCCGACGGCACCGCTGAGCTAACTACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 ACTGCTGCTACACGGTTTATGAAGGATCTTCATTTTACAGGGACTAATGGTGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GTTGGCCGTGGGATAGCGCTTACCTTGTTTAACCTTGCTGATACACTTCTCGGCGGGCTC 302

RESULT 522
AF296160
LOCUS       AF296160                304 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus strain TW261E nucleocapsid protein gene, partial
            cds.
ACCESSION   AF296160
VERSION     AF296160.1  GI:22384856
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2000) Department of Medicine, Division of
            Gastroenterology, Taipei Veterans General Hospital, Institute of
            Clinical Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW261E"
                     /db_xref="taxon:12461"
                     /note="from patient serum"
     CDS             <1. .>304
                     /codon_start=3
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                     /product="nucleocapsid protein"
                     /protein_id="AAM96007.1"
                     /db_xref="GI:22384857"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              329             Length:         304
Score:                  94.00           Matches:        94
Percent Similarity:     94.00%          Conservative:   0
Best Local Similarity:  94.00%          Mismatches:     6
Query Match:            17.12%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF296160 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          3 CCTGTGAACTCCTATACCAATACACCTTATACTGGTGCTCTCGGCCTGCTCGACTTCGCG 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTCGTAATTTGACACCTGGTAATACAAACACGCGCGTTTCTCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||    ||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        123 TCGAGCAGTGCACGCCACAAATTGCGCCGAGGGGCCGACGGCACCGCTGAGCTAACTACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||
Db        183 ACTGCTGCTACACGGTTTATGAAGGATCTTCATTTTACAGGGACTAATGGTGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        243 GTTGGCCGTGGGATAGCGCTTACCTTGTTTAACCTTGCTGATACACTTCTCGGCGGGCTC 302

RESULT 523
AY052774
LOCUS       AY052774                304 bp    RNA     linear   VRL 01-SEP-2002
DEFINITION  Hepatitis E virus TW6345-1E nucleocapsid protein gene, partial cds.
ACCESSION   AY052774
VERSION     AY052774.1  GI:22651424
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   WU,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-AUG-2001) Department of Medicine, Institute of
            Clinical Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW6345-1E"
                     /db_xref="taxon:12461"
     CDS             <1. .>304
                     /codon_start=3
                     /product="nucleocapsid protein"
                     /protein_id="AAL14260.1"
                     /db_xref="GI:22651425"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              329             Length:         304
Score:                  94.00           Matches:        94
Percent Similarity:     94.00%          Conservative:   0
Best Local Similarity:  94.00%          Mismatches:     6
Query Match:            17.12%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AY052774 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          3 CCTGTGAACTCCTATACCAATACACCTTATACTGGTGCCCTCGGCCTGCTCGACTTCGCG 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTCGTAATTTGACACCTGGTAATACAAACACGCGCGTTTCTCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||    ||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        123 TCGAGCAGTGCACGCCACAAATTGCGCCGAGGGGCCGACGGCACCGCTGAGCTAACTACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||
Db        183 ACTGCTGCTACACGGTTTATGAAGGATCTTCATTTTACAGGGACTAATGGTGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        243 GTTGGCCGTGGGATAGCGCTTACCTTGTTTAACCTTGCTGATACACTTCTCGGCGGGCTC 302

RESULT 524
AF324501
LOCUS       AF324501                299 bp    RNA     linear   VRL 26-AUG-2002
DEFINITION  Swine hepatitis E virus isolate IND-SW1 nucleocapsid protein gene,
            partial cds.
ACCESSION   AF324501
VERSION     AF324501.1  GI:22476826
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 299)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 299)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B.R. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-NOV-2000) Hepatitis Department, National Institute of
            Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune,
            Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .299
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW1"
                     /specific_host="swine"
                     /db_xref="taxon:63421"
                     /country="India"
     CDS             <1. .>299
                     /codon_start=1
                     /product="nucleocapsid protein"
                     /protein_id="AAM97324.1"
                     /db_xref="GI:22476827"
                     /translation="NTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRR
                     GADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPTELIS"

Alignment Scores:
Pred. No.:              333             Length:         299
Score:                  93.00           Matches:        93
Percent Similarity:     93.94%          Conservative:   0
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Best Local Similarity:  93.94%        Mismatches:    6
Query Match:            16.94%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AF324501 (1-299)

Qy        179 AsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArg 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATACACCCTACACCGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGT 60

Qy        199 AsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHis 218
              |||||||||      ||||||||||||||||||||||||||||||||    |||||||||
Db         61 AACTTAACACCTGGCAATACGAACACTCGTGTGTCCCGTTACTCGAGCAGCGCGCGTCAT 120

Qy        219 ArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPhe 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGTTGCGCCGGGGGGCTGATGGTACTGCTGAGTTAACCACTACTGCTGCTACACGTTTT 180

Qy        239 MetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAla 258
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        181 ATGAAGGACCTCCACTTTACTGGGACCAATGGTGTTGGTGAAGTCGGTCGTGGTATAGCG 240

Qy        259 LeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              |||||||||    ||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGACCTTATTTAATCTTGCTGATACACTGCTCGGCGGCCTGCCGACAGAATTGATT 297

RESULT 525
AF324502
LOCUS       AF324502                299 bp    RNA     linear   VRL 26-AUG-2002
DEFINITION  Swine hepatitis E virus isolate IND-SW2 nucleocapsid protein gene,
            partial cds.
ACCESSION   AF324502
VERSION     AF324502.1  GI:22476828
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 299)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 299)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B.R. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-NOV-2000) Hepatitis Department, National Institute of
            Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune,
            Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .299
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW2"
                     /specific_host="swine"
                     /db_xref="taxon:63421"
                     /country="India"
     CDS             <1. .>299
                     /codon_start=1
                     /product="nucleocapsid protein"
                     /protein_id="AAM97325.1"
                     /db_xref="GI:22476829"
                     /translation="NTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRR
                     GADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPTELIS"

Alignment Scores:
Pred. No.:              333           Length:        299
Score:                  93.00         Matches:       93
Percent Similarity:     93.94%        Conservative:  0
Best Local Similarity:  93.94%        Mismatches:    6
Query Match:            16.94%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AF324502 (1-299)

Qy        179 AsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArg 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATACACCTTACACCGGCGCCCTCGGTCTGCTCGATTTTGCGCTCGAACTCGAGTTTCGT 60

Qy        199 AsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHis 218
              |||||||||      ||||||||||||||||||||||||||||||||    |||||||||
Db         61 AACTTAACACCTGGTAATACGAATACCCGTGTGTCCCGTTATTCGAGCAGTGCGCGTCAT 120

Qy        219 ArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPhe 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGCTGCGCCGAGGGGCTGATGGTACTGCTGAGTTAACCACTACTGCCGCTACACGCTTT 180

Qy        239 MetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAla 258
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        181 ATGAAGGACCTTCACTTTACTGGGACCAACGGTGTTGGTGAAGTTGGCCGTGGTATAGCG 240

Qy        259 LeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              |||||||||    ||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGACCCTATTTAATCTTGCTGATACACTTCTCGGCGGGCTCCCGACAGAATTGATT 297

RESULT 526
AF324503
LOCUS       AF324503                299 bp    RNA     linear   VRL 26-AUG-2002
DEFINITION  Swine hepatitis E virus isolate IND-SW3 nucleocapsid protein gene,
            partial cds.
ACCESSION   AF324503
VERSION     AF324503.1  GI:22476830
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 299)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 299)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B.R. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-NOV-2000) Hepatitis Department, National Institute of
            Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune,
            Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .299
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW3"
                     /specific_host="swine"
                     /db_xref="taxon:63421"
                     /country="India"
     CDS             <1. .>299
                     /codon_start=1
                     /product="nucleocapsid protein"
                     /protein_id="AAM97326.1"
                     /db_xref="GI:22476831"
                     /translation="NTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRR
                     GADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLPTELIS"

Alignment Scores:
Pred. No.:              333           Length:        299
Score:                  93.00         Matches:       93
Percent Similarity:     93.94%        Conservative:  0
Best Local Similarity:  93.94%        Mismatches:    6
Query Match:            16.94%        Indels:        0
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DB:                    1             Gaps:          0

US-09-769-066-16 (1-549) x AF324503 (1-299)

Qy        179 AsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArg 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATACACCTTACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGT 60

Qy        199 AsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHis 218
              |||||||||      ||||||||||||||||||||||||||||||   |||||||||
Db         61 AACTTAACACCTGGCAATACGAACACCCGTGTGTCCCGTTACTCGAGCAGCGCGCGTCAT 120

Qy        219 ArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPhe 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGTTGCGCCGGGGGGCTGATGGCACTGCTGAGTTAACCACTACTGCTGCTACACGTTTT 180

Qy        239 MetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAla 258
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        181 ATGAAGGACCTCCATTTTACTGGGACCAACGGTGTTGGTGAAGTTGGTCGTGGTATAGCG 240

Qy        259 LeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGACCTTATTTAATCTTGCTGATACACTTCTCGGCGGGCTTCCGACAGAATTGATT 297

RESULT 527
HEE428852
LOCUS       HEE428852               300 bp    RNA     linear   VRL 12-JUL-2002
DEFINITION  Hepatitis E virus type 4 partial polyprotein gene for capsid
            protein, swine isolate SB2.
ACCESSION   AJ428852
VERSION     AJ428852.1  GI:18447771
KEYWORDS    capsid protein; polyprotein gene.
SOURCE      Hepatitis E virus type 4
  ORGANISM  Hepatitis E virus type 4
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Xia,N., Peng,G., Lan,H., Zhuang,H., Zhu,Y.,
            Li,S., Tian,K., Gu,W., Lin,J., Wu,X., Li,H. and Harrison,T.J.
  TITLE     Prevalence, isolation, and partial sequence analysis of hepatitis E
            virus from domestic animals in China
  JOURNAL   J. Med. Virol. 67 (4), 516-521 (2002)
  MEDLINE   22110701
   PUBMED   12115997
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2002) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Hepatitis E virus type 4"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="SB2"
                     /specific_host="Sus scrofa"
                     /db_xref="taxon:185580"
                     /country="China:Beijing"
     CDS             <1. .>300
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="CAD21788.1"
                     /db_xref="GI:18447772"
                     /db_xref="GOA:Q8UZ76"
                     /db_xref="UniProt/TrEMBL:Q8UZ76"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGG"

Alignment Scores:
Pred. No.:              333           Length:        300
Score:                  93.00         Matches:       93
Percent Similarity:     93.94%        Conservative:  0
Best Local Similarity:  93.94%        Mismatches:    6
Query Match:            16.94%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x HEE428852 (1-300)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTGAACTCTTATACCAATACACCCTATACCGGTGCCCTCGGCCTGCTCGACTTTGCG 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              |||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTCGTAATTTGACACCTGGCAATACGAATACGCGCGTCTCTCGCTAC 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||   |||||||||   ||||||||||||||||||||||||||||||||||||||
Db        123 TCGAGCAGTGCGCGCCACAAACTGCGCCGAGGGGCCGATGGTACTGCTGAGTTGACTACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 ACTGCTGCTACACGGTTTATGAAGGACCTTCATTTTACAGGGACTAATGGTGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGly 271
              |||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        243 GTTGGCCGTGGGATTGCACTTACCTTGTTTAACCTTGCTGACACACTTCTCGGCGGG 299

RESULT 528
AF134812
LOCUS       AF134812                301 bp    RNA     linear   VRL 15-AUG-2002
DEFINITION  Hepatitis E virus capsid protein gene, partial cds.
ACCESSION   AF134812
VERSION     AF134812.1  GI:4530608
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Li,K., Zhuang,H. and Zhu,W.
  TITLE     Partial nucleotide sequencing of hepatitis E viruses detected in
            sera of patients with hepatitis E from 14 cities in China
  JOURNAL   Chin. Med. J. 115 (7), 1058-1063 (2002)
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Li,K., Zhuang,H. and Zhu,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAR-1999) Department of Microbiology, Beijing Medical
            University, 38 Xueyuan Road, Beijing 100083, P.R.China
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="HF-044"
                     /db_xref="taxon:12461"
                     /country="China"
     CDS             <1. .>301
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAD22115.1"
                     /db_xref="GI:4530609"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              333           Length:        301
Score:                  93.00         Matches:       93
Percent Similarity:     93.94%        Conservative:  0
Best Local Similarity:  93.94%        Mismatches:    6
Query Match:            16.94%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AF134812 (1-301)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTGAACTCCTACACTAATACACCCTACACTGGTGCCCTTGGCCTGCTCGATTTTGCG 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
                |||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTCGCAATTTGACACCTGGTAATACAAACACGCGCGTCTCTCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
                ||||||   |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TCGAGTAGTGCGCGCCATAAACTGCGCCGAGGGGCTGACGGCACTGCTGAGCTGACTACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 ACTGCTGCTACACGATTTATGAAGGATCTTCATTTTACAGGGACTAATGGCGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGly 271
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GTTGGCCGCGGGATAGCGCTTACCCTGTTTAACCTTGCTGATACACTTCTCGGCGGG 299

RESULT 529
AF134917
LOCUS       AF134917                 301 bp ss-RNA     linear   VRL 15-AUG-2002
DEFINITION  Hepatitis E virus strain HF-054/China capsid protein gene, partial
            cds.
ACCESSION   AF134917
VERSION     AF134917.1  GI:4836760
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Li,K., Zhuang,H. and Zhu,W.
  TITLE     Partial nucleotide sequencing of hepatitis E viruses detected in
            sera of patients with hepatitis E from 14 cities in China
  JOURNAL   Chin. Med. J. 115 (7), 1058-1063 (2002)
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Li,K., Zhuang,H. and Zhu,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-1999) Department of Microbiology, Beijing Medical
            University, 38 Xueyuan Road, Beijing 100083, P.R.China
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="HF-054/China"
                     /db_xref="taxon:12461"
     CDS             <1. .>301
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAD30543.1"
                     /db_xref="GI:4836761"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              333           Length:         301
Score:                  93.00         Matches:        93
Percent Similarity:     93.94%        Conservative:   0
Best Local Similarity:  93.94%        Mismatches:     6
Query Match:            16.94%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF134917 (1-301)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTGAACTCCTACACCAATACACCCTATACCGGTGCTCTTGGCCTGCTCGATTTTGCG 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
                |||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTCGTAATTTGACACCTGGCAATACGAATACGCGCGTCTCTCGTTAC 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
                ||||||   |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TCGAGCAGTGCGCGCCACAAACTGCGTCGAGGGGCCGATGGTACCGCTGAGTTAACTACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 ACTGCTGCTACACGGTTTATGAAGGACCTTCATTTTACAGGGACTAATGGCGTTGGCGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGly 271
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GTTGGCCGTGGGATAGCACTTACCTTGTTTAACCTTGCTGACACACTTCTCGGCGGG 299

RESULT 530
AY621101
LOCUS       AY621101                 302 bp    RNA     linear   VRL 27-JUN-2004
DEFINITION  Swine hepatitis E virus isolate swCH103 capsid protein gene,
            partial cds.
ACCESSION   AY621101
VERSION     AY621101.1  GI:49036124
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 302)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 302)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .302
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="swCH103"
                     /isolation_source="pig feces"
                     /db_xref="taxon:63421"
     CDS             <1. .>302
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT48735.1"
                     /db_xref="GI:49036125"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLA"

Alignment Scores:
Pred. No.:              334           Length:         302
Score:                  93.00         Matches:        93
Percent Similarity:     93.00%        Conservative:   0
Best Local Similarity:  93.00%        Mismatches:     7
Query Match:            16.94%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AY621101 (1-302)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
                ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCATGTTTTGCATACATGGCTCACCTGTGAATTCTTACACTAATACACCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db         61 GCCCTCGGCCTACTTGATTTCGCACTTGAGCTTGAGTTCCGTAATTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACTAATACGCGTGTTTCTCGTTACTCGAGTAGCGCGCGACACAAATTGCGCCGAGGGGCT 180
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Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGTACTGCTGAGCTTACTACCACTGCTGCCACACGTTTTATGAAAGACCTTCACTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||    ||||||||||||||||||||||||||||||||||||||    ||||||
Db        241 ACGGGAACTAATGGTGTTGGCGAGGTCGGTCGTGGTATAGCGTTAACCCTGTTTAATCTT 300

RESULT 531
AY621102
LOCUS       AY621102                302 bp    RNA     linear   VRL 27-JUN-2004
DEFINITION  Swine hepatitis E virus isolate swCH100 capsid protein gene,
            partial cds.
ACCESSION   AY621102
VERSION     AY621102.1  GI:49036126
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 302)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Detection and analysis of partial sequences of swine hepatitis E
            virus in Xinjiang
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 302)
  AUTHORS   Ma,X. and Lu,C.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2004) College of Animal Medicine, Nanjing
            Agricultural University, Tong Wei Road No.1, Nanjing, Jiangsu
            210095, P. R. China
FEATURES             Location/Qualifiers
     source          1. .302
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="swCH100"
                     /isolation_source="pig feces"
                     /db_xref="taxon:63421"
     CDS             <1. .>302
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAT48736.1"
                     /db_xref="GI:49036127"
                     /translation="VMFCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                     VSRYSSSARHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLA"

Alignment Scores:
Pred. No.:              334             Length:         302
Score:                  93.00           Matches:        93
Percent Similarity:     93.00%          Conservative:   0
Best Local Similarity:  93.00%          Mismatches:     7
Query Match:            16.94%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AY621102 (1-302)

Qy        165 ValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrProTyrThrGly 184
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCATGTTTTGCATACATGGCTCACCTGTGAATTCTTACACTAATACACCTTACACCGGT 60

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db         61 GCCCTCGGCCTACTTGATTTCGCACTTGAGCTTGAGTTCCGTAATTTGACACCTGGCAAC 120

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||||||
Db        121 ACTAATACGCGTGTTTCTCGTTACTCGAGTAGCGCGCGACACAAATTGCGCCGAGGGGCT 180

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGGTACTGCTGAGCTTACTACCACTGCTGCCACACGTTTTATGAAAGACCTTCACTTT 240

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              ||||||    ||||||||||||||||||||||||||||||||||||||    ||||||
Db        241 ACGGGAACTAATGGTGTTGGCGAGGTCGGTCGTGGTATAGCGTTAACCCTGTTTAATCTT 300

RESULT 532
AF093896
LOCUS       AF093896                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate K75 polyprotein gene, partial cds.
ACCESSION   AF093896
VERSION     AF093896.1  GI:4336439
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="K75"
                     /db_xref="taxon:12461"
                     /country="India: Karnal"
                     /note="isolated in 1987"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17807.1"
                     /db_xref="GI:4336455"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              334             Length:         304
Score:                  93.00           Matches:        93
Percent Similarity:     93.00%          Conservative:   0
Best Local Similarity:  93.00%          Mismatches:     7
Query Match:            16.94%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF093896 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACCGCCGAGCTTACCACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||    ||||||      ||||||||||||||||
Db        183 ACGGCCGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAG 242
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Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        243 ATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 533
AF093897
LOCUS       AF093897               304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate K45 polyprotein gene, partial cds.
ACCESSION   AF093897
VERSION     AF093897.1  GI:4336440
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="K45"
                     /db_xref="taxon:12461"
                     /country="India: Karnal"
                     /note="isolated in 1987"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17808.1"
                     /db_xref="GI:4336456"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              334             Length:         304
Score:                  93.00           Matches:        93
Percent Similarity:     93.00%          Conservative:   0
Best Local Similarity:  93.00%          Mismatches:     7
Query Match:            16.94%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF093897 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTCTCCCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACCGCCGAGCTTACCACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||  ||||||  ||||||||||||||||||||
Db        183 ACGGCCGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        243 ATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 534
AF093898
LOCUS       AF093898               304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate Y2 polyprotein gene, partial cds.
ACCESSION   AF093898
VERSION     AF093898.1  GI:4336441
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="Y2"
                     /db_xref="taxon:12461"
                     /country="India: Yamunanagar"
                     /note="isolated in 1989"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17809.1"
                     /db_xref="GI:4336457"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              334             Length:         304
Score:                  93.00           Matches:        93
Percent Similarity:     93.00%          Conservative:   0
Best Local Similarity:  93.00%          Mismatches:     7
Query Match:            16.94%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF093898 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTCTCCCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACCGCCGAGCTTACCACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
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                 ||||||||||||||||||||||||||||||||   ||||||      ||||||||||||||||
Db        183 ACGGCCGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
                 ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        243 ATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 535
AF093900
LOCUS       AF093900                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate M67 polyprotein gene, partial cds.
ACCESSION   AF093900
VERSION     AF093900.1  GI:4336443
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="M67"
                     /db_xref="taxon:12461"
                     /country="India: Meerut"
                     /note="isolated in 1996"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17811.1"
                     /db_xref="GI:4336459"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              334             Length:         304
Score:                  93.00           Matches:        93
Percent Similarity:     93.00%          Conservative:   0
Best Local Similarity:  93.00%          Mismatches:     7
Query Match:            16.94%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF093900 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTCGCAACCTTACCCCTGGTAACACTAATACGCGGGTCTCCCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||   ||||||      ||||||||||||||||
Db        183 ACGGCTGCTACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        243 ATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 536
AF093901
LOCUS       AF093901                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate M82 polyprotein gene, partial cds.
ACCESSION   AF093901
VERSION     AF093901.1  GI:4336444
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="M82"
                     /db_xref="taxon:12461"
                     /country="India: Meerut"
                     /note="isolated in 1996"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17812.1"
                     /db_xref="GI:4336460"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              334             Length:         304
Score:                  93.00           Matches:        93
Percent Similarity:     93.00%          Conservative:   0
Best Local Similarity:  93.00%          Mismatches:     7
Query Match:            16.94%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF093901 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          3 CCCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACC 182
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Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||  ||||||     ||||||||||||||||
Db        183 ACGGCTGCTACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAACGGTGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        243 ATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 537
AF093902
LOCUS       AF093902                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate M70 polyprotein gene, partial cds.
ACCESSION   AF093902
VERSION     AF093902.1  GI:4336445
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="M70"
                     /db_xref="taxon:12461"
                     /country="India: Meerut"
                     /note="isolated in 1996"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17813.1"
                     /db_xref="GI:4336461"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              334             Length:         304
Score:                  93.00           Matches:        93
Percent Similarity:     93.00%          Conservative:   0
Best Local Similarity:  93.00%          Mismatches:     7
Query Match:            16.94%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF093902 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          3 CCCGTAAACTCTTATACTAATACACCTTATACCGGTGCCCTCGGGCTGTTGGACTTCGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTCCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||  ||||||     ||||||||||||||||
Db        183 ACGGCTGCTACCCGCTTTATGAAGGACCTTTATTTTACTAGTACTAATGGTGTCGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        243 ATCGGCCGCGGGATAGCCCTCACCCTTTTTAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 538
AF093903
LOCUS       AF093903                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate 331 polyprotein gene, partial cds.
ACCESSION   AF093903
VERSION     AF093903.1  GI:4336446
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="331"
                     /db_xref="taxon:12461"
                     /country="India: Lucknow"
                     /note="sporadic hepatitis E; isolated in 1996"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17814.1"
                     /db_xref="GI:4336462"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              334             Length:         304
Score:                  93.00           Matches:        93
Percent Similarity:     93.00%          Conservative:   0
Best Local Similarity:  93.00%          Mismatches:     7
Query Match:            16.94%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF093903 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCCGTAAATTCTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db         63 CTCGAACTTGAGTTCCGCAACCTTACCCCCGGCAACACCAATACTCGGGTCTCTCGTTAC 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
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Db        123 TCCAGCACTGCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
                ||||||||||||||||||||||||||||||||    ||||||      ||||||||||||||||
Db        183 ACGGCTGCCACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
                   |||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db        243 ATCGGCCGCGGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTA 302

RESULT 539
AF093904
LOCUS       AF093904                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate K46 polyprotein gene, partial cds.
ACCESSION   AF093904
VERSION     AF093904.1  GI:4336447
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="K46"
                     /db_xref="taxon:12461"
                     /country="India: Karnal"
                     /note="isolated in 1987"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17815.1"
                     /db_xref="GI:4336463"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              334           Length:        304
Score:                  93.00         Matches:       93
Percent Similarity:     93.00%        Conservative:  0
Best Local Similarity:  93.00%        Mismatches:    7
Query Match:            16.94%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AF093904 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          3 CCCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
                ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACCGCCGAGCTTACCACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
                ||||||||||||||||||||||||||||||||    ||||||      ||||||||||||||||
Db        183 ACGGCCGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
                   |||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db        243 ATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 540
AF093905
LOCUS       AF093905                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate K70 polyprotein gene, partial cds.
ACCESSION   AF093905
VERSION     AF093905.1  GI:4336448
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="K70"
                     /db_xref="taxon:12461"
                     /country="India: Karnal"
                     /note="isolated in 1987"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17816.1"
                     /db_xref="GI:4336464"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              334           Length:        304
Score:                  93.00         Matches:       93
Percent Similarity:     93.00%        Conservative:  0
Best Local Similarity:  93.00%        Mismatches:    7
Query Match:            16.94%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AF093905 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
                ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTAT 122
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Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACCGCCGAGCTTACCACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||    ||||||      ||||||||||||||||
Db        183 ACGGCCGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db        243 ATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 541
AF093906
LOCUS       AF093906                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate K74 polyprotein gene, partial cds.
ACCESSION   AF093906
VERSION     AF093906.1  GI:4336449
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="K74"
                     /db_xref="taxon:12461"
                     /country="India: Karnal"
                     /note="isolated in 1987"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17817.1"
                     /db_xref="GI:4336465"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              334             Length:         304
Score:                  93.00           Matches:        93
Percent Similarity:     93.00%          Conservative:   0
Best Local Similarity:  93.00%          Mismatches:     7
Query Match:            16.94%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF093906 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
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Db         63 CTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACCGCCGAGCTTACCACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||    ||||||      ||||||||||||||||
Db        183 ACGGCCGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db        243 ATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 542
AF093907
LOCUS       AF093907                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate Y3 polyprotein gene, partial cds.
ACCESSION   AF093907
VERSION     AF093907.1  GI:4336450
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="Y3"
                     /db_xref="taxon:12461"
                     /country="India: Yamunanagar"
                     /note="isolated in 1989"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17818.1"
                     /db_xref="GI:4336466"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              334             Length:         304
Score:                  93.00           Matches:        93
Percent Similarity:     93.00%          Conservative:   0
Best Local Similarity:  93.00%          Mismatches:     7
Query Match:            16.94%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF093907 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
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Db         63 CTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTCTCCCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACCGCCGAGCTTACCACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              |||||||||||||||||||||||||||||    ||||||      ||||||||||||||||
Db        183 ACGGCCGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        243 ATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 543
AF093908
LOCUS       AF093908                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate Y11 polyprotein gene, partial cds.
ACCESSION   AF093908
VERSION     AF093908.1  GI:4336451
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="Y11"
                     /db_xref="taxon:12461"
                     /country="India: Yamunanagar"
                     /note="isolated in 1989"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17819.1"
                     /db_xref="GI:4336467"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              334             Length:         304
Score:                  93.00           Matches:        93
Percent Similarity:     93.00%          Conservative:   0
Best Local Similarity:  93.00%          Mismatches:     7
Query Match:            16.94%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF093908 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTCTCCCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACCGCCGAGCTTACCACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              |||||||||||||||||||||||||||||   ||||||      ||||||||||||||||
Db        183 ACGGCCGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        243 ATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 544
AF093909
LOCUS       AF093909                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate Y66 polyprotein gene, partial cds.
ACCESSION   AF093909
VERSION     AF093909.1  GI:4336452
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="Y66"
                     /db_xref="taxon:12461"
                     /country="India: Yamunanagar"
                     /note="isolated in 1989"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17820.1"
                     /db_xref="GI:4336468"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              334             Length:         304
Score:                  93.00           Matches:        93
Percent Similarity:     93.00%          Conservative:   0
Best Local Similarity:  93.00%          Mismatches:     7
Query Match:            16.94%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF093909 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCC 62
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Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
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Db         63 CTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTCTCCCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACCGCCGAGCTTACCACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||    ||||||      ||||||||||||||||
Db        183 ACGGCCGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        243 ATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 545
AF093910
LOCUS       AF093910                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate Y67 polyprotein gene, partial cds.
ACCESSION   AF093910
VERSION     AF093910.1  GI:4336453
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
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                     /mol_type="genomic RNA"
                     /isolate="Y67"
                     /db_xref="taxon:12461"
                     /country="India: Yamunanagar"
                     /note="isolated in 1989"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17821.1"
                     /db_xref="GI:4336469"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
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Alignment Scores:
Pred. No.:              334             Length:         304
Score:                  93.00           Matches:        93
Percent Similarity:     93.00%          Conservative:   0
Best Local Similarity:  93.00%          Mismatches:     7
Query Match:            16.94%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF093910 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          3 CCCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
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Db         63 CTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAATACTAATACGCGGGTCTCCCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
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Db        123 TCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACCGCCGAGCTTACCACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
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Db        183 ACGGCCGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        243 ATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 546
AF302068
LOCUS       AF302068                304 bp    mRNA    linear   VRL 02-DEC-2001
DEFINITION  Hepatitis E virus strain TW11SW capsid protein mRNA, partial cds.
ACCESSION   AF302068
VERSION     AF302068.1  GI:17224601
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.C.
  TITLE     Hepatitis E virus cross-species infection in human and swine
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-AUG-2000) Division of Gastroenterology, Taipei
            Veterans General Hospital & Institute of Clinical Medicine,
            National Yang-Ming University, 201 Shih-Pai Road, Sec. 2, Taipei
            112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
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                     /db_xref="taxon:12461"
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     CDS             <1. .>304
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                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAL37038.1"
                     /db_xref="GI:17224602"
                     /translation="PVNSYTNTPYTGALGLLDSALELEFRNLTPGNTNTRVSRYSSSA
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Alignment Scores:
Pred. No.:              334             Length:         304
Score:                  93.00           Matches:        93
Percent Similarity:     93.00%          Conservative:   0
Best Local Similarity:  93.00%          Mismatches:     7
Query Match:            16.94%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF302068 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          3 CCTGTGAACTCCTATACCAATACACCTTATACCGGTGCCCTCGGCCTGCTCGACTCCGCG 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
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Db         63 CTTGAGCTTGAGTTTCGTAATTTGACACCTGGTAATACAAACACGCGCGTTTCTCGTTAT 122
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Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
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Db        123 TCGAGCAGTGCACGCCACAAATTGCGCCGAGGGGCCGACGGCACCGCTGAGCTAACTACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
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Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        243 GTTGGCCGTGGGATAGCGCTTACCTTGTTTAACCTTGCTGATACACTTCTCGGCGGGCTC 302

RESULT 547
AF324504
LOCUS       AF324504                299 bp    RNA     linear   VRL 26-AUG-2002
DEFINITION  Swine hepatitis E virus isolate IND-SW4 nucleocapsid protein gene,
            partial cds.
ACCESSION   AF324504
VERSION     AF324504.1  GI:22476832
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 299)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 299)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B.R. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-NOV-2000) Hepatitis Department, National Institute of
            Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune,
            Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .299
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW4"
                     /specific_host="swine"
                     /db_xref="taxon:63421"
                     /country="India"
     CDS             <1. .>299
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                     /product="nucleocapsid protein"
                     /protein_id="AAM97327.1"
                     /db_xref="GI:22476833"
                     /translation="NTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRR
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Alignment Scores:
Pred. No.:              338           Length:        299
Score:                  92.00         Matches:       92
Percent Similarity:     92.93%        Conservative:  0
Best Local Similarity:  92.93%        Mismatches:    7
Query Match:            16.76%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AF324504 (1-299)

Qy        179 AsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArg 198
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Db          1 AATACACCTTACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGT 60

Qy        199 AsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHis 218
              |||||||||     ||||||||||||||||||||||||||||||   |||||||||
Db         61 AACTTAACACCTGGCAATACGAACACCCGTGTGTCTCGTTACTCGAGCAGCGCGCGTCAT 120

Qy        219 ArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPhe 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGTTGCGCCGGGGGGCTGATGGCACTGCTGAGTTAACCACTACTGCTGCTACACGTTTT 180

Qy        239 MetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAla 258
              ||||||||||||||||||||||   ||||||||||||||||||   |||||||||
Db        181 ATGAAGGACCTCCATTTTACTGGGACCAACGGTGTTGGTGAAGTCGGTTGTGGTATAGCG 240

Qy        259 LeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGACCTTATTTAATCTTGCTGATACACTTCTCGGCGGGCTTCCGACAGAATTGATT 297

RESULT 548
HEE428853
LOCUS       HEE428853               300 bp    RNA     linear   VRL 12-JUL-2002
DEFINITION  Hepatitis E virus type 4 partial polyprotein gene for capsid
            protein, swine isolate G6.
ACCESSION   AJ428853
VERSION     AJ428853.1  GI:18447773
KEYWORDS    capsid protein; polyprotein gene.
SOURCE      Hepatitis E virus type 4
  ORGANISM  Hepatitis E virus type 4
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Xia,N., Peng,G., Lan,H., Zhuang,H., Zhu,Y.,
            Li,S., Tian,K., Gu,W., Lin,J., Wu,X., Li,H. and Harrison,T.J.
  TITLE     Prevalence, isolation, and partial sequence analysis of hepatitis E
            virus from domestic animals in China
  JOURNAL   J. Med. Virol. 67 (4), 516-521 (2002)
  MEDLINE   22110701
   PUBMED   12115997
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2002) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .300
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                     /virion
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                     /db_xref="taxon:185580"
                     /country="China:Beijing"
     CDS             <1. .>300
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                     /protein_id="CAD21789.1"
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Alignment Scores:
Pred. No.:              338           Length:        300
Score:                  92.00         Matches:       92
Percent Similarity:     92.93%        Conservative:  0
Best Local Similarity:  92.93%        Mismatches:    7
Query Match:            16.76%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x HEE428853 (1-300)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          3 CCTGTGAATTCTTACACTAATACACCCTACACCGGTGCCCTCGGCTTACTTGATTTTGCA 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
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Db         63 CTCGAGCTCGAGTTCCGCAATTTAACACCTGGTAACACTAACACGCGCGTTTCTCGCTAC 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
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Db        123 TCGAGTAGCGCACGTCACAAATTGCGCCGAGGGCCTGATGGTACTGCTGAGTTAACTACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
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Db        183 ACTGCTGCCACACGCTTTATGAAAGACCTCCATTTCACGGGGACTAATGGTGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGly 271
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Db        243 GTCGGTCGTGGTATAGCGCTGACCTTGTTTAATCTTGCTGATACGCTTCTCGGCGGG 299

RESULT 549
HEE428854
LOCUS       HEE428854               300 bp    RNA     linear   VRL 12-JUL-2002
DEFINITION  Hepatitis E virus type 4 partial polyprotein gene for capsid
            protein, swine isolate G8.
ACCESSION   AJ428854
VERSION     AJ428854.1  GI:18447775
KEYWORDS    capsid protein; polyprotein gene.
SOURCE      Hepatitis E virus type 4
  ORGANISM  Hepatitis E virus type 4
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Xia,N., Peng,G., Lan,H., Zhuang,H., Zhu,Y.,
            Li,S., Tian,K., Gu,W., Lin,J., Wu,X., Li,H. and Harrison,T.J.
  TITLE     Prevalence, isolation, and partial sequence analysis of hepatitis E
            virus from domestic animals in China
  JOURNAL   J. Med. Virol. 67 (4), 516-521 (2002)
  MEDLINE   22110701
   PUBMED   12115997
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2002) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
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                     /isolate="G8"
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                     /country="China:Beijing"
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                     /protein_id="CAD21790.1"
                     /db_xref="GI:18447776"
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Alignment Scores:
Pred. No.:              338             Length:         300
Score:                  92.00           Matches:        92
Percent Similarity:     92.93%          Conservative:   0
Best Local Similarity:  92.93%          Mismatches:     7
Query Match:            16.76%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x HEE428854 (1-300)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
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Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
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Db        123 TCGAGTAGCGCGCGTCACAAACTGCGCCGAGGGCCTGATGGTACCGCTGAGTTGACTACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
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Db        183 ACTGCTGCCACACGTTTTATGAAAGACCTCCATTTTACGGGGACTAATGGTGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGly 271
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        243 GTCGGTCGTGGTATAGCGTTAACTTTGTTTAATCTTGCTGATACGCTTCTCGGTGGG 299

RESULT 550
HEE428855
LOCUS       HEE428855               300 bp    RNA     linear   VRL 12-JUL-2002
DEFINITION  Hepatitis E virus type 4 partial polyprotein gene for capsid
            protein, swine isolate SH1.
ACCESSION   AJ428855
VERSION     AJ428855.1  GI:18447777
KEYWORDS    capsid protein; polyprotein gene.
SOURCE      Hepatitis E virus type 4
  ORGANISM  Hepatitis E virus type 4
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Xia,N., Peng,G., Lan,H., Zhuang,H., Zhu,Y.,
            Li,S., Tian,K., Gu,W., Lin,J., Wu,X., Li,H. and Harrison,T.J.
  TITLE     Prevalence, isolation, and partial sequence analysis of hepatitis E
            virus from domestic animals in China
  JOURNAL   J. Med. Virol. 67 (4), 516-521 (2002)
  MEDLINE   22110701
   PUBMED   12115997
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2002) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
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                     /organism="Hepatitis E virus type 4"
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                     /isolate="SH1"
                     /specific_host="Sus scrofa"
                     /db_xref="taxon:185580"
                     /country="China:Henan"
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                     /protein_id="CAD21791.1"
                     /db_xref="GI:18447778"
                     /db_xref="GOA:Q8UZ73"
                     /db_xref="UniProt/TrEMBL:Q8UZ73"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
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Alignment Scores:
Pred. No.:              338             Length:         300
Score:                  92.00           Matches:        92
Percent Similarity:     92.93%          Conservative:   0
Best Local Similarity:  92.93%          Mismatches:     7
Query Match:            16.76%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x HEE428855 (1-300)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db          3 CCTGTAAATTCTTATACTAATACGCCTTATACTGGCGCTCTTGGCTTGCTTGACTTCGCG 62

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              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||

Db         63 CTCGAGCTTGAGTTCCGTAATTTGACACCTGGCAACACGAATACTCGTGTATCTCGTTAC 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||    |||||||||    ||||||||||||    ||||||||||||||||||||||

Db        123 TCGAGTAGCGCGCGCCACAAGTTACGCCGTGGGCCCGATGGCACTGCTGAATTGACTACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||

Db        183 ACTGCTGCTACACGCTTTATGAAGGACCTTCATTTCACGGGGACTAATGGTGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGly 271
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Db        243 GTCGGTCGTGGCATAGCGTTAACCCTGTTTAACCTTGCTGATACGCTTCTCGGTGGG 299

RESULT 551
AF103940
LOCUS       AF103940                301 bp ss-RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus capsid protein gene, partial cds.
ACCESSION   AF103940
VERSION     AF103940.1  GI:4324410
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Li,K., Zhuang,H., Wang,Y., Zhu,W., Tang,R., Bi,Y., Wei,Q., Liao,D.,
            Guo,Q., Wei,F. and Huang,Y.
  TITLE     A variant of hepatitis E virus isolated from a hepatitis E patient
            with negative anti-HEV
  JOURNAL   Zhonghua Wei Sheng Wu Xue He Mian Yi Xue Za Zhi 20 (2), 164-166
            (2000)
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Li,K., Zhuang,H. and Zhu,W.
  TITLE     Partial nucleotide sequencing of hepatitis E viruses detected in
            sera of patients with hepatitis E from 14 cities in China
  JOURNAL   Chin. Med. J. 115 (7), 1058-1063 (2002)
REFERENCE   3  (bases 1 to 301)
  AUTHORS   Li,K., Zhuang,H., Wang,Y., Zhu,W., Tang,R., Bi,Y., Wei,Q., Liao,D.,
            Guo,Q., Wei,F. and Huang,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-NOV-1998) Dept. of Microbiology, Beijing Medical
            University, 38 Xueyuan Road, Beijing, Beijing 100083, China
FEATURES             Location/Qualifiers
     source          1. .301
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                     /strain="LZ-105/China"
                     /db_xref="taxon:12461"
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                     /protein_id="AAD16876.1"
                     /db_xref="GI:4324411"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
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Alignment Scores:
Pred. No.:              338             Length:         301
Score:                  92.00           Matches:        92
Percent Similarity:     92.93%          Conservative:   0
Best Local Similarity:  92.93%          Mismatches:     7
Query Match:            16.76%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF103940 (1-301)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          3 CCTGTAAATTCTTACACTAACACACCTTACACCGGCGCCCTCGGTCTGCTTGACTTCGCA 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||

Db         63 CTCGAGCTCGAGTTTCGCAATTTGACACCTGGTAACACGAACACGCGCGTCTCCCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||    |||||||||    ||||||||||||    ||||||||||||||||||||||

Db        123 TCGAGTAGCGCGCGTCATAAGCTGCGCCGAGGGCCTGACGGCACTGCGGAGCTAACTACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||

Db        183 ACTGCTGCTACACGTTTTATGAAAGATCTTCATTTCACTGGGACTAATGGTGTTGGTGAA 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGly 271
              ||||||||||||||||||||||||||    ||||||||||||||||||||||||||

Db        243 GTTGGTCGTGGTATAGCACTGACCCTGTTTAATCTTGCTGATACGCTTCTCGGCGGG 299

RESULT 552
AF134916
LOCUS       AF134916                301 bp ss-RNA     linear   VRL 15-AUG-2002
DEFINITION  Hepatitis E virus strain HF-030/China capsid protein gene, partial
            cds.
ACCESSION   AF134916
VERSION     AF134916.1  GI:4836758
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Li,K., Zhuang,H. and Zhu,W.
  TITLE     Partial nucleotide sequencing of hepatitis E viruses detected in
            sera of patients with hepatitis E from 14 cities in China
  JOURNAL   Chin. Med. J. 115 (7), 1058-1063 (2002)
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Li,K., Zhuang,H. and Zhu,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-1999) Department of Microbiology, Beijing Medical
            University, 38 Xueyuan Road, Beijing 100083, P.R.China
FEATURES             Location/Qualifiers
     source          1. .301
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="HF-030/China"
                     /db_xref="taxon:12461"
     CDS             <1. .>301
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAD30542.1"
                     /db_xref="GI:4836759"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGADGTAELTTTAATRFMKDLHLTGTNGVGEVGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              338             Length:         301
Score:                  92.00           Matches:        92
Percent Similarity:     92.93%          Conservative:   0
Best Local Similarity:  92.93%          Mismatches:     7
Query Match:            16.76%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF134916 (1-301)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          3 CCTGTGAACTCTTACACCAATACACCCTATACCGGTGCTCTTGGCCTGCTCGATTTTGCG 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||

Db         63 CTTGAGCTCGAGTTTCGTAATTTGACACCTGGTAATACGAATACGCGCGTCTCTCGTTAT 122
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Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||  |||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        123 TCGAGTAGTGCGCGCCACAAACTGCGCCGAGGGGCCGACGGTACTGCTGAGTTAACTACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||    ||||||   ||||||||||||||||
Db        183 ACTGCTGCTACACGGTTTATGAAGGACCTTCATTTGACAGGGACTAATGGCGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGly 271
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        243 GTTGGCCGTGGGATAGCGCTTACCCTGTTTAACCTTGCTGACACACTTCTCGGCGGG 299

RESULT 553
AF093899
LOCUS       AF093899                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate M73 polyprotein gene, partial cds.
ACCESSION   AF093899
VERSION     AF093899.1  GI:4336442
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="M73"
                     /db_xref="taxon:12461"
                     /country="India: Meerut"
                     /note="isolated in 1996"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17810.1"
                     /db_xref="GI:4336458"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFASTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              338             Length:         304
Score:                  92.00           Matches:        92
Percent Similarity:     92.00%          Conservative:   0
Best Local Similarity:  92.00%          Mismatches:     8
Query Match:            16.76%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF093899 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||

Db         63 CTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||    |||   ||||||||||||||||
Db        183 ACGGCTGCTACCCGCTTCATGAAGGACCTCTATTTTGCTAGTACTAACGGTGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        243 ATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 554
AF093911
LOCUS       AF093911                304 bp ss-RNA     linear   VRL 04-MAR-1999
DEFINITION  Hepatitis E virus isolate M75 polyprotein gene, partial cds.
ACCESSION   AF093911
VERSION     AF093911.1  GI:4336454
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Genetic variability of hepatitis E virus within and between three
            epidemics in India
  JOURNAL   Virus Res. 59 (1), 35-48 (1999)
  MEDLINE   20311225
   PUBMED   10854164
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Aggarwal,R., McCaustland,K.A., Dilawari,J.B., Sinha,S.D. and
            Robertson,B.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) Hepatitis Branch, Division of Viral and
            Rickettsial Diseases, National Center for Infectious Diseases,
            Centers for Disease Control and Prevention (CDC), 1600 Clifton
            Road, Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="M75"
                     /db_xref="taxon:12461"
                     /country="India: Meerut"
                     /note="isolated in 1996"
     CDS             <1. .>304
                     /note="orf2"
                     /codon_start=3
                     /product="polyprotein"
                     /protein_id="AAD17822.1"
                     /db_xref="GI:4336470"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFASTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              338             Length:         304
Score:                  92.00           Matches:        92
Percent Similarity:     92.00%          Conservative:   0
Best Local Similarity:  92.00%          Mismatches:     8
Query Match:            16.76%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF093911 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGCTGGATTTTGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
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                  ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db          63 CTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACTAATACGCGGGTCTCCCGTTAT 122

Qy         213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         123 TCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACC 182

Qy         233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
                  ||||||||||||||||||||||||||||||    |||          ||||||||||||||
Db         183 ACGGCTGCTACCCGCTTCATGAAGGACCTCTATTTTGCTAGTACTAACGGTGTTGGTGAG 242

Qy         253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
                     ||||||||||||||||||||||    ||||||||||||||||||||||||||||
Db         243 ATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTG 302

RESULT 555
AF296161
LOCUS       AF296161                304 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus strain TW2896E nucleocapsid protein gene, partial
            cds.
ACCESSION   AF296161
VERSION     AF296161.1  GI:22384859
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2000) Department of Medicine, Division of
            Gastroenterology, Taipei Veterans General Hospital, Institute of
            Clinical Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW2896E"
                     /db_xref="taxon:12461"
                     /note="from patient serum"
     CDS             <1. .>304
                     /codon_start=3
                     /product="nucleocapsid protein"
                     /protein_id="AAM96008.1"
                     /db_xref="GI:22384860"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGPDGTAELTTTAATRFMKDLHFTGTNGVGEVGHGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:                338             Length:         304
Score:                    92.00           Matches:        92
Percent Similarity:       92.00%          Conservative:   0
Best Local Similarity:    92.00%          Mismatches:     8
Query Match:              16.76%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF296161 (1-304)

Qy         173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           3 CCTGTAAATTCTTATACTAATACACCCTATACTGGTGCTCTCGGTCTGCTTGATTTTGCA 62

Qy         193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
                  ||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db          63 CTCGAACTTGAGTTTCGCAATTTGACACCTGGCAATACAAACACGCGTGTCTCTCGTTAC 122

Qy         213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
                  ||||||   |||||||||   ||||||||||||   ||||||||||||||||||||||||
Db         123 TCGAGTAGCGCGCGCCACAAGCTACGCCGAGGACCTGATGGTACAGCAGAGCTAACCACT 182

Qy         233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
                  ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||
Db         183 ACTGCTGCTACACGCTTTATGAAGGATCTTCATTTCACCGGGACTAACGGTGTTGGTGAG 242

Qy         253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
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Db         243 GTTGGTCATGGTATAGCATTAACCCTGTTTAATCTTGCTGATACGCTTCTCGGCGGGCTT 302

RESULT 556
AF296162
LOCUS       AF296162                304 bp    RNA     linear   VRL 12-SEP-2001
DEFINITION  Hepatitis E virus strain TW6345E nonfunctional nucleocapsid protein
            gene, partial sequence.
ACCESSION   AF296162
VERSION     AF296162.1  GI:15558948
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2000) Department of Medicine, Division of
            Gastroenterology, Taipei Veterans General Hospital, Institute of
            Clinical Medicine, National Yang-Ming University School of
            Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW6345E"
                     /db_xref="taxon:12461"
                     /note="from Taiwanese patient serum"
     misc_feature    <1. .>304
                     /note="nonfunctional nucleocapsid protein due to mutation"

Alignment Scores:
Pred. No.:                338             Length:         304
Score:                    92.00           Matches:        92
Percent Similarity:       92.00%          Conservative:   0
Best Local Similarity:    92.00%          Mismatches:     8
Query Match:              16.76%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF296162 (1-304)

Qy         173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
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Db           3 CCTGTGAACTCCTATACCAATACACCTTATACTGGTGCCCTCGGCCTGCTCGACTTCGCG 62

Qy         193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
                  ||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db          63 CTTGAGCTTGAGTTTCGTAATTTGACACCTGGTAATACAAACACGCGCGTTTCTCGTTAT 122

Qy         213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
                  ||||||   |||||||||   ||||||   ||||||||||||||||||||||||||||||
Db         123 TCGAGCAGTGCACGCCACAAATTGCGCTGAGGGGCCGACGGCACCGCTGAGCTAACTACT 182

Qy         233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
                  ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||
Db         183 ACTGCTGCTACACGGTTTATGAAGGATCTTCATTTTGCAGGGACTAATGGTGTTGGTGAG 242

Qy         253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
                  ||||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db         243 GTTGGCCGTGGGATAGCGCTTACCTTGTTTAACCTTGCTGATACACTTCTCGGCGGGCTC 302

RESULT 557
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AF296164
LOCUS       AF296164                304 bp    RNA     linear   VRL 12-SEP-2001
DEFINITION  Hepatitis E virus strain TW5856E nucleocapsid protein gene, partial
            cds.
ACCESSION   AF296164
VERSION     AF296164.1  GI:15558951
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2000) Department of Medicine, Division of
            Gastroenterology, Taipei Veterans General Hospital, Institute of
            Clinical Medicine, National Yang-Ming University School of
            Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW5856E"
                     /db_xref="taxon:12461"
                     /note="from Taiwanese patient serum"
     CDS             <1. .>304
                     /codon_start=3
                     /product="nucleocapsid protein"
                     /protein_id="AAL02058.1"
                     /db_xref="GI:15558952"
                     /translation="PVNSYTNTPYTGALGPLDFALELEFRNLTPGNTSTRVSRYSSSA
                     RHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              338             Length:         304
Score:                  92.00           Matches:        92
Percent Similarity:     92.00%          Conservative:   0
Best Local Similarity:  92.00%          Mismatches:     8
Query Match:            16.76%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF296164 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db          3 CCTGTGAACTCCTATACCAATACACCTTATACTGGTGCCCTCGGCCCGCTCGACTTCGCG 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              |||||||||||||||||||||||||||      ||||||   ||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTCGTAATTTGACACCTGGTAATACAAGCACGCGCGTTTCTCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||   ||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        123 TCGAGCAGTGCACGCCACAAATTGCGCCGAGGGGCCGACGGCACCGCTGAGCTAACTACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        183 ACTGCTGCTACACGGTTTATGAAGGATCTTCATTTTACAGGGACTAATGGTGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        243 GTTGGCCGTGGGATAGCGCTTACCTTGTTTAACCTTGCTGATACACTTCTCGGCGGGCTC 302

RESULT 558
AF296167
LOCUS       AF296167                304 bp    RNA     linear   VRL 12-SEP-2001
DEFINITION  Hepatitis E virus strain TW3SW nucleocapsid protein gene, partial
            cds.
ACCESSION   AF296167
VERSION     AF296167.1  GI:15558957
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2000) Department of Medicine, Division of
            Gastroenterology, Taipei Veterans General Hospital, Institute of
            Clinical Medicine, National Yang-Ming University School of
            Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW3SW"
                     /db_xref="taxon:12461"
                     /note="from 3 month old swine serum"
     CDS             <1. .>304
                     /codon_start=3
                     /product="nucleocapsid protein"
                     /protein_id="AAL02061.1"
                     /db_xref="GI:15558958"
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                     RHRLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNLAYTLLGGLS"

Alignment Scores:
Pred. No.:              338             Length:         304
Score:                  92.00           Matches:        92
Percent Similarity:     92.00%          Conservative:   0
Best Local Similarity:  92.00%          Mismatches:     8
Query Match:            16.76%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF296167 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db          3 CCTGTTAATTCTTATACTAACACACCTCATAATGGCGCACTTGGACTTCTTGATTTTGCG 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              |||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         63 CTGGAGCTTGAATTTAGGAATCTGACACCCGGGAACACTAACACCCGTGTTTCCCGATAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ACTAGTACAGCCCGCCACCGACTGCGCCGTGGTGCAGACGGGACTGCTGAGCTTACAACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        183 ACAGCAGCCACGCGCTTCATGAAAGACCTGCATTTTACAGGCACGAATGGGGTCGGCGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        243 GTGGGCCGCGGTATTGCTCTTACATTGTTCAATCTTGCTTACACTCTCCTTGGTGGGTTG 302

RESULT 559
AF302069
LOCUS       AF302069                304 bp    mRNA    linear   VRL 02-DEC-2001
DEFINITION  Hepatitis E virus strain Nepal 7138 capsid protein mRNA, partial
            cds.
ACCESSION   AF302069
VERSION     AF302069.1  GI:17224603
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
```

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            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.C.
  TITLE     Hepatitis E virus cross-species infection in human and swine
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-AUG-2000) Division of Gastroenterology, Taipei
            Veterans General Hospital & Institute of Clinical Medicine,
            National Yang-Ming University, 201 Shih-Pai Road, Sec. 2, Taipei
            112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="mRNA"
                     /strain="Nepal 7138"
                     /db_xref="taxon:12461"
                     /country="Nepal"
                     /note="isolated from patient's serum"
     CDS             <1. .>304
                     /note="ORF2"
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAL37039.1"
                     /db_xref="GI:17224604"
                     /translation="PVNFYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              338           Length:         304
Score:                  92.00         Matches:        92
Percent Similarity:     92.00%        Conservative:   0
Best Local Similarity:  92.00%        Mismatches:     8
Query Match:            16.76%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF302069 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCCGTAAATTTTTATACTAACACACCCTACACCGGTGCCCTTGGGCTGTTGGACTTTGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         63 CTCGAACTTGAGTTCCGTAACCTTACCCCCGGCAACACCAATACTCGGGTTTCTCGTTAC 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TCCAGCACTGCTCGCCACCGTCTTCGCCGCGGTGCAGATGGGACTGCCGAGCTCACCACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              |||||||||||||||||||||||||||||||    ||||||      ||||||||||||||||
Db        183 ACGGCTGCCACCCGCTTTATGAAAGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
                  ||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        243 ATCGGCCGCGGGATAGCCCTTACCCTGTTTAATCTTGCTGACACTCTGCTTGGCGGCCTA 302

RESULT 560
HEE428851
LOCUS       HEE428851               300 bp    RNA     linear   VRL 12-JUL-2002
DEFINITION  Hepatitis E virus type 1 partial polyprotein gene for capsid
            protein, human isolate F8.
ACCESSION   AJ428851
VERSION     AJ428851.1  GI:18447769
KEYWORDS    capsid protein; polyprotein gene.
SOURCE      Hepatitis E virus type 1
  ORGANISM  Hepatitis E virus type 1
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Xia,N., Peng,G., Lan,H., Zhuang,H., Zhu,Y.,
            Li,S., Tian,K., Gu,W., Lin,J., Wu,X., Li,H. and Harrison,T.J.
  TITLE     Prevalence, isolation, and partial sequence analysis of hepatitis E
            virus from domestic animals in China
  JOURNAL   J. Med. Virol. 67 (4), 516-521 (2002)
  MEDLINE   22110701
   PUBMED   12115997
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2002) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Hepatitis E virus type 1"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="F8"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:185579"
                     /country="China:Xinjiang"
     CDS             <1. .>300
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="CAD21787.1"
                     /db_xref="GI:18447770"
                     /db_xref="GOA:Q8UZ77"
                     /db_xref="UniProt/TrEMBL:Q8UZ77"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTA
                     RHRLRRGTDGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGG"

Alignment Scores:
Pred. No.:              342           Length:         300
Score:                  91.00         Matches:        91
Percent Similarity:     91.92%        Conservative:   0
Best Local Similarity:  91.92%        Mismatches:     8
Query Match:            16.58%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x HEE428851 (1-300)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTAAATTCTTATACTAACACACCTTATACCGGTGCCCTTGGGCTGTTGGATTTTGCC 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         63 CTCGAACTTGAGTTCCGCAACCTCACCCCCGGTAATACCAACACGCGGGTCTCCCGTTAC 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||
Db        123 TCCAGCACTGCCCGTCACCGCCTTCGTCGCGGTACAGATGGGACTGCCGAGCTCACCACC 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||   ||||||      ||||||||||||||||
Db        183 ACGGCTGCTACCCGCTTCATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGly 271
                  ||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        243 ATCGGCCGCGGGATAGCGCTTACCCTGTTTAACCTTGCTGACACCCTGCTTGGCGGT 299

RESULT 561
HEE428856
LOCUS       HEE428856               300 bp    RNA     linear   VRL 12-JUL-2002
DEFINITION  Hepatitis E virus type 4 partial polyprotein gene for capsid
            protein, swine isolate SJ14.
ACCESSION   AJ428856
VERSION     AJ428856.1  GI:18447779
KEYWORDS    capsid protein; polyprotein gene.
SOURCE      Hepatitis E virus type 4
  ORGANISM  Hepatitis E virus type 4
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
```

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REFERENCE   1
  AUTHORS   Wang,Y., Zhang,H., Xia,N., Peng,G., Lan,H., Zhuang,H., Zhu,Y.,
            Li,S., Tian,K., Gu,W., Lin,J., Wu,X., Li,H. and Harrison,T.J.
  TITLE     Prevalence, isolation, and partial sequence analysis of hepatitis E
            virus from domestic animals in China
  JOURNAL   J. Med. Virol. 67 (4), 516-521 (2002)
  MEDLINE   22110701
   PUBMED   12115997
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Harrison,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2002) Harrison T.J., Centre for Hepatology,
            University College London, Royal Free Campus, Rowland Hill Street,
            London, NW3 2PF, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .300
                     /organism="Hepatitis E virus type 4"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="SJ14"
                     /specific_host="Sus scrofa"
                     /db_xref="taxon:185580"
                     /country="China:Zhejiang"
     CDS             <1. .>300
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="CAD21792.1"
                     /db_xref="GI:18447780"
                     /db_xref="GOA:Q8UZ72"
                     /db_xref="UniProt/TrEMBL:Q8UZ72"
                     /translation="PVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSA
                     RHKLRRGPDGTAELTTTAATRFMKDLHFTGTDGVGEVGRGIALTLFNLADTLLGG"

Alignment Scores:
Pred. No.:                342             Length:         300
Score:                    91.00           Matches:        91
Percent Similarity:       91.92%          Conservative:   0
Best Local Similarity:    91.92%          Mismatches:     8
Query Match:              16.58%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x HEE428856 (1-300)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCCGTAAATTCTTACACTAATACACCTTACACTGGCGCCCTCGGCCTGCTTGACTTTGCA 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         63 CTCGAGCTCGAGTTCCGCAACCTGACACCTGGTAATACGAACACGCGTGTCTCCCGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||    |||||||||    ||||||||||||    ||||||||||||||||||||||||
Db        123 TCGAGTAGCGCGCGTCACAAGTTACGCCGAGGGCCTGACGGCACTGCGGAGCTAACTACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 ACTGCTGCTACACGTTTCATGAAAGATCTTCATTTTACTGGGACTGATGGTGTTGGTGAA 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGly 271
              ||||||||||||||||||||||||||    ||||||||||||||||||||||||||||
Db        243 GTTGGCCGTGGTATAGCATTGACCTTGTTTAATCTTGCTGATACACTTCTCGGCGGG 299

RESULT 562
AF296163
LOCUS       AF296163                 304 bp    RNA     linear   VRL 12-SEP-2001
DEFINITION  Hepatitis E virus strain TW7924E nucleocapsid protein gene, partial
            cds.
ACCESSION   AF296163
VERSION     AF296163.1  GI:15558949
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Subclinical infection of HEV in human and swine in Taiwan area
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wu,J.-C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-2000) Department of Medicine, Division of
            Gastroenterology, Taipei Veterans General Hospital, Institute of
            Clinical Medicine, National Yang-Ming University School of
            Medicine, 201 Shih-Pai Road, Sec. 2, Taipei 112, Taiwan
FEATURES             Location/Qualifiers
     source          1. .304
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /strain="TW7924E"
                     /db_xref="taxon:12461"
                     /note="from Thai human"
     CDS             <1. .>304
                     /codon_start=3
                     /product="nucleocapsid protein"
                     /protein_id="AAL02057.1"
                     /db_xref="GI:15558950"
                     /translation="PVNSYTNTPYTSALGLLDFALELEFRNLTPGNTNTRVSCYSSSA
                     RHKLRRGADGTAELTTTAATRFMKDLHFTGTNGVGEVARGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:                342             Length:         304
Score:                    91.00           Matches:        91
Percent Similarity:       91.00%          Conservative:   0
Best Local Similarity:    91.00%          Mismatches:     9
Query Match:              16.58%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF296163 (1-304)

Qy        173 ProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAla 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCTGTGAACTCCTATACCAATACACCTTATACTAGTGCCCTCGGCCTGCTCGACTTCGCG 62

Qy        193 LeuGluLeuGluPheArgAsnLeuThrThrCysAsnThrAsnThrArgValSerArgTyr 212
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||||
Db         63 CTTGAGCTTGAGTTTCGTAATTTGACACCTGGTAATACAAACACGCGCGTTTCTTGTTAT 122

Qy        213 SerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThr 232
              ||||||    |||||||||    ||||||||||||||||||||||||||||||||||||||||
Db        123 TCGAGCAGTGCACGCCACAAATTGCGCCGAGGGGCCGACGGCACCGCTGAGCTAACTACT 182

Qy        233 ThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyValGlyGlu 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 ACTGCTGCTACACGGTTTATGAAGGATCTTCATTTTACAGGGACTAATGGTGTTGGTGAG 242

Qy        253 ValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              |||    ||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        243 GTTGCCCGTGGGATAGCGCTTACCTTGTTCAACCTTGCTGATACACTTCTCGGCGGGCTC 302

RESULT 563
AF446092
LOCUS       AF446092                 295 bp    RNA     linear   VRL 02-JAN-2003
DEFINITION  Hepatitis E virus isolate AKOLA99 structural protein 2 gene,
            partial cds.
ACCESSION   AF446092
VERSION     AF446092.1  GI:27462552
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 295)
  AUTHORS   Chobe,L.P., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE     Hepatitis E Outbreaks in Maharashtra (1999-2000), India:
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           Phylogenetic Analysis of Currently Prevalent HEV Isolates
  JOURNAL  Unpublished
REFERENCE  2  (bases 1 to 295)
  AUTHORS  Chobe,L.P., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
  TITLE    Direct Submission
  JOURNAL  Submitted (09-NOV-2001) Hepatitis, National Institute of Virology,
           20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .295
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="AKOLA99"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>295
                     /note="ORF2"
                     /codon_start=3
                     /product="structural protein 2"
                     /protein_id="AAO15472.1"
                     /db_xref="GI:27462553"
                     /translation="PYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGA
                     DGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELIS"

Alignment Scores:
Pred. No.:                346           Length:         295
Score:                    90.00         Matches:        90
Percent Similarity:       92.78%        Conservative:   0
Best Local Similarity:    92.78%        Mismatches:     7
Query Match:              16.39%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-16 (1-549) x AF446092 (1-295)

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTCGAGCTTGAGTTTCGCAACCTT 62

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 ACCCCCGGTAACACTAATACGCGGGTTTCCCGTTATTCCAGCACTGCCCGCCACCGCCTT 122

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CGTCGCGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTCATGAAG 182

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||  ||||||      ||||||||||||||   ||||||||||||||||||||||
Db        183 GACCTCTATTTTACTAGTACTAATGGTGTTGGTGAGATCGGCCGCGGGATAGCCCTCACC 242

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              |||   ||||||||||||||||||||||||||||||||||||||||||||
Db        243 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATT 293

RESULT 564
AF105021
LOCUS       AF105021                 296 bp    RNA     linear   VRL 01-DEC-2000
DEFINITION  Hepatitis E virus structural protein 2 gene, partial cds.
ACCESSION   AF105021
VERSION     AF105021.1  GI:6650540
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 296)
  AUTHORS   He,J., Binn,L.N., Tsarev,S.A., Hayes,C.G., Frean,J.A., Isaacson,M.
            and Innis,B.L.
  TITLE     Molecular characterization of a hepatitis E virus isolate from
            Namibia
  JOURNAL   J. Biomed. Sci. 7 (4), 334-338 (2000)
  MEDLINE   20355243
   PUBMED   10895057
REFERENCE   2  (bases 1 to 296)
  AUTHORS   He,J., Binn,L., Tsarev,S., Frean,J. and Innis,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-NOV-1998) Department of Virus Diseases, WRAIR,
            Washington, DC 20307
FEATURES             Location/Qualifiers
     source          1. .296
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="83-Namibia"
                     /db_xref="taxon:12461"
                     /country="Namibia"
     CDS             <1. .>296
                     /note="ORF-2"
                     /codon_start=3
                     /product="structural protein 2"
                     /protein_id="AAF21896.1"
                     /db_xref="GI:6650541"
                     /translation="STIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTASDQLL
                     IENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLEDTLDYPARAHTFD"

Alignment Scores:
Pred. No.:                355           Length:         296
Score:                    88.00         Matches:        88
Percent Similarity:       90.72%        Conservative:   0
Best Local Similarity:    90.72%        Mismatches:     9
Query Match:              16.03%        Indels:         0
DB:                       1             Gaps:           0

US-09-769-066-16 (1-549) x AF105021 (1-296)

Qy        417 ThrValGluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPhe 436
              |||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ACGATTCAGCAGTATTCGAAGACTTTCTTCGTCCTGCCGCTTCGTGGCAAGCTCTCCTTC 65

Qy        437 TrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAsp 456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 TGGGAGGCGGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACTACTGCTAGCGAC 125

Qy        457 GlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArg 476
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CAATTGCTTATCGAGAACGCCGCTGGGCATCGGGTGGCCATTTCTACTTATACCACTAGC 185

Qy        477 LeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeu 496
              ||||||||||||||||   |||||||||   ||||||||||||||   |||||||||
Db        186 TTGGGTGCAGGCCCTGTTTCCATCTCCGCGGTCGCTGTTCTAGCCCCCCACTCTGCTTTA 245

Qy        497 AlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAsp 513
              ||||||||||||||||   |||||||||   ||||||||||||||||||
Db        246 GCATTGCTCGAGGATACCTTGGATTACCCTGCCCGTGCTCATACTTTTGAT 296

RESULT 565
AY697426
LOCUS       AY697426                 283 bp    DNA     linear   VRL 12-OCT-2004
DEFINITION  Hepatitis E virus isolate osh89-5 capsid protein gene, partial cds.
ACCESSION   AY697426
VERSION     AY697426.1  GI:53854289
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 283)
  AUTHORS   Lu,L., Drobeniuc,J., Kobylnikov,N., Usmanov,R.K., Robertson,B.H.,
            Favorov,M.O. and Margolis,H.S.
  TITLE     Complete sequence of a Kygyzstan swine hepatitis E virus (HEV)
            isolated from a piglet thought to be experimentally infected with
            human HEV
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 283)
  AUTHORS   Lu,L., Drobeniuc,J., Kobylnikov,N., Usmanov,R.K., Robertson,B.H.,
            Favorov,M.O. and Margolis,H.S.
  TITLE     Direct Submission
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  JOURNAL   Submitted (26-JUL-2004) Laboratory Branch, Division of Viral
            Hepatitis, National Center for Infectious Disease, Centers for
            Disease Control and Prevention, 1600 Clifton Road NE., MS A33,
            Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .283
                     /organism="Hepatitis E virus"
                     /mol_type="genomic DNA"
                     /isolate="osh89-5"
                     /isolation_source="Human fecal sample"
                     /db_xref="taxon:12461"
                     /country="Kyrgyzstan: 1989"
                     /note="genotype: I"
     CDS             <1. .>283
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAU95601.1"
                     /db_xref="GI:53854290"
                     /translation="TPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRG
                     ADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              363             Length:         283
Score:                  86.00           Matches:        86
Percent Similarity:     92.47%          Conservative:   0
Best Local Similarity:  92.47%          Mismatches:     7
Query Match:            15.66%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AY697426 (1-283)

Qy        180 ThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsn 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ACACCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCTCTCGAACTTGAGTTCCGCAAC 62

Qy        200 LeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArg 219
              ||||||      ||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CTCACCCCCGGTAATACCAACACTCGGGTCTCCCGCTACTCCAGCACTGCTCGCCACCGT 122

Qy        220 LeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMet 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CTCCGTCGTGGTGCGGATGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATG 182

Qy        240 LysAspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeu 259
              |||||||||   ||||||      ||||||||||||||||   ||||||||||||||||||
Db        183 AAGGATCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTT 242

Qy        260 ThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeu 272
              ||||||   ||||||||||||||||||||||||||||||
Db        243 ACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTA 281

RESULT 566
AX181958
LOCUS       AX181958                250 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 240 from Patent WO0146696.
ACCESSION   AX181958
VERSION     AX181958.1  GI:15133241
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 240 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="3p.pile {hpenssp} shown in Figure 9F-9G"

Alignment Scores:
Pred. No.:              374             Length:         250
Score:                  83.00           Matches:        83
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            15.12%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AX181958 (1-250)

Qy        258 AlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTCTAACATTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCA 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCC 181

Qy        318 HisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CACGATATCGATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAG 241

Qy        338 GlnAspArg 340
              ||||||||
Db        242 CAGGATCGG 250

RESULT 567
BD077326
LOCUS       BD077326                250 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077326
VERSION     BD077326.1  GI:22622929
KEYWORDS    JP 2001520384-A/205.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 250)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 205 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/205
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   3p.pile {hpenssp} shown in Figure 9C
            FH   Key             Location/Qualifiers
            FT   source          1. .250
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                        virus)'.
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              374             Length:         250
Score:                  83.00           Matches:        83
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Percent Similarity:     100.00%         Conservative:  0
Best Local Similarity:  100.00%         Mismatches:    0
Query Match:            15.12%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-16 (1-549) x BD077326 (1-250)

Qy        258 AlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCTCTAACATTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCA 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCC 181

Qy        318 HisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CACGATATCGATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAG 241

Qy        338 GlnAspArg 340
              |||||||||
Db        242 CAGGATCGG 250

RESULT 568
AY697428
LOCUS       AY697428                 266 bp    DNA     linear   VRL 12-OCT-2004
DEFINITION  Hepatitis E virus isolate osh89-4 capsid protein gene, partial cds.
ACCESSION   AY697428
VERSION     AY697428.1  GI:53854293
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 266)
  AUTHORS   Lu,L., Drobeniuc,J., Kobylnikov,N., Usmanov,R.K., Robertson,B.H.,
            Favorov,M.O. and Margolis,H.S.
  TITLE     Complete sequence of a Kygyzstan swine hepatitis E virus (HEV)
            isolated from a piglet thought to be experimentally infected with
            human HEV
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 266)
  AUTHORS   Lu,L., Drobeniuc,J., Kobylnikov,N., Usmanov,R.K., Robertson,B.H.,
            Favorov,M.O. and Margolis,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-JUL-2004) Laboratory Branch, Division of Viral
            Hepatitis, National Center for Infectious Disease, Centers for
            Disease Control and Prevention, 1600 Clifton Road NE., MS A33,
            Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .266
                     /organism="Hepatitis E virus"
                     /mol_type="genomic DNA"
                     /isolate="osh89-4"
                     /isolation_source="Human fecal sample"
                     /db_xref="taxon:12461"
                     /country="Kyrgyzstan: 1989"
                     /note="genotype: I"
     CDS             <1. .>266
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAU95603.1"
                     /db_xref="GI:53854294"
                     /translation="ALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTA
                     ELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGL"

Alignment Scores:
Pred. No.:              384             Length:        266
Score:                  81.00           Matches:       81
Percent Similarity:     92.05%          Conservative:  0
Best Local Similarity:  92.05%          Mismatches:    7
Query Match:            14.75%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-16 (1-549) x AY697428 (1-266)

Qy        185 AlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsn 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db          2 GCCCTCGGGCTGCTGGACTTTGCTCTCGAACTTGAGTTCCGCAACCTCACCCCCGGTAAT 61

Qy        205 ThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAla 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ACCAACACTCGGGTCTCCCGCTACTCCAGCACTGCTCGCCACCGTCTCCGTCGTGGTGCG 121

Qy        225 AspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPhe 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        122 GATGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAGGATCTCTATTTT 181

Qy        245 ThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              |||     ||||||||||||||   ||||||||||||||||||||||||   ||||||
Db        182 ACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTTACCCTGTTCAACCTT 241

Qy        265 AlaAspThrLeuLeuGlyGlyLeu 272
              |||||||||||||||||||||||
Db        242 GCTGACACTCTGCTTGGCGGCCTA 265

RESULT 569
AX181955
LOCUS       AX181955                 250 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 237 from Patent WO0146696.
ACCESSION   AX181955
VERSION     AX181955.1  GI:15133238
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 237 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="3p.pile {hpea} shown in Figure 9F-9G"

Alignment Scores:
Pred. No.:              388             Length:        250
Score:                  80.00           Matches:       80
Percent Similarity:     96.39%          Conservative:  0
Best Local Similarity:  96.39%          Mismatches:    3
Query Match:            14.57%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-16 (1-549) x AX181955 (1-250)

Qy        258 AlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGCTTACCCTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGTGGCCAGCTGTTCTACTCTCGCCCCGTCGTCTCAGCCAATGGCGAGCCG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        122 ACTGTTAAGCTGTATACATCTGTGGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCG 181
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Qy        318 HisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        182 CATGACATCGACCTCGGGGAATCCCGTGTAGTTATTCAGGATTATGACAACCAACATGAG 241

Qy        338 GlnAspArg 340
              |||||||||
Db        242 CAGGACCGA 250

RESULT 570
AX181956
LOCUS       AX181956                250 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 238 from Patent WO0146696.
ACCESSION   AX181956
VERSION     AX181956.1  GI:15133239
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 238 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="3p.pile (hpeuigh) shown in Figure 9F-9G"

Alignment Scores:
Pred. No.:              388             Length:         250
Score:                  80.00           Matches:        80
Percent Similarity:     96.39%          Conservative:   0
Best Local Similarity:  96.39%          Mismatches:     3
Query Match:            14.57%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AX181956 (1-250)

Qy        258 AlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGCTTACCCTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGTGGCCAGCTGTTCTACTCTCGCCCCGTCGTCTCAGCCAATGGCGAGCCG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||||    |||||||||
Db        122 ACTGTTAAGCTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCG 181

Qy        318 HisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        182 CATGACATCGACCTCGGGGAATCTCGAGTTGTTATTCAGGATTATGACAACCAACATGAG 241

Qy        338 GlnAspArg 340
              |||||||||
Db        242 CAGGACCGG 250

RESULT 571
AX181957
LOCUS       AX181957                250 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 239 from Patent WO0146696.
ACCESSION   AX181957
VERSION     AX181957.1  GI:15133240
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 239 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="3p.pile (hpesvp) shown in Figure 9F-9G"

Alignment Scores:
Pred. No.:              388             Length:         250
Score:                  80.00           Matches:        80
Percent Similarity:     96.39%          Conservative:   0
Best Local Similarity:  96.39%          Mismatches:     3
Query Match:            14.57%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AX181957 (1-250)

Qy        258 AlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||||    |||||||||
Db        122 ACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCG 181

Qy        318 HisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        182 CATGACATTGACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAA 241

Qy        338 GlnAspArg 340
              |||||||||
Db        242 CAAGATCGG 250

RESULT 572
BD077323
LOCUS       BD077323                250 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077323
VERSION     BD077323.1  GI:22622926
KEYWORDS    JP 2001520384-A/202.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 250)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 202 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/202
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   3p.pile (hpea) shown in Figure 9C
            FH   Key             Location/Qualifiers
            FT   source          1. .250
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          FT                   /organism='Hepatitis virus (hepatitis E  FT
                              virus)'.
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              388             Length:         250
Score:                  80.00           Matches:        80
Percent Similarity:     96.39%          Conservative:   0
Best Local Similarity:  96.39%          Mismatches:     3
Query Match:            14.57%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x BD077323 (1-250)

Qy        258 AlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGCTTACCCTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGTGGCCAGCTGTTCTACTCTCGCCCCGTCGTCTCAGCCAATGGCGAGCCG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACTGTTAAGCTGTATACATCTGTGGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCG 181

Qy        318 HisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        182 CATGACATCGACCTCGGGGAATCCCGTGTAGTTATTCAGGATTATGACAACCAACATGAG 241

Qy        338 GlnAspArg 340
              |||||||||
Db        242 CAGGACCGA 250

RESULT 573
BD077324
LOCUS       BD077324                 250 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077324
VERSION     BD077324.1  GI:22622927
KEYWORDS    JP 2001520384-A/203.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 250)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 203 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/203
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   3p.pile {hpeuigh} shown in Figure 9C
            FH   Key             Location/Qualifiers
            FT   source          1. .250
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                              virus)'.
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              388             Length:         250
Score:                  80.00           Matches:        80
Percent Similarity:     96.39%          Conservative:   0
Best Local Similarity:  96.39%          Mismatches:     3
Query Match:            14.57%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x BD077324 (1-250)

Qy        258 AlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGCTTACCCTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGTGGCCAGCTGTTCTACTCTCGCCCCGTCGTCTCAGCCAATGGCGAGCCG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACTGTTAAGCTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCG 181

Qy        318 HisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        182 CATGACATCGACCTCGGGGAATCTCGAGTTGTTATTCAGGATTATGACAACCAACATGAG 241

Qy        338 GlnAspArg 340
              |||||||||
Db        242 CAGGACCGG 250

RESULT 574
BD077325
LOCUS       BD077325                 250 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077325
VERSION     BD077325.1  GI:22622928
KEYWORDS    JP 2001520384-A/204.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 250)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 204 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/204
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   3p.pile {hpesvp} shown in Figure 9C
            FH   Key             Location/Qualifiers
            FT   source          1. .250
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                              virus)'.
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              388             Length:         250
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Score:                  80.00          Matches:       80
Percent Similarity:     96.39%         Conservative:  0
Best Local Similarity:  96.39%         Mismatches:    3
Query Match:            14.57%         Indels:        0
DB:                     1              Gaps:          0

US-09-769-066-16 (1-549) x BD077325 (1-250)

Qy        258 AlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCG 181

Qy        318 HisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        182 CATGACATTGACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAA 241

Qy        338 GlnAspArg 340
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Db        242 CAAGATCGG 250

RESULT 575
AY697427
LOCUS       AY697427                 265 bp    DNA     linear   VRL 12-OCT-2004
DEFINITION  Hepatitis E virus isolate osh89-3 capsid protein gene, partial cds.
ACCESSION   AY697427
VERSION     AY697427.1  GI:53854291
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 265)
  AUTHORS   Lu,L., Drobeniuc,J., Kobylnikov,N., Usmanov,R.K., Robertson,B.H.,
            Favorov,M.O. and Margolis,H.S.
  TITLE     Complete sequence of a Kygyzstan swine hepatitis E virus (HEV)
            isolated from a piglet thought to be experimentally infected with
            human HEV
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 265)
  AUTHORS   Lu,L., Drobeniuc,J., Kobylnikov,N., Usmanov,R.K., Robertson,B.H.,
            Favorov,M.O. and Margolis,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-JUL-2004) Laboratory Branch, Division of Viral
            Hepatitis, National Center for Infectious Disease, Centers for
            Disease Control and Prevention, 1600 Clifton Road NE., MS A33,
            Atlanta, GA 30333, USA
FEATURES             Location/Qualifiers
     source          1. .265
                     /organism="Hepatitis E virus"
                     /mol_type="genomic DNA"
                     /isolate="osh89-3"
                     /isolation_source="Human fecal sample"
                     /db_xref="taxon:12461"
                     /country="Kyrgyzstan: 1989"
                     /note="genotype: I"
     CDS             <1. .>265
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAU95602.1"
                     /db_xref="GI:53854292"
                     /translation="LGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAE
                     LTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLP"

Alignment Scores:
Pred. No.:              389            Length:        265
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Score:                  80.00          Matches:       80
Percent Similarity:     91.95%         Conservative:  0
Best Local Similarity:  91.95%         Mismatches:    7
Query Match:            14.57%         Indels:        0
DB:                     1              Gaps:          0

US-09-769-066-16 (1-549) x AY697427 (1-265)

Qy        186 LeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThr 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||      ||||||
Db          3 CTCGGGCTGCTGGACTTTGCTCTCGAACTTGAGTTCCGCAACCTCACCCCCGGTAATACC 62

Qy        206 AsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAsp 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 AACACTCGGGTCTCCCGCTACTCCAGCACTGCTCGCCACCGTCTCCGTCGTGGTGCGGAT 122

Qy        226 GlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThr 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        123 GGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAGGATCTCTATTTTACT 182

Qy        246 GlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeuAla 265
              ||||||||||||||||   ||||||||||||||||||||||   |||||||||
Db        183 AGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTTACCCTGTTCAACCTTGCT 242

Qy        266 AspThrLeuLeuGlyGlyLeu 272
              |||||||||||||||||||||
Db        243 GACACTCTGCTTGGCGGCCTA 263

RESULT 576
AF228533
LOCUS       AF228533                 255 bp    RNA     linear   VRL 02-FEB-2001
DEFINITION  Hepatitis E virus isolate 93-Dji 42031 structural protein gene,
            partial cds.
ACCESSION   AF228533
VERSION     AF228533.1  GI:12656044
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 255)
  AUTHORS   van Cuyck,H. and Viret,J.
  TITLE     Introduction for a modelization of Hepatitis E virus (HEV)
            evolution
  JOURNAL   Acta Biotheor. (2000) In press
REFERENCE   2  (bases 1 to 255)
  AUTHORS   Buisson,Y., Grandadam,M., Tsarev,S. and Masseron,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Transmissible Agents, CRSSA, 24 Ave des
            Maquis du Gresivaudan, BP87, La Tronche 38702, France
FEATURES             Location/Qualifiers
     source          1. .255
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="93-Dji 42031"
                     /db_xref="taxon:12461"
                     /country="Djibouti"
                     /note="isolated from sporadic case in 1993"
     CDS             <1. .>255
                     /note="ORF2"
                     /codon_start=1
                     /product="structural protein"
                     /protein_id="AAK00718.1"
                     /db_xref="GI:12656045"
                     /translation="FWEAGTTKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGA
                     GPVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECR"

Alignment Scores:
Pred. No.:              398            Length:        255
Score:                  78.00          Matches:       78
Percent Similarity:     91.76%         Conservative:  0
Best Local Similarity:  91.76%         Mismatches:    7
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Query Match:            14.21%      Indels:        0
DB:                     1           Gaps:          0

US-09-769-066-16 (1-549) x AF228533 (1-255)

Qy        436 PheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSer 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTCTGGGAGGCGGGTACTACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGC 60

Qy        456 AspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThr 475
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACCAATTGCTCATCGAGAATGCCGCCGGACATCGGGTGGCTATTTCCACCTATACCACT 120

Qy        476 ArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAla 495
                ||||||||||||||||||   |||||||||   ||||||||||||||   ||||||
Db        121 AGCCTAGGTGCTGGCCCTGTTTCCATCTCCGCGGTCGCTGTTCTAGCCCCCCACTCTGCT 180

Qy        496 LeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPhe 515
              ||||||||||||||||||||   |||||||||   ||||||||||||||||||||||||
Db        181 TTAGCACTGCTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTC 240

Qy        516 CysProGluCysArg 520
              ||||||||||||||||
Db        241 TGCCCGGAGTGCCGT 255

RESULT 577
AF228529
LOCUS       AF228529                256 bp    RNA     linear   VRL 02-FEB-2001
DEFINITION  Hepatitis E virus isolate 93-Som structural protein gene, partial
            cds.
ACCESSION   AF228529
VERSION     AF228529.1  GI:12656036
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 256)
  AUTHORS   van Cuyck,H. and Viret,J.
  TITLE     Introduction for a modelization of Hepatitis E virus (HEV)
            evolution
  JOURNAL   Acta Biotheor. (2000) In press
REFERENCE   2  (bases 1 to 256)
  AUTHORS   Masseron,T., Buisson,Y., Grandadam,M. and Nicand,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Transmissible Agents, CRSSA, 24 Ave des
            Maquis du Gresivaudan, BP87, La Tronche 38702, France
FEATURES             Location/Qualifiers
     source          1. .256
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="93-Som"
                     /db_xref="taxon:12461"
     CDS             <1. .>256
                     /note="ORF2"
                     /codon_start=1
                     /product="structural protein"
                     /protein_id="AAK00714.1"
                     /db_xref="GI:12656037"
                     /translation="FWEAGTTKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGA
                     GPVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECR"

Alignment Scores:
Pred. No.:              398         Length:        256
Score:                  78.00       Matches:       78
Percent Similarity:     91.76%      Conservative:  0
Best Local Similarity:  91.76%      Mismatches:    7
Query Match:            14.21%      Indels:        0
DB:                     1           Gaps:          0

US-09-769-066-16 (1-549) x AF228529 (1-256)

Qy        436 PheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSer 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTTTGGGAGGCGGGTACTACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGT 60

Qy        456 AspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThr 475
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACCAATTGCTCATCGAGAATGCCGCCGGACATCGGGTGGCTATTTCCACCTATACCACT 120

Qy        476 ArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAla 495
                ||||||||||||||||||   |||||||||   ||||||||||||||   ||||||
Db        121 AGCCTAGGTGCTGGCCCTGTCTCCATCTCCGCGGTCGCTGTTCTAGCCCCCCACTCTGCT 180

Qy        496 LeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPhe 515
              ||||||||||||||||||||   |||||||||   ||||||||||||||||||||||||
Db        181 TTAGCGCTGCTTGAGGACACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTC 240

Qy        516 CysProGluCysArg 520
              ||||||||||||||||
Db        241 TGCCCGGAGTGCCGC 255

RESULT 578
AF228530
LOCUS       AF228530                256 bp    RNA     linear   VRL 02-FEB-2001
DEFINITION  Hepatitis E virus isolate 95-Alg Tan 11 structural protein gene,
            partial cds.
ACCESSION   AF228530
VERSION     AF228530.1  GI:12656038
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 256)
  AUTHORS   van Cuyck,H. and Viret,J.
  TITLE     Introduction for a modelization of Hepatitis E virus (HEV)
            evolution
  JOURNAL   Acta Biotheor. (2000) In press
REFERENCE   2  (bases 1 to 256)
  AUTHORS   Larouze,B., Buisson,Y., Grandadam,M., Nicand,E. and Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Transmissible Agents, CRSSA, 24 Ave des
            Maquis du Gresivaudan, BP87, La Tronche 38702, France
FEATURES             Location/Qualifiers
     source          1. .256
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="95-Alg Tan 11"
                     /db_xref="taxon:12461"
                     /country="Algeria: Tanedfou"
                     /note="isolated from 1995 epidemic outbreak case"
     CDS             <1. .>256
                     /note="ORF2"
                     /codon_start=1
                     /product="structural protein"
                     /protein_id="AAK00715.1"
                     /db_xref="GI:12656039"
                     /translation="FWEAGTTKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGA
                     GPVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECR"

Alignment Scores:
Pred. No.:              398         Length:        256
Score:                  78.00       Matches:       78
Percent Similarity:     91.76%      Conservative:  0
Best Local Similarity:  91.76%      Mismatches:    7
Query Match:            14.21%      Indels:        0
DB:                     1           Gaps:          0

US-09-769-066-16 (1-549) x AF228530 (1-256)

Qy        436 PheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSer 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTCTGGGAGGCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGC 60
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Qy        456 AspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThr 475
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACCAATTGCTTATTGAGAACGCCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACT 120

Qy        476 ArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAla 495
              ||||||||||||||||||  |||||||||  ||||||||||||||||  ||||||
Db        121 AGCCTAGGTGCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCATTCTGCT 180

Qy        496 LeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPhe 515
              ||||||||||||||||||||  |||||||||  ||||||||||||||||||||||||||
Db        181 TTAGCACTGCTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTC 240

Qy        516 CysProGluCysArg 520
              ||||||||||||||||
Db        241 TGTCCGGAGTGCCGT 255

RESULT 579
AF228534
LOCUS       AF228534                256 bp    RNA     linear   VRL 02-FEB-2001
DEFINITION  Hepatitis E virus isolate 95-Dji 26-3 93393 structural protein
            gene, partial cds.
ACCESSION   AF228534
VERSION     AF228534.1  GI:12656046
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 256)
  AUTHORS   van Cuyck,H. and Viret,J.
  TITLE     Introduction for a modelization of Hepatitis E virus (HEV)
            evolution
  JOURNAL   Acta Biotheor. (2000) In press
REFERENCE   2  (bases 1 to 256)
  AUTHORS   Masseron,T., Buisson,Y., Grandadam,M. and Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Transmissible Agents, CRSSA, 24 Ave des
            Maquis du Gresivaudan, BP87, La Tronche 38702, France
FEATURES             Location/Qualifiers
     source          1. .256
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="95-Dji 26-3 93393"
                     /db_xref="taxon:12461"
                     /country="Djibouti"
                     /note="isolated from sporadic case in 1995; Djibouti
                     resident"
     CDS             <1. .>256
                     /note="ORF2"
                     /codon_start=1
                     /product="structural protein"
                     /protein_id="AAK00719.1"
                     /db_xref="GI:12656047"
                     /translation="FWEAGTTKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGA
                     GPVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECR"

Alignment Scores:
Pred. No.:              398           Length:         256
Score:                  78.00         Matches:        78
Percent Similarity:     91.76%        Conservative:   0
Best Local Similarity:  91.76%        Mismatches:     7
Query Match:            14.21%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF228534 (1-256)

Qy        436 PheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSer 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTCTGGGAGGCGGGTACTACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGT 60

Qy        456 AspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThr 475
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACCAATTGCTCATTGAGAATGCCGCCGGACATCGGGTGGCTATTTCCACCTATACCACT 120

Qy        476 ArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAla 495
              ||||||||||||||||||  |||||||||  ||||||||||||||||  ||||||
Db        121 AGCCTAGGTGCTGGCCCTGTTTCCATCTCCGCGGTCGCTGTTTTAGCCCCCCACTCTGCT 180

Qy        496 LeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPhe 515
              ||||||||||||||||||||  |||||||||  ||||||||||||||||||||||||||
Db        181 TTAGCACTGCTTGAGGATACCCTGGATTACCCTGCCCGCGCTCACACTTTCGATGATTTC 240

Qy        516 CysProGluCysArg 520
              ||||||||||||||||
Db        241 TGCCCGGAGTGCCGC 255

RESULT 580
AF228535
LOCUS       AF228535                256 bp    RNA     linear   VRL 02-FEB-2001
DEFINITION  Hepatitis E virus isolate 96-Dji 28-1 99402 structural protein
            gene, partial cds.
ACCESSION   AF228535
VERSION     AF228535.1  GI:12656048
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 256)
  AUTHORS   van Cuyck,H. and Viret,J.
  TITLE     Introduction for a modelization of Hepatitis E virus (HEV)
            evolution
  JOURNAL   Acta Biotheor. (2000) In press
REFERENCE   2  (bases 1 to 256)
  AUTHORS   Masseron,T., Buisson,Y., Grandadam,M. and Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Transmissible Agents, CRSSA, 24 Ave des
            Maquis du Gresivaudan, BP87, La Tronche 38702, France
FEATURES             Location/Qualifiers
     source          1. .256
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="96-Dji 28-1 99402"
                     /db_xref="taxon:12461"
                     /country="Djibouti"
                     /note="isolated from sporadic case in 1996; French
                     soldier"
     CDS             <1. .>256
                     /note="ORF2"
                     /codon_start=1
                     /product="structural protein"
                     /protein_id="AAK00720.1"
                     /db_xref="GI:12656049"
                     /translation="FWEAGTTKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGA
                     GPVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECR"

Alignment Scores:
Pred. No.:              398           Length:         256
Score:                  78.00         Matches:        78
Percent Similarity:     91.76%        Conservative:   0
Best Local Similarity:  91.76%        Mismatches:     7
Query Match:            14.21%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF228535 (1-256)

Qy        436 PheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSer 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTCTGGGAGGCGGGTACTACTAAAGCCGGGTACCCTTATAACTATAACACCACTGCTAGT 60

Qy        456 AspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThr 475
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACCAATTGCTCATTGAGAATGCCGCCGGACATCGGGTGGCTATTTCCACCTATACCACT 120
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Qy        476 ArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAla 495
              ||||||||||||||||||   |||||||||   ||||||||||||||||   ||||||
Db        121 AGCCTAGGTGCTGGCCCTGTTTCCATCTCCGCGGTCGCTGTTTTAGCCCCCCACTCTGCT 180

Qy        496 LeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPhe 515
              ||||||||||||||||||||||   |||||||||   |||||||||||||||||||||||
Db        181 TTAGCACTGCTTGAGGATACTCTGGATTACCCTGCCCGCGCTCACACTTTCGATGATTTC 240

Qy        516 CysProGluCysArg 520
              ||||||||||||||
Db        241 TGCCCGGAGTGCCGC 255

RESULT 581
AF228537
LOCUS       AF228537                256 bp    RNA     linear   VRL 02-FEB-2001
DEFINITION  Hepatitis E virus isolate 95-Alg Tan 4 10TE structural protein
            gene, partial cds.
ACCESSION   AF228537
VERSION     AF228537.1  GI:12656052
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 256)
  AUTHORS   van Cuyck,H. and Viret,J.
  TITLE     Introduction for a modelization of Hepatitis E virus (HEV)
            evolution
  JOURNAL   Acta Biotheor. (2000) In press
REFERENCE   2  (bases 1 to 256)
  AUTHORS   Larouze,B., Siriwardana,M.G., Buisson,Y., Grandadam,M. and
            Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Transmissible Agents, CRSSA, 24 Ave des
            Maquis du Gresivaudan, BP87, La Tronche 38702, France
FEATURES             Location/Qualifiers
     source          1. .256
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="95-Alg Tan 4 10TE"
                     /db_xref="taxon:12461"
                     /country="Algeria: Tanedfou"
                     /note="isolated from epidemic outbreak case in 1995"
     CDS             <1. .>256
                     /note="ORF2"
                     /codon_start=1
                     /product="structural protein"
                     /protein_id="AAK00722.1"
                     /db_xref="GI:12656053"
                     /translation="FWEAGTTKAGYPYNYNTTASDQLLIENAAGHRVAISTYTTSLGA
                     GPVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECR"

Alignment Scores:
Pred. No.:              398           Length:        256
Score:                  78.00         Matches:       78
Percent Similarity:     91.76%        Conservative:  0
Best Local Similarity:  91.76%        Mismatches:    7
Query Match:            14.21%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AF228537 (1-256)

Qy        436 PheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSer 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTCTGGGAGGCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCCAGC 60

Qy        456 AspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThr 475
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACCAATTGCTTATTGAGAACGCCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACT 120

Qy        476 ArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAla 495
              ||||||||||||||||||   |||||||||   ||||||||||||||||   ||||||
Db        121 AGCCTAGGCGCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCT 180

Qy        496 LeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPhe 515
              ||||||||||||||||||||||   |||||||||   |||||||||||||||||||||||
Db        181 TTAGCACTGCTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTC 240

Qy        516 CysProGluCysArg 520
              ||||||||||||||
Db        241 TGTCCGGAGTGCCGT 255

RESULT 582
AF407560
LOCUS       AF407560                249 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW5 capsid protein gene, partial cds.
ACCESSION   AF407560
VERSION     AF407560.1  GI:22347436
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 249)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 249)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .249
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW5"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>249
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM95904.1"
                     /db_xref="GI:22347437"
                     /translation="YTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGAD
                     GTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNL"

Alignment Scores:
Pred. No.:              402           Length:        249
Score:                  77.00         Matches:       77
Percent Similarity:     92.77%        Conservative:  0
Best Local Similarity:  92.77%        Mismatches:    6
Query Match:            14.03%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AF407560 (1-249)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGTAACTTAACA 60

Qy        202 ThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              ||||||||||||||||||||||||||||||||||||  |||||||||  ||||||
Db         61 CCTGGCAATACGAACACCCGTGTGTCTCGTTACTCGAGCAGCGCGCGTCATAAGTTGCGC 120

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGGGGCTGATGGCACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGAC 180
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Qy        242 LeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeu 261
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCCATTTTACTGGGACCAACGGTGTTGGTGAAGTTGGTCGTGGTATAGCGCTGACCTTA 240

Qy        262 LeuAsnLeu 264
              |||||||
Db        241 TTTAATCTA 249
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RESULT 583
AF407567
LOCUS AF407567 249 bp RNA linear VRL 21-AUG-2002
DEFINITION Hepatitis E virus IND-SW12 capsid protein gene, partial cds.
ACCESSION AF407567
VERSION AF407567.1 GI:22347453
KEYWORDS .
SOURCE Hepatitis E virus
ORGANISM Hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 249)
AUTHORS Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and Walimbe,A.M.
TITLE Human and swine hepatitis E viruses from Western India belong to different genotypes
JOURNAL J. Hepatol. 36 (3), 417-425 (2002)
MEDLINE 21856722
PUBMED 11867187
REFERENCE 2 (bases 1 to 249)
AUTHORS Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-2001) Hepatitis, National Institute of Virology, 20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES Location/Qualifiers
source 1. .249
/organism="Hepatitis E virus"
/mol_type="genomic RNA"
/isolate="IND-SW12"
/specific_host="pig"
/db_xref="taxon:12461"
/country="India"
CDS <1. .>249
/note="ORF2"
/codon_start=1
/product="capsid protein"
/protein_id="AAM95908.1"
/db_xref="GI:22347454"
/translation="YTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGAD
GTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNL"

Alignment Scores:

Pred. No.:	402	Length:	249
Score:	77.00	Matches:	77
Percent Similarity:	92.77%	Conservative:	0
Best Local Similarity:	92.77%	Mismatches:	6
Query Match:	14.03%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AF407567 (1-249)

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Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGTAACTTAACA 60

Qy        202 ThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              |||||||||||||||||||||||||||||||  |||||||||  ||||||
Db         61 CCTGGCAATACGAACACCCGTGTGTCTCGTTACTCGAGCAGCGCGCGTCATAAGTTGCGC 120

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGGGGCTGATGGCACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGAC 180

Qy        242 LeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeu 261
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCCATTTTACTGGGACCAACGGTGTTGGTGAAGTTGGTCGTGGTATAGCGCTGACCTTA 240

Qy        262 LeuAsnLeu 264
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Db        241 TTTAATCTA 249
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RESULT 584
AF505860
LOCUS AF505860 249 bp ss-RNA linear VRL 01-MAY-2003
DEFINITION Swine hepatitis E virus isolate IND-SW17 ORF2 gene, partial cds.
ACCESSION AF505860
VERSION AF505860.1 GI:30269361
KEYWORDS .
SOURCE Swine hepatitis E virus
ORGANISM Swine hepatitis E virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae; Hepevirus.
REFERENCE 1 (bases 1 to 249)
AUTHORS Arankalle,V.A., Chobe,L.P., Walimbe,A.M., Yergolkar,P.N. and George,J.P.
TITLE Incidence of Swine HEV Infection in South India and Phylogenetic Analysis (1985-1999)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 249)
AUTHORS Arankalle,V.A., Chobe,L.P., Walimbe,A.M., Yergolkar,P.N. and George,J.P.
TITLE Direct Submission
JOURNAL Submitted (15-APR-2002) Hepatitis Department, National Institute of Virology, 20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES Location/Qualifiers
source 1. .249
/organism="Swine hepatitis E virus"
/mol_type="genomic RNA"
/isolate="IND-SW17"
/db_xref="taxon:63421"
/country="India: South"
CDS <1. .>249
/codon_start=1
/product="ORF2"
/protein_id="AAP29642.1"
/db_xref="GI:30269362"
/translation="YTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGAD
GTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNL"

Alignment Scores:

Pred. No.:	402	Length:	249
Score:	77.00	Matches:	77
Percent Similarity:	92.77%	Conservative:	0
Best Local Similarity:	92.77%	Mismatches:	6
Query Match:	14.03%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AF505860 (1-249)

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Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
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Db          1 TACACTGGCGCCCTCGGTCTGCTCGACTTTGCGCTTGAACTCGAGTTTCGTAATTTAACA 60

Qy        202 ThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              |||||||||||||||||||||||||||||||  |||||||||  ||||||
Db         61 CCTGGCAATACGAATACCCGTGTGTCCCGTTATTCGAGCAGCGCACGTCACAAGTTGCGC 120

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGAGGGGCTGATGGTACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGAT 180

Qy        242 LeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeu 261
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCCATTTTACTGGGACCAACGGTGTTGGTGAAGTTGGCCGTGGTATAGCGCTGACCTTA 240

Qy        262 LeuAsnLeu 264
              |||||||
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Db        241 TTTAATCTC 249

RESULT 585
AF228538
LOCUS       AF228538                256 bp    RNA     linear   VRL 02-FEB-2001
DEFINITION  Hepatitis E virus isolate 95-Alg Tan 6 Al17 structural protein
            gene, partial cds.
ACCESSION   AF228538
VERSION     AF228538.1  GI:12656054
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 256)
  AUTHORS   van Cuyck,H. and Viret,J.
  TITLE     Introduction for a modelization of Hepatitis E virus (HEV)
            evolution
  JOURNAL   Acta Biotheor. (2000) In press
REFERENCE   2  (bases 1 to 256)
  AUTHORS   Larouze,B., Siriwardana,M.G., Buisson,Y., Grandadam,M. and
            Tsarev,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2000) Transmissible Agents, CRSSA, 24 Ave des
            Maquis du Gresivaudan, BP87, La Tronche 38702, France
FEATURES             Location/Qualifiers
     source          1. .256
                     /organism="Hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="95-Alg Tan 6 Al17"
                     /db_xref="taxon:12461"
                     /country="Algeria: Tanedfou"
                     /note="isolated from epidemic outbreak case in 1995"
     CDS             <1. .>256
                     /note="ORF2"
                     /codon_start=1
                     /product="structural protein"
                     /protein_id="AAK00723.1"
                     /db_xref="GI:12656055"
                     /translation="FWEAGTTKAGYPYNYNTTASDQLLIENVAGHRVAISTYTTSLGA
                     GPVSISAVAVLAPHSALALLEDTLDYPARAHTFDDFCPECR"

Alignment Scores:
Pred. No.:              403           Length:         256
Score:                  77.00         Matches:        77
Percent Similarity:     90.59%        Conservative:   0
Best Local Similarity:  90.59%        Mismatches:     8
Query Match:            14.03%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF228538 (1-256)

Qy        436 PheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSer 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTCTGGGAGGCAGGTACCACTAAAGCCGGGTACCCTTATAATTATAATACCACTGCTAGC 60

Qy        456 AspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThr 475
              ||||||   ||||||||||||  ||||||||||||||||||||||||||||||||||||
Db         61 GACCAATTGCTTATTGAGAACGTCGCCGGGCATCGGGTGGCTATTTCCACTTATACCACT 120

Qy        476 ArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAla 495
              ||||||||||||||||||   |||||||||   ||||||||||||||||   ||||||
Db        121 AGCCTAGGTGCTGGCCCTGTCTCTATTTCTGCGGTCGCTGTTTTAGCTCCCCACTCTGCT 180

Qy        496 LeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPhe 515
              ||||||||||||||||||||||   |||||||||   ||||||||||||||||||||||
Db        181 TTAGCACTGCTTGAGGATACCCTGGATTACCCTGCCCGCGCCCATACTTTTGATGATTTC 240

Qy        516 CysProGluCysArg 520
              ||||||||||||||||
Db        241 TGTCCGGAGTGCCGT 255
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RESULT 586
AF407562
LOCUS       AF407562                244 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW7 capsid protein gene, partial cds.
ACCESSION   AF407562
VERSION     AF407562.1  GI:22347441
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 244)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 244)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .244
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW7"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>244
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM95905.1"
                     /db_xref="GI:22347442"
                     /translation="GALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGADGT
                     AELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNL"

Alignment Scores:
Pred. No.:              412           Length:         244
Score:                  75.00         Matches:        75
Percent Similarity:     92.59%        Conservative:   0
Best Local Similarity:  92.59%        Mismatches:     6
Query Match:            13.66%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AF407562 (1-244)

Qy        184 GlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCys 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGTAACCTAACACCTGGC 61

Qy        204 AsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGly 223
              ||||||||||||||||||||||||||||||   |||||||||   ||||||||||||
Db         62 AATACGAACACCCGTGTGTCTCGTTACTCGAGCAGCGCGCGTCATAAGTTGCGCCGGGGG 121

Qy        224 AlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHis 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GCTGATGGCACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGACCTCCAT 181

Qy        244 PheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsn 263
              |||||||||   ||||||||||||||||||||||||||||||||||||||||   |||
Db        182 TTTACTGGGACCAACGGTGTTGGTGAAGTTGGTCGTGGTATAGCGCTGACCTTATTTAAT 241

Qy        264 Leu 264
              |||
Db        242 CTA 244

RESULT 587
AF407561
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LOCUS       AF407561                246 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW6 nonfunctional capsid protein gene,
            partial sequence.
ACCESSION   AF407561
VERSION     AF407561.1  GI:22347439
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 246)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 246)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .246
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW6"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     misc_feature    <1. .>246
                     /note="nonfunctional capsid protein due to mutation; ORF2"

Alignment Scores:
Pred. No.:                412             Length:         246
Score:                    75.00           Matches:        75
Percent Similarity:       93.75%          Conservative:   0
Best Local Similarity:    93.75%          Mismatches:     5
Query Match:              13.66%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF407561 (1-246)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGTAACTTAACA 60

Qy        202 ThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              |||||||||||||||||||||||||||||||   |||||||||   ||||||
Db         61 CCTGGCAATACGAACACCCGTGTGTCTCGTTACTCGAGCAGCGCGCGTCATAAGTTGCGC 120

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGGGGCTGATGGCACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGAC 180

Qy        242 LeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeu 261
              |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCCATTTTACTGGGACCAACGGTGTTGGTGAAGTTGGTCGTGGTATAGCGCTGACCTTA 240

RESULT 588
AF407564
LOCUS       AF407564                247 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW9 capsid protein gene, partial cds.
ACCESSION   AF407564
VERSION     AF407564.1  GI:22347447
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 247)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 247)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .247
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW9"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>247
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM95907.1"
                     /db_xref="GI:22347448"
                     /translation="YTGALGLLDFALELEFRSLTPGNTNTRVSRYSSSARHKLRRGAD
                     GTAELTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFN"

Alignment Scores:
Pred. No.:                412             Length:         247
Score:                    75.00           Matches:        75
Percent Similarity:       91.46%          Conservative:   0
Best Local Similarity:    91.46%          Mismatches:     7
Query Match:              13.66%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF407564 (1-247)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGTAGCTTAACA 60

Qy        202 ThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              |||||||||||||||||||||||||||||||   |||||||||   ||||||
Db         61 CCTGGCAATACGAACACCCGTGTGTCTCGTTACTCGAGCAGCGCGCGTCATAAGTTGCGC 120

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGGGGCCGATGGTACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGAC 180

Qy        242 LeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeu 261
              |||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCCATTTTACTGGGACCAACGGTGTTGGTGAAGTTGGTCGTGGTATAGCGCTGACCTTA 240

Qy        262 LeuAsn 263
              |||
Db        241 TTTAAT 246

RESULT 589
AF407569
LOCUS       AF407569                247 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW14 capsid protein gene, partial cds.
ACCESSION   AF407569
VERSION     AF407569.1  GI:22347459
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 247)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
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          different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 247)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,.
          20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .247
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW14"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>247
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM95910.1"
                     /db_xref="GI:22347460"
                     /translation="YTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGAD
                     GTAELTTTAATRFMKDLHFTGTNGVGEVGCGIALTLFN"

Alignment Scores:
Pred. No.:              412             Length:         247
Score:                  75.00           Matches:        75
Percent Similarity:     91.46%          Conservative:   0
Best Local Similarity:  91.46%          Mismatches:     7
Query Match:            13.66%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF407569 (1-247)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TACACTGGCGCCCTCGGTCTGCTCGATTTTGCGCTTGAACTCGAGTTTCGTAATTTAACA 61

Qy        202 ThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              |||||||||||||||||||||||||||||||   |||||||||   ||||||
Db         62 CCTGGTAATACGAACACCCGTGTGTCCCGTTATTCGAGCAGCGCGCGTCACAAGTTGCGC 121

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CGAGGGGCTGATGGTACTGCTGAGTTAACTACTACTGCTGCCACACGTTTTATGAAGGAC 181

Qy        242 LeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeu 261
              ||||||||||||||   ||||||||||||||||||   ||||||||||||||||||
Db        182 CTCCATTTTACTGGGACCAATGGTGTTGGTGAAGTTGGTTGTGGTATAGCGCTGACCTTA 241

Qy        262 LeuAsn 263
                 |||
Db        242 TTTAAT 247

RESULT 590
AF505861
LOCUS       AF505861                 249 bp ss-RNA     linear   VRL 01-MAY-2003
DEFINITION  Swine hepatitis E virus isolate IND-SW18 ORF2 gene, partial cds.
ACCESSION   AF505861
VERSION     AF505861.1  GI:30269363
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
          Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
          Hepevirus.
REFERENCE   1  (bases 1 to 249)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Walimbe,A.M., Yergolkar,P.N. and
          George,J.P.
  TITLE     Incidence of Swine HEV Infection in South India and Phylogenetic
          Analysis (1985-1999)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 249)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Walimbe,A.M., Yergolkar,P.N. and
          George,J.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-2002) Hepatitis Department, National Institute of
          Virology, 20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .249
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW18"
                     /db_xref="taxon:63421"
                     /country="India: South"
     CDS             <1. .>249
                     /codon_start=2
                     /product="ORF2"
                     /protein_id="AAP29643.1"
                     /db_xref="GI:30269364"
                     /translation="YTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGAD
                     GTAELTTTAATRFMKDPHFTGTNGVGEVGRGIALTLFNL"

Alignment Scores:
Pred. No.:              412             Length:         249
Score:                  75.00           Matches:        75
Percent Similarity:     91.46%          Conservative:   0
Best Local Similarity:  91.46%          Mismatches:     7
Query Match:            13.66%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF505861 (1-249)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TACACTGGCGCCCTCGGTCTGCTCGATTTTGCGCTTGAACTCGAGTTTCGTAATTTAACA 61

Qy        202 ThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              |||||||||||||||||||||||||||||||   |||||||||   ||||||
Db         62 CCTGGCAATACGAATACCCGTGTGTCCCGTTATTCGAGCAGCGCACGTCACAAGTTGCGC 121

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CGAGGGGCTGATGGTACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGAT 181

Qy        242 LeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeu 261
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CCCCATTTTACTGGGACCAACGGTGTTGGTGAAGTTGGCCGTGGTATAGCGCTGACCTTA 241

Qy        262 LeuAsn 263
                 |||
Db        242 TTTAAT 247

RESULT 591
AF407570
LOCUS       AF407570                 250 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW15 capsid protein gene, partial cds.
ACCESSION   AF407570
VERSION     AF407570.1  GI:22347462
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
          Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
          Hepevirus.
REFERENCE   1  (bases 1 to 250)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
          Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
          different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 250)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
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  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW15"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>250
                     /note="ORF2"
                     /codon_start=2
                     /product="capsid protein"
                     /protein_id="AAM95911.1"
                     /db_xref="GI:22347463"
                     /translation="YTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGAD
                     GTAELTSTAATRFMKDLHFTGTNGVGEVGCGIALTLFNL"

Alignment Scores:
Pred. No.:                412             Length:         250
Score:                    75.00           Matches:        75
Percent Similarity:       90.36%          Conservative:   0
Best Local Similarity:    90.36%          Mismatches:     8
Query Match:              13.66%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF407570 (1-250)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGTAATTTAACA 61

Qy        202 ThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              |||||||||||||||||||||||||||||||    |||||||||    ||||||
Db         62 CCTGGTAATACGAACACCCGTGTGTCCCGTTATTCGAGCAGCGCGCGTCACAAGTTGCGC 121

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              |||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        122 CGAGGGGCTGATGGTACTGCTGAGTTAACCTCTACTGCTGCTACACGTTTTATGAAGGAT 181

Qy        242 LeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeu 261
              ||||||||||||||    ||||||||||||||||||||    ||||||||||||||||||
Db        182 CTCCATTTTACTGGGACCAATGGTGTTGGTGAAGTTGGTTGTGGTATAGCGCTGACCTTA 241

Qy        262 LeuAsnLeu 264
                 |||||||
Db        242 TTTAATCTA 250

RESULT 592
AF407563
LOCUS       AF407563                247 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW8 capsid protein gene, partial cds.
ACCESSION   AF407563
VERSION     AF407563.1  GI:22347444
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 247)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 247)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .247
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW8"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>247
                     /note="ORF2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAM95906.1"
                     /db_xref="GI:22347445"
                     /translation="YTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGAD
                     GTAELTTTAATRFMKDLHFTGTNGVGEVGCGLALTLFN"

Alignment Scores:
Pred. No.:                417             Length:         247
Score:                    74.00           Matches:        74
Percent Similarity:       90.24%          Conservative:   0
Best Local Similarity:    90.24%          Mismatches:     8
Query Match:              13.48%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF407563 (1-247)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGTAACTTAACA 60

Qy        202 ThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              |||||||||||||||||||||||||||||||    |||||||||    ||||||
Db         61 CCTGGCAATACGAACACCCGTGTGTCTCGTTACTCGAGCAGCGCGCGTCATAAGTTGCGC 120

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGGGGCTGATGGTACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGAC 180

Qy        242 LeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeu 261
              ||||||||||||||    ||||||||||||||||||||    |||    ||||||||||||
Db        181 CTCCATTTTACTGGGACCAACGGTGTTGGTGAAGTCGGTTGTGGTCTAGCGCTGACCTTA 240

Qy        262 LeuAsn 263
                 |||
Db        241 TTTAAT 246

RESULT 593
AF407568
LOCUS       AF407568                239 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW13 capsid protein gene, partial cds.
ACCESSION   AF407568
VERSION     AF407568.1  GI:22347456
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 239)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 239)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .239
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                     /organism="Hepatitis E virus"
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                     /isolate="IND-SW13"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     CDS             <1. .>239
                     /note="ORF2"
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAM95909.1"
                     /db_xref="GI:22347457"
                     /translation="LGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGADGTAE
                     LTTTAATRFMKDLHFTGTNGVGEVGRGIALTLFNL"

Alignment Scores:
Pred. No.:                421             Length:         239
Score:                    73.00           Matches:        73
Percent Similarity:       92.41%          Conservative:   0
Best Local Similarity:    92.41%          Mismatches:     6
Query Match:              13.30%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AF407568 (1-239)

Qy        186 LeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThrThrCysAsnThr 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||      ||||||
Db          3 CTCGGTCTGCTCGATTTTGCGCTTGAACTCGAGTTTCGTAATTTAACACCTGGTAATACG 62

Qy        206 AsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAsp 225
              |||||||||||||||||||||||||   |||||||||   ||||||||||||||||||
Db         63 AACACCCGTGTGTCCCGTTACTCGAGCAGCGCGCGTCATAAGTTGCGCCGGGGGGCTGAT 122

Qy        226 GlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThr 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GGCACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGACCTCCATTTTACT 182

Qy        246 GlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsnLeu 264
              |||   ||||||||||||||||||||||||||||||||||||||||   ||||||
Db        183 GGGACCAACGGTGTTGGTGAAGTTGGTCGTGGTATAGCGCTGACCTTATTTAATCTA 239

RESULT 594
AY753554
LOCUS       AY753554                 227 bp    RNA     linear   VRL 12-OCT-2004
DEFINITION  Hepatitis E virus isolate Lucknow_Sw_208 capsid protein gene,
            partial cds.
ACCESSION   AY753554
VERSION     AY753554.1  GI:53854173
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 227)
  AUTHORS   Aggarwal,R., Shukla,P. and Naik,S.
  TITLE     Hepatitis E virus among swine in northern India
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 227)
  AUTHORS   Aggarwal,R., Shukla,P. and Naik,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-SEP-2004) Gastroenterology, Sanjay Gandhi
            Postgraduate Institute of Medical Sciences, Raebareli Road,
            Lucknow, UP 226014, India
FEATURES             Location/Qualifiers
     source          1. .227
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="Lucknow_Sw_208"
                     /specific_host="swine"
                     /db_xref="taxon:12461"
                     /country="India: Lucknow"
     CDS             <1. .>227
                     /note="Orf2"
                     /codon_start=1
                     /product="capsid protein"
                     /protein_id="AAU95557.1"
                     /db_xref="GI:53854174"
                     /translation="YTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRGAD
                     GTAELTTTAATRFMKDLHFTGTNGVGEVGRG"

Alignment Scores:
Pred. No.:                435             Length:         227
Score:                    70.00           Matches:        70
Percent Similarity:       93.33%          Conservative:   0
Best Local Similarity:    93.33%          Mismatches:     5
Query Match:              12.75%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AY753554 (1-227)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACACTGGCGCCCTCGGTCTGCTCGACTTTGCACTTGAGCTTGAGTTTCGTAATTTGACA 60

Qy        202 ThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              |||||||||||||||||||||||||||||||||||   |||||||||   ||||||
Db         61 CCCGGGAATACCAACACACGTGTGTCTCGTTACTCGAGCAGTGCGCGCCACAAATTGCGT 120

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGGGCGCTGATGGGACCGCCGAGTTAACCACTACAGCAGCTACTCGGTTTATGAAGGAT 180

Qy        242 LeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGly 256
              ||||||||||||||   ||||||||||||||||||||||||||
Db        181 TTACATTTTACTGGGACTAATGGTGTTGGTGAGGTTGGGCGTGGT 225

RESULT 595
AF407566
LOCUS       AF407566                 249 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW11 nonfunctional capsid protein gene,
            partial sequence.
ACCESSION   AF407566
VERSION     AF407566.1  GI:22347451
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 249)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 249)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .249
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW11"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     misc_feature    <1. .>249
                     /note="nonfunctional capsid protein due to mutation; ORF2"

Alignment Scores:
Pred. No.:                442             Length:         249
Score:                    69.00           Matches:        69
Percent Similarity:       86.25%          Conservative:   0
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Best Local Similarity:  86.25%          Mismatches:     11
Query Match:            12.57%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF407566 (1-249)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTTGAACTCGAGTTCCGTAATCTAACA 60

Qy        202 ThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCCGGTAATACGAACACCCGTGTGTCTCGTTATTCGAGCAGCGCGCGTCACAAGTTGCGC 120

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGAGGGGCTGATGGTACTGCTGAGTTAACCACTACTGCTGCTACACGCTTTATGAAGGAC 180

Qy        242 LeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeu 261
              |||||||||||||||   ||||||||||||||||||||                   |||
Db        181 CTTCATTTTACTGGGACCAACGGTGTTGGTGAAGTTGGTCTGTGGTATAGCGCTGACCTT 240

RESULT 596
AF407565
LOCUS       AF407565                 251 bp    RNA     linear   VRL 21-AUG-2002
DEFINITION  Hepatitis E virus IND-SW10 nonfunctional capsid protein gene,
            partial sequence.
ACCESSION   AF407565
VERSION     AF407565.1  GI:22347450
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 251)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Chadha,M.S., Kundu,B. and
            Walimbe,A.M.
  TITLE     Human and swine hepatitis E viruses from Western India belong to
            different genotypes
  JOURNAL   J. Hepatol. 36 (3), 417-425 (2002)
  MEDLINE   21856722
   PUBMED   11867187
REFERENCE   2  (bases 1 to 251)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Joshi,M.V., Kundu,B. and Walimbe,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Hepatitis, National Institute of Virology,
            20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .251
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW10"
                     /specific_host="pig"
                     /db_xref="taxon:12461"
                     /country="India"
     misc_feature    <1. .>251
                     /note="nonfunctional capsid protein due to mutation; ORF2"

Alignment Scores:
Pred. No.:              442             Length:         251
Score:                  69.00           Matches:        69
Percent Similarity:     86.25%          Conservative:   0
Best Local Similarity:  86.25%          Mismatches:     11
Query Match:            12.57%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF407565 (1-251)

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TACACTGGCGCCCTCGGTCTGCTTGATTTTGCACTCGAACTCGAGTTTCGTAACTTAACA 61

Qy        202 ThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCAGGCAACACGAACACCCGTGTGTCCCGTTACTCGAGCAGCGCGCGTCATAAGTTGCGC 121

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CGGGGGGCTGATGGTACTGCTGAGTTAACCACTACTGCTGCTACACGTTTTATGAAGGAC 181

Qy        242 LeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeu 261
              |||||||||||||||   ||||||||||||||||||||                   |||
Db        182 CTCCATTTTACTGGGACCAACGGTGTTGGTGAAGTTGGTCTGTGGTATAGCGCTGACCTT 241

RESULT 597
AF347692
LOCUS       AF347692                 212 bp    RNA     linear   VRL 01-NOV-2001
DEFINITION  Swine hepatitis E virus capsid protein gene, partial cds.
ACCESSION   AF347692
VERSION     AF347692.1  GI:16565781
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 212)
  AUTHORS   Yoo,D., Willson,P., Pei,Y., Hayes,M.A., Deckert,A., Dewey,C.E.,
            Friendship,R.M., Yoon,Y., Gottschalk,M., Yason,C. and Giulivi,A.
  TITLE     Prevalence of hepatitis E virus antibodies in Canadian swine herds
            and identification of a novel variant of swine hepatitis E virus
  JOURNAL   Clin. Diagn. Lab. Immunol. 8 (6), 1213-1219 (2001)
  MEDLINE   21546646
   PUBMED   11687465
REFERENCE   2  (bases 1 to 212)
  AUTHORS   Pei,Y. and Yoo,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-FEB-2001) Department of Pathobiology, University of
            Guelph, Guelph, Ontario N1G 2W1, Canada
FEATURES             Location/Qualifiers
     source          1. .212
                     /organism="Swine hepatitis E virus"
                     /virion
                     /mol_type="genomic RNA"
                     /isolate="SK3"
                     /db_xref="taxon:63421"
                     /country="Canada: Saskatchewan"
     CDS             <1. .>212
                     /note="ORF2"
                     /codon_start=3
                     /product="capsid protein"
                     /protein_id="AAL26294.1"
                     /db_xref="GI:16565782"
                     /translation="NPLLPLQDGTNTHIMATEASNYAQYRVVRATIRYRPLVPNAVGG
                     YAISISFWPQTTTTPTSVDMNSITST"

Alignment Scores:
Pred. No.:              445             Length:         212
Score:                  68.00           Matches:        68
Percent Similarity:     97.14%          Conservative:   0
Best Local Similarity:  97.14%          Mismatches:     2
Query Match:            12.39%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AF347692 (1-212)

Qy         50 AsnProProLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSer 69
              |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 AACCCCCTTTTACCCCTCCAGGACGGAACCAATACTCATATCATGGCCACCGAGGCGTCC 62

Qy         70 AsnTyrAlaGlnTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsn 89
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db         63 AACTATGCCCAGTATCGGGTCGTCCGAGCTACGATCCGTTACCGCCCGCTGGTGCCTAAT 122

Qy         90 AlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThr 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GCTGTTGGCGGTTACGCTATTTCTATTTCTTTCTGGCCCCAAACTACAACTACTCCTACT 182
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Qy        110 SerValAspMetAsnSerIleThrSerThr 119
              |||||||||||||||||||||||||||||||
Db        183 TCTGTTGATATGAATTCCATCACTTCTACT 212

RESULT 598
AF505859
LOCUS       AF505859                217 bp ss-RNA     linear   VRL 01-MAY-2003
DEFINITION  Swine hepatitis E virus isolate IND-SW16 ORF2 gene, partial cds.
ACCESSION   AF505859
VERSION     AF505859.1  GI:30269359
KEYWORDS    .
SOURCE      Swine hepatitis E virus
  ORGANISM  Swine hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 217)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Walimbe,A.M., Yergolkar,P.N. and
            George,J.P.
  TITLE     Incidence of Swine HEV Infection in South India and Phylogenetic
            Analysis (1985-1999)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 217)
  AUTHORS   Arankalle,V.A., Chobe,L.P., Walimbe,A.M., Yergolkar,P.N. and
            George,J.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-2002) Hepatitis Department, National Institute of
            Virology, 20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India
FEATURES             Location/Qualifiers
     source          1. .217
                     /organism="Swine hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="IND-SW16"
                     /db_xref="taxon:63421"
                     /country="India: South"
     CDS             <1. .>217
                     /codon_start=1
                     /product="ORF2"
                     /protein_id="AAP29641.1"
                     /db_xref="GI:30269360"
                     /translation="TPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSSARHKLRRG
                     ADGTAELTTTAATRFMKDLHFTGTNGVG"

Alignment Scores:
Pred. No.:              450          Length:         217
Score:                  67.00        Matches:        67
Percent Similarity:     93.06%       Conservative:   0
Best Local Similarity:  93.06%       Mismatches:     5
Query Match:            12.20%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AF505859 (1-217)

Qy        180 ThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsn 199
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACACCTTACACTGGCGCCCTCGGTCTGCTCGATTTTGCACTCGAACTCGAGTTTCGTAAT 60

Qy        200 LeuThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArg 219
              ||||||     |||||||||||||||||||||||||||||||||   |||||||||
Db         61 TTGACACCTGGTAATACGAACACTCGTGTGTCTCGTTATTCGAGCAGCGCGCGTCATAAG 120

Qy        220 LeuArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMet 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTGCGCCGAGGGGCTGATGGTACTGCTGAGCTAACTACTACTGCTGCTACACGCTTTATG 180

Qy        240 LysAspLeuHisPheThrGlyLeuAsnGlyValGly 251
              ||||||||||||||||||||    ||||||||||||
Db        181 AAGGACCTCCATTTTACTGGGACCAATGGTGTTGGT 216

RESULT 599
AX181959
LOCUS       AX181959                250 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 241 from Patent WO0146696.
ACCESSION   AX181959
VERSION     AX181959.1  GI:15133242
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 241 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="3p.pile {840453p} shown in Figure 9F-9G"

Alignment Scores:
Pred. No.:              463          Length:         250
Score:                  65.00        Matches:        65
Percent Similarity:     78.31%       Conservative:   0
Best Local Similarity:  78.31%       Mismatches:     18
Query Match:            11.84%       Indels:         0
DB:                     1            Gaps:           0

US-09-769-066-16 (1-549) x AX181959 (1-250)

Qy        258 AlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||    ||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCCTGACTCTGTTTAATCTTGCTGATACGCTTCTTGGTGGTTTACCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              |||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCTGTTCAGAATTGATTTCGTCGGCTG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIlePro 317
              |||        |||              ||||||||||||||||||      ||||||
Db        122 GGGGTCAACTGTTTTACTCCCGCCCTGTTTGCGCAGCAAGACAAGGGCATCACCATTCCA 181

Qy        318 HisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CACGACATAGATTTAGGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCACGAA 241

Qy        338 GlnAspArg 340
              ||||||||
Db        242 CAAGATCGA 250

RESULT 600
BD077327
LOCUS       BD077327                250 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077327
VERSION     BD077327.1  GI:22622930
KEYWORDS    JP 2001520384-A/206.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 250)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 206 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/206
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
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           PI   ISA K MASHAWER
           PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
           PC   C07K14/08,
           PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
           CC   3p.pile {840453p} shown in Figure 9C
           FH   Key             Location/Qualifiers
           FT   source          1. .250
           FT                   /organism='Hepatitis virus (hepatitis E  FT
                        virus)'.
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:                463             Length:         250
Score:                    65.00           Matches:        65
Percent Similarity:       78.31%          Conservative:   0
Best Local Similarity:    78.31%          Mismatches:     18
Query Match:              11.84%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x BD077327 (1-250)

Qy         258 AlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
               ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db           2 GCCCTGACTCTGTTTAATCTTGCTGATACGCTTCTTGGTGGTTTACCGACAGAATTGATT 61

Qy         278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
               ||||||||||||||||||||||||||||||||||||
Db          62 TCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCTGTTCAGAATTGATTTCGTCGGCTG 121

Qy         298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIlePro 317
                  |||         |||           ||||||||||||||||||      ||||||
Db         122 GGGGTCAACTGTTTTACTCCCGCCCTGTTTGCGCAGCAAGACAAGGGCATCACCATTCCA 181

Qy         318 HisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         182 CACGACATAGATTTAGGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCACGAA 241

Qy         338 GlnAspArg 340
               |||||||||
Db         242 CAAGATCGA 250

RESULT 601
AX181929
LOCUS       AX181929                197 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 211 from Patent WO0146696.
ACCESSION   AX181929
VERSION     AX181929.1  GI:15141762
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 211 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .197
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="1440o2.seq"
     CDS             <2. .>196
                     /note="unnamed protein product; Greek Isolate 2 Orf2"
                     /codon_start=1
                     /protein_id="CAC50185.1"
                     /db_xref="GI:15141763"
                     /translation="TELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIP
                     HDIDLGDSRVVIQDYDNQHEQ"

Alignment Scores:
Pred. No.:                464             Length:         197
Score:                    64.00           Matches:        64
Percent Similarity:       98.46%          Conservative:   0
Best Local Similarity:    98.46%          Mismatches:     1
Query Match:              11.66%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AX181929 (1-197)

Qy         274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 ACAGAATTRATTTCGTCGGCTGGAGGTCAACTGTTCTACTCCCGCCCGGTTGTCTCAGCC 61

Qy         294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 AATGGCGAGCCGACTGTTAAGTTATACACCTCTGTCGAGAATGCACAGCAGGATAAGGGC 121

Qy         314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         122 ATTGCTATACCACATGATATAGACTTAGGGGATTCCCGTGTGGTTATACAAGATTATGAY 181

Qy         334 AsnGlnHisGluGln 338
               |||||||||||||||
Db         182 AACCARCAYGAACAA 196

RESULT 602
AX181933
LOCUS       AX181933                197 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 215 from Patent WO0146696.
ACCESSION   AX181933
VERSION     AX181933.1  GI:15141766
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 215 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .197
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="2015o2.seq"
     CDS             <2. .>196
                     /note="unnamed protein product; Greek Isolate 2 Orf2"
                     /codon_start=1
                     /protein_id="CAC50187.1"
                     /db_xref="GI:15141767"
                     /translation="TELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIP
                     HDIDLGDSRVVIQDYDNQHEQ"

Alignment Scores:
Pred. No.:                464             Length:         197
Score:                    64.00           Matches:        64
Percent Similarity:       98.46%          Conservative:   0
Best Local Similarity:    98.46%          Mismatches:     1
Query Match:              11.66%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AX181933 (1-197)

Qy         274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 ACAGAATTRATTTCGTCGGCTGGAGGCCAGCTCTTCTACTCCCGCCCAGTCGTCTCAGCC 61
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Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTTAAATTGTATACATCCGTCGAGAATGCGCAGCAGGACAAGGGC 121

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ATTGCCATACCACATGATATAGATCTAGGAGATTCCCGCGTGGTTATCCAGGATTATGAY 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCARCAYGAACAA 196

RESULT 603
AX181963
LOCUS       AX181963                197 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 245 from Patent WO0146696.
ACCESSION   AX181963
VERSION     AX181963.1  GI:15141774
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 245 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .197
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="Aulo2-wlao2.pat"
     CDS             <2. .>196
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC50192.1"
                     /db_xref="GI:15141775"
                     /translation="TELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIP
                     HDIDLGDSRVVIQDYDNQHEQ"

Alignment Scores:
Pred. No.:                464             Length:         197
Score:                    64.00           Matches:        64
Percent Similarity:       98.46%          Conservative:   0
Best Local Similarity:    98.46%          Mismatches:     1
Query Match:              11.66%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AX181963 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTRATTTCGTCGGCTGGGGGACAGTTATTCTACTCCCGCCCTGTYGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTTAAATTATATACATCTGTAGAGAATGCGCAGCAGGACAAGGGG 121

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ATTGCCATCCCACATGATATAGATCTGGGCGACTCTCGTGTGGTGATCCAGGATTATGAY 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCARCAYGAACAA 196

RESULT 604
AX181971
LOCUS       AX181971                197 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 253 from Patent WO0146696.
ACCESSION   AX181971
VERSION     AX181971.1  GI:15141782
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 253 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .197
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="Ar2o2-f7702.pat"
     CDS             <2. .>196
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC50196.1"
                     /db_xref="GI:15141783"
                     /translation="TELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIP
                     HDIDLGDSRVVIQDYDNQHEQ"

Alignment Scores:
Pred. No.:                464             Length:         197
Score:                    64.00           Matches:        64
Percent Similarity:       98.46%          Conservative:   0
Best Local Similarity:    98.46%          Mismatches:     1
Query Match:              11.66%          Indels:         0
DB:                       1               Gaps:           0

US-09-769-066-16 (1-549) x AX181971 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTRATTTCGTCGGCTGGGGGTCAGTTGTTTTACTCCCGCCCTGTCGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTTAAGTTGTATACATCTGTGGAGAATGCGCAGCAGGATAAAGGA 121

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ATCGCCATCCCACACGACATAGATCTGGGCGATTCCCGTGTGGTTATTCAGGATTATGAY 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCARCAYGAACAA 196

RESULT 605
BD077306
LOCUS       BD077306                197 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077306
VERSION     BD077306.1  GI:22622909
KEYWORDS    JP 2001520384-A/185.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 197)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 185 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/185
            PD   30-OCT-2001
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            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   1440o2.seq
            CC   Xaa = Unknown or Other at position 3
            CC   Xaa = Unknown or Other at position 60
            CC   Xaa = Unknown or Other at positions 62-63
            FH   Key             Location/Qualifiers
            FT   CDS             (2). .(196).
FEATURES              Location/Qualifiers
     source           1. .197
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              464           Length:         197
Score:                  64.00         Matches:        64
Percent Similarity:     98.46%        Conservative:   0
Best Local Similarity:  98.46%        Mismatches:     1
Query Match:            11.66%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x BD077306 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTRATTTCGTCGGCTGGAGGTCAACTGTTCTACTCCCGCCCGGTTGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTTAAGTTATACACCTCTGTCGAGAATGCACAGCAGGATAAGGGC 121

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ATTGCTATACCACATGATATAGACTTAGGGGATTCCCGTGTGGTTATACAAGATTATGAY 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCARCAYGAACAA 196

RESULT 606
BD077308
LOCUS       BD077308                 197 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077308
VERSION     BD077308.1  GI:22622911
KEYWORDS    JP 2001520384-A/187.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 197)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 187 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/187
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   2015o2.seq
            CC   Xaa = Unknown or Other at position 3
            CC   Xaa = Unknown or Other at position 60
            CC   Xaa = Unknown or Other at positions 62-63
            FH   Key             Location/Qualifiers
            FT   CDS             (2). .(196).
FEATURES              Location/Qualifiers
     source           1. .197
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              464           Length:         197
Score:                  64.00         Matches:        64
Percent Similarity:     98.46%        Conservative:   0
Best Local Similarity:  98.46%        Mismatches:     1
Query Match:            11.66%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x BD077308 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTRATTTCGTCGGCTGGAGGCCAGCTCTTCTACTCCCGCCCAGTCGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTTAAATTGTATACATCCGTCGAGAATGCGCAGCAGGACAAGGGC 121

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ATTGCCATACCACATGATATAGATCTAGGAGATTCCCGCGTGGTTATCCAGGATTATGAY 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCARCAYGAACAA 196

RESULT 607
AX181869
LOCUS       AX181869                 197 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 151 from Patent WO0146696.
ACCESSION   AX181869
VERSION     AX181869.1  GI:15133190
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 151 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES              Location/Qualifiers
     source           1. .197
                      /organism="Hepatitis E virus"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:12461"
                      /note="us2-orf2"

Alignment Scores:
Pred. No.:              470           Length:         197
Score:                  63.00         Matches:        63
Percent Similarity:     96.92%        Conservative:   0
Best Local Similarity:  96.92%        Mismatches:     2
Query Match:            11.48%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AX181869 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            2 ACAGAATTGATTTCGTCGGCTGGGGGCCAACTGTTTTACTCCCGCCCGGTTGTCTCAGCC 61

Qy          294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           62 AATGGCGAGCCAACAGTAAAGTTATATACATCTGTTGAGAATGCGCAGCAAGACAAGGGC 121

Qy          314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          122 ATCACCATTCCACATGATATAGACCTGGGTGACTCCCGTGTGGTTATCCAGGATTATGAT 181

Qy          334 AsnGlnHisGluGln 338
                ||||||||||||||||
Db          182 AACCAGCAYGAGCAA 196

RESULT 608
AX181899
LOCUS       AX181899                197 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 181 from Patent WO0146696.
ACCESSION   AX181899
VERSION     AX181899.1  GI:15133209
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mushahwar,I.K.
  TITLE     Methods and compositions for detecting hepatitis e virus
  JOURNAL   Patent: WO 0146696-A 181 28-JUN-2001;
            ABBOTT LABORATORIES (US)
FEATURES             Location/Qualifiers
     source          1. .197
                     /organism="Hepatitis E virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:12461"
                     /note="z12-orf2.con"

Alignment Scores:
Pred. No.:              470             Length:         197
Score:                  63.00           Matches:        63
Percent Similarity:     96.92%          Conservative:   0
Best Local Similarity:  96.92%          Mismatches:     2
Query Match:            11.48%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AX181899 (1-197)

Qy          274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            2 ACAGAATTAATTTCGTCGGCTGGGGGTCAACTGTTCTACTCCCGCCCTGTCGTCTCAGCC 61

Qy          294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           62 AATGGCGAGCCGACTGTCAAGTTATACACATCTGTTGAGAATGCACAGCAGGATAAGGGG 121

Qy          314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
                    ||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db          122 ATAGCTATTCCACATGACATAGATTTGGGCGACTCTCGTTTGGTAATCCAGGATTATGAT 181

Qy          334 AsnGlnHisGluGln 338
                ||||||||||||||||
Db          182 AACCAACACGAACAA 196

RESULT 609
BD077269
LOCUS       BD077269                197 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077269
VERSION     BD077269.1  GI:22622872
KEYWORDS    JP 2001520384-A/148.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 197)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 148 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
            PN   JP 2001520384-A/148
            PD   30-OCT-2001
            PF   15-OCT-1998 JP 2000516232
            PR   15-OCT-1997 US    60/061199
            PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
            DAWSON,
            PI   ISA K MASHAWER
            PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
            PC   C07K14/08,
            PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
            CC   us2-orf2
            FH   Key             Location/Qualifiers
            FT   source          1. .197
            FT                   /organism='Hepatitis virus (hepatitis E  FT
                        virus)'.
FEATURES             Location/Qualifiers
     source          1. .197
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              470             Length:         197
Score:                  63.00           Matches:        63
Percent Similarity:     96.92%          Conservative:   0
Best Local Similarity:  96.92%          Mismatches:     2
Query Match:            11.48%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x BD077269 (1-197)

Qy          274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            2 ACAGAATTGATTTCGTCGGCTGGGGGCCAACTGTTTTACTCCCGCCCGGTTGTCTCAGCC 61

Qy          294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           62 AATGGCGAGCCAACAGTAAAGTTATATACATCTGTTGAGAATGCGCAGCAAGACAAGGGC 121

Qy          314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          122 ATCACCATTCCACATGATATAGACCTGGGTGACTCCCGTGTGGTTATCCAGGATTATGAT 181

Qy          334 AsnGlnHisGluGln 338
                ||||||||||||||||
Db          182 AACCAGCAYGAGCAA 196

RESULT 610
BD077288
LOCUS       BD077288                197 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method and compositions for detecting hepatitis E virus.
ACCESSION   BD077288
VERSION     BD077288.1  GI:22622891
KEYWORDS    JP 2001520384-A/167.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 197)
  AUTHORS   Schlauder,G.G., Erker,J.C., Desai,S.M., Dawson,G.J. and
            Mashawer,I.K.
  TITLE     Method and compositions for detecting hepatitis E virus
  JOURNAL   Patent: JP 2001520384-A 167 30-OCT-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Hepatitis virus (hepatitis E virus)
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           PN   JP 2001520384-A/167
           PD   30-OCT-2001
           PF   15-OCT-1998 JP 2000516232
           PR   15-OCT-1997 US    60/061199
           PI   GEORGE G SCHLAUDER,JAMES C ERKER,SURESH M DESAI,GEORGE J  PI
           DAWSON,
           PI   ISA K MASHAWER
           PC   G01N33/576,A61K35/12,A61K39/29,A61K48/00,A61P1/16,A61P31/20,
           PC   C07K14/08,
           PC   C07K16/10,C12N15/09,C12Q1/68,G01N33/577
           CC   z12-orf2.con
           FH   Key             Location/Qualifiers
           FT   source          1. .197
           FT                   /organism='Hepatitis virus (hepatitis E  FT
                          virus)'.
FEATURES             Location/Qualifiers
     source          1. .197
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Alignment Scores:
Pred. No.:              470             Length:         197
Score:                  63.00           Matches:        63
Percent Similarity:     96.92%          Conservative:   0
Best Local Similarity:  96.92%          Mismatches:     2
Query Match:            11.48%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x BD077288 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTAATTTCGTCGGCTGGGGGTCAACTGTTCTACTCCCGCCCTGTCGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTCAAGTTATACACATCTGTTGAGAATGCACAGCAGGATAAGGGG 121

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
              |||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        122 ATAGCTATTCCACATGACATAGATTTGGGCGACTCTCGTTTGGTAATCCAGGATTATGAT 181

Qy        334 AsnGlnHisGluGln 338
              ||||||||||||||||
Db        182 AACCAACACGAACAA 196

RESULT 611
AY626041
LOCUS       AY626041                189 bp    RNA     linear   VRL 12-JUN-2004
DEFINITION  Hepatitis E virus isolate MP13 structural protein gene, partial
            cds.
ACCESSION   AY626041
VERSION     AY626041.1  GI:48374467
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 189)
  AUTHORS   Mansuy,J.M., Peron,J.M., Bureau,C., Alric,L., Vinel,J.P. and
            Izopet,J.
  TITLE     Immunologically silent autochthonous acute hepatitis E virus
            infection in France
  JOURNAL   J. Clin. Microbiol. 42 (2), 912-913 (2004)
   PUBMED   14766888
REFERENCE   2  (bases 1 to 189)
  AUTHORS   Mansuy,J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-MAY-2004) Virology Laboratory, University Hospital
            Purpan, Palce du Dr Baylac TSA 40031, Toulouse 31059, France
FEATURES             Location/Qualifiers
     source          1. .189
                     /organism="Hepatitis E virus"
                     /mol_type="genomic RNA"
                     /isolate="MP13"
                     /isolation_source="serum"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:12461"
                     /country="France: Toulouse"
     CDS             <1. .>189
                     /note="ORF2"
                     /codon_start=2
                     /product="structural protein"
                     /protein_id="AAT42068.1"
                     /db_xref="GI:48374468"
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                     HDIDLGDSRVVIQDYDNQ"

Alignment Scores:
Pred. No.:              480             Length:         189
Score:                  61.00           Matches:        61
Percent Similarity:     98.39%          Conservative:   0
Best Local Similarity:  98.39%          Mismatches:     1
Query Match:            11.11%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AY626041 (1-189)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
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Db          2 ACAGAATTRATTTCGTCGGCTGGAGGTCAACTGTTCTACTCCCGCCCGGTTGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTTAAGTTATACACCTCTGTCGAGAATGCACAGCAGGACAAGGGC 121

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ATCGCTATACCACATGATATAGATTTAGGGGATTCCCGCGTGGTTATACAGGATTATGAC 181

Qy        334 AsnGln 335
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Db        182 AACCAR 187

RESULT 612
AY626042
LOCUS       AY626042                189 bp    RNA     linear   VRL 12-JUN-2004
DEFINITION  Hepatitis E virus isolate MP14 structural protein gene, partial
            cds.
ACCESSION   AY626042
VERSION     AY626042.1  GI:48374469
KEYWORDS    .
SOURCE      Hepatitis E virus
  ORGANISM  Hepatitis E virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;
            Hepevirus.
REFERENCE   1  (bases 1 to 189)
  AUTHORS   Mansuy,J.M., Peron,J.M., Bureau,C., Alric,L., Vinel,J.P. and
            Izopet,J.
  TITLE     Immunologically silent autochthonous acute hepatitis E virus
            infection in France
  JOURNAL   J. Clin. Microbiol. 42 (2), 912-913 (2004)
   PUBMED   14766888
REFERENCE   2  (bases 1 to 189)
  AUTHORS   Mansuy,J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-MAY-2004) Virology Laboratory, University Hospital
            Purpan, Palce du Dr Baylac TSA 40031, Toulouse 31059, France
FEATURES             Location/Qualifiers
     source          1. .189
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                     /mol_type="genomic RNA"
                     /isolate="MP14"
                     /isolation_source="stool"
                     /specific_host="Homo sapiens"
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                /country="France: Toulouse"
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                /note="ORF2"
                /codon_start=2
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Alignment Scores:
Pred. No.:              480             Length:         189
Score:                  61.00           Matches:        61
Percent Similarity:     98.39%          Conservative:   0
Best Local Similarity:  98.39%          Mismatches:     1
Query Match:            11.11%          Indels:         0
DB:                     1               Gaps:           0

US-09-769-066-16 (1-549) x AY626042 (1-189)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTGATTTCGTCGGCTGGAGGTCAACTGTTCTACTCCCGCCCGGTTGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTTAAGTTATACACCTCTGTCGAGAATGCACAGCAGGACAAGGGC 121

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ATCGCTATACCACATGATATAGATTTAGGGGATTCCCGCGTGGTTATACAGGATTATGAC 181

Qy        334 AsnGln 335
              ||||||
Db        182 AACCAR 187


Search completed: July 26, 2005, 09:22:25
Job time : 282 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2005, 09:39:11 ; Search time 25 Seconds
(without alignments)
2.308 Million cell updates/sec

Title: US-09-769-066-16
Perfect score: 549
Sequence: 1 AVAPAHDTSPVPDVDSRGAI.....QSTVAELQRLKVKVGKTREL 549

Scoring table: UNITARY_AA
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 47 seqs, 52546 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 47 summaries

Command line parameters:
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-DB=rng16.seq -SUFFIX=pto -OUT=foley066-16.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=unitary_AA -TRANS=human40.cdi
-LIST=47 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=47
-MODE=LOCAL -OUTFMT=pto -NORM=stat -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-NCPU=6 -NEG_SCORES=0 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : rng16.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	549	100.0	1647	1	AAT27110	Hepatitis E virus
2	549	100.0	2058	1	AAT27108	Hepatitis E virus
3	535.5	97.5	1980	1	AAT96960	Hepatitis E virus
4	521	94.9	1647	1	AAV61686	Hepatitis E virus
5	520	94.7	1647	1	AAT27109	Hepatitis E virus
6	535.5	97.5	2100	1	AAQ47130	HEV third and seco
7	534.5	97.4	2100	1	AAQ46814	Mexico strain HEV
8	521	94.9	1983	1	AAV61688	Hepatitis E virus
9	521	94.9	1984	1	AAQ86592	Hepatitis E virus
10	521	94.9	1990	1	ABL60053	Hepatitis E virus
11	521	94.9	1990	1	ADB97808	HEV ORF2 DNA #SEQ
12	520	94.7	1983	1	AAT96959	Hepatitis E virus
13	521	94.9	2054	1	AAS01448	Hepatitis E virus
14	520	94.7	2049	1	AAT27107	Hepatitis E virus
15	513	93.4	1980	1	ABZ23919	Swine HEV open rea
16	508	92.5	1989	1	ABL60054	Hepatitis E virus
17	508	92.5	1989	1	ADB97809	HEV related DNA #S
18	460.5	83.9	1643	1	AAQ27436	DNA encoding epide
19	327	59.6	984	1	AAT27112	Hepatitis E virus
20	327	59.6	984	1	AAT96966	Hepatitis E virus
21	323	58.8	1020	1	AAZ00231	Nucleic acid seque
22	305	55.6	984	1	AAT27111	Hepatitis E virus
23	305	55.6	984	1	AAT96965	Hepatitis E virus
24	300	54.6	1026	1	AAZ00279	HEV US and CMP-KDO
25	292	53.2	960	1	AAZ00282	HEV US recombinant
26	285	51.9	899	1	AAZ00129	Nucleic acid seque
27	256	46.6	960	1	AAZ00193	Nucleic acid seque
28	250	45.5	920	1	AAZ00277	Nucleic acid seque
29	237	43.2	810	1	AAS01434	Hepatitis E virus
30	236	43.0	901	1	AAZ00255	Nucleic acid seque
31	234	42.6	890	1	AAZ00276	Nucleic acid seque
32	209	38.1	678	1	AAZ00212	Nucleic acid seque
33	83	15.1	250	1	AAZ00310	Conserved Nucleic
34	80	14.6	250	1	AAZ00309	Conserved Nucleic
35	80	14.6	250	1	AAZ00307	Conserved Nucleic
36	80	14.6	250	1	AAZ00308	Conserved Nucleic
37	64	11.7	197	1	AAZ00290	HEV isolate 1440o2
38	64	11.7	197	1	AAZ00292	HEV isolate 2015o2
39	63	11.5	197	1	AAZ00272	Nucleic acid seque
40	63	11.5	197	1	AAZ00253	Nucleic acid seque
41	115	20.9	450	1	ADD24381	Hepatitis E virus
42	114	20.8	449	1	AAV66325	ET-NANB (HEV) Mexi
43	114	20.8	449	1	AAV54733	Nucleic acid encod
44	114	20.8	449	1	AAA99263	Hepatitis E virus
45	114	20.8	449	1	AAF83499	HEV-Mexican strain
46	114	20.8	449	1	AAL50390	Hepatitis E virus
47	65	11.8	250	1	AAZ00311	Conserved Nucleic

ALIGNMENTS

RESULT 1
AAT27110
ID AAT27110 standard; DNA; 1647 BP.
XX
AC AAT27110;
XX
DT 16-OCT-2003 (revised)
DT 06-AUG-1996 (first entry)
XX
DE Hepatitis E virus (Mexico strain) 62K antigen DNA.
XX
KW HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW capsid; ds.
XX
OS Hepatitis E virus; Mexico strain.
XX
PN WO9612807-A2.
XX
PD 02-MAY-1996.
XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
DR P-PSDB; AAR96092.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Disclosure; Page 73-74; 125pp; English.
XX
CC A DNA sequence (AAT27110) codes for 62K antigen (AAR96092) comprising the
CC C-terminal 549 amino acids of hepatitis E virus (HEV) Mexico strain
CC capsid protein (AAR96090). It is obtd. by PCR amplification of HEV Mexico
CC ORF-2 (AAT27108). The amplified fragment is inserted into vector pGEX for
CC prodn. 62K in E. coli cells. Expression of full-length ORF-2 in Sf9
CC insect cells using a baculovirus system also results in prodn. of 62K
CC antigen (see also AAR96101 and AAR96103). 62K represents an improved
CC antigen, in comparison to bacterial expressed proteins, for use in HEV
CC diagnostic assays, and also has excellent immunogenic properties.

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CC   (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 1647 BP; 327 A; 497 C; 400 G; 423 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                0.418          Length:          1647
Score:                    549.00         Matches:         549
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-16 (1-549) x AAT27110 (1-1647)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 60

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 120

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 180

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 240

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 300

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 360

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 420

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 480

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 540

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 600

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACGGCCCGTCACCGGCTC 660

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 720

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 780

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 840

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 900

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 960

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1020

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1080

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1140

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1200

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1260

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1320

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1380

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1440

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1500

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1560

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1620

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1621 GTTAAGGTGGGTAAAACTCGGGAGTTG 1647

RESULT 2
AAT27108
ID   AAT27108 standard; DNA; 2058 BP.
XX
AC   AAT27108;
XX
DT   16-OCT-2003  (revised)
DT   06-AUG-1996  (first entry)
XX
DE   Hepatitis E virus (Mexico strain) ORF-2.
XX
KW   HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW   diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW   capsid; ds.
XX
OS   Hepatitis E virus; Mexico strain.
XX
PN   WO9612807-A2.
XX
PD   02-MAY-1996.
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XX
PF 23-OCT-1995; 95WO-US013703.
XX
PR 24-OCT-1994; 94US-00327952.
PR 13-OCT-1995; 95US-00542634.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fuerst TR, Mcatee CP, Yarbough PO, Zhang Y;
XX
DR WPI; 1996-230608/23.
DR P-PSDB; AAR96090.
XX
PT Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT diagnostic reagents for determining HEV infection and in vaccines.
XX
PS Disclosure; Page 71-72; 125pp; English.
XX
CC The hepatitis E virus (HEV) Mexico strain ORF-2 (AAT27108) codes for the
CC putative capsid protein (AAR96090). PCR amplification of ORF-2 allows
CC prodn. of capsid protein or of C-terminal regions of the capsid protein
CC (see also AAR96092, AAR96094 and AAR96096) and expression in Spodoptera
CC frugiperda Sf9 insect cells using a baculovirus vector provides
CC recombinant C-terminal regions (see also AAR96102 and AAR96104) useful as
CC diagnostic reagents and in vaccines. The HEV Burma strain ORF-2
CC (AAT27107) may similarly be used. (Updated on 16-OCT-2003 to standardise
CC OS field)
XX
SQ Sequence 2058 BP; 372 A; 649 C; 507 G; 530 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.501	Length:	2058
Score:	549.00	Matches:	549
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AAT27108 (1-2058)

```
Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACGGCCCGTCACCGGCTC 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1774 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1833

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1893

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1894 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1953

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1954 GTTAAGGTGGGTAAAACTCGGGAGTTG 1980

RESULT 3
AAT96960
ID   AAT96960 standard; DNA; 1980 BP.
XX
AC   AAT96960;
XX
DT   17-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   26-FEB-1998  (first entry)
XX
DE   Hepatitis E virus Mexico strain ORF2.
XX
KW   Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
KW   diagnosis; HEV; ds.
XX
OS   Hepatitis E virus; - Mexico strain.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1980
FT                   /*tag=  a
FT                   /product= "ORF2_protein"
XX
PN   US5686239-A.
XX
PD   11-NOV-1997.
XX
PF   09-MAY-1994;   94US-00240049.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   17-JAN-1992;   92US-00822335.
PR   20-APR-1992;   92US-00870985.
PR   01-MAY-1992;   92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Tam AW,  Reyes GR,  Yarbough PO;
XX
DR   WPI; 1997-558132/51.
DR   P-PSDB; AAW35827.
XX
PT   Diagnosis of hepatitis E virus Burma and Mexico strain infection - by
PT   immunoassay with hepatitis E virus peptide antigens.
XX
PS   Disclosure; Col 25-28; 36pp; English.
XX
CC   A method has been developed for detecting hepatitis E virus (HEV)
CC   antibodies (Ab). The method comprises: (a) reacting a serum sample with a
CC   HEV peptide antigen; and (b) examining the peptide for the presence of
CC   bound Ab, where the presence of bound Ab indicates the presence of HEV
CC   Ab. The present sequence encodes the protein from the open reading frame,
CC   ORF2, from HEV Mexico strain. The method can be used to diagnose
CC   infection with the enterically transmitted non-A/non-B viral hepatitis
CC   agent HEV, specifically the HEV Burma and Mexico strains. (Updated on 25-
CC   MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to standardise OS
CC   field)
XX
SQ   Sequence 1980 BP; 364 A; 624 C; 493 G; 499 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0.575          Length:        1980
Score:                  535.50         Matches:       546
Percent Similarity:     99.45%         Conservative:  0

Best Local Similarity:  99.45%         Mismatches:    2
Query Match:            97.54%         Indels:        1
DB:                     1              Gaps:          1

US-09-769-066-16 (1-549) x AAT96960 (1-1980)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCAC---TCC 990

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1050

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1110

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1170

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1230

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1290

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1291 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1350
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Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1410

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1411 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1470

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1471 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1530

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1531 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1590

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1591 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1650

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1651 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1710

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1711 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1770

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1771 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1830

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1831 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1890

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1891 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1950

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1951 GTTAAGGTGGGTAAAACTCGGGAGTTG 1977
```

RESULT 4
AAV61686
ID AAV61686 standard; DNA; 1647 BP.
XX
AC AAV61686;
XX
DT 03-DEC-1998 (first entry)
XX
DE Hepatitis E virus hollow particle protein ORF2 DNA.
XX
KW Hollow particle protein; virus; antibody; detection; immunoassay;
KW infection; ss.
XX
OS Hepatitis virus.
XX
FH Key Location/Qualifiers
FT CDS 1. .1647
FT /*tag= a
FT /product= "hollow particle protein"
FT /note= "No start codon given for ORF2"
XX
PN JP10234383-A.
XX
PD 08-SEP-1998.
XX
PF 28-FEB-1997; 97JP-00062445.
XX
PR 28-FEB-1997; 97JP-00062445.
XX
PA (DENK-) DENKA SEIKEN KK.
PA (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR WPI; 1998-535037/46.
DR P-PSDB; AAW76367.
XX
PT Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids
PT encoding it - useful for more accurate detection of HEV in samples, using
PT immuno-assays and nucleic acid hybridisation.
XX
PS Claim 1; Page 15-17; 29pp; Japanese.
XX
CC This sequence encodes a Hepatitis E viral hollow particle protein
CC described as ORF2. This polypeptide can be used to raise antibodies to
CC detect HEV infection in samples, e.g. by immuno-assay based techniques,
CC and the nucleic acid can be used for the same in nucleic acid
CC hybridisation assays. The polypeptide and nucleic acid allow more
CC accurate detection of HEV than previously possible
XX
SQ Sequence 1647 BP; 303 A; 535 C; 390 G; 419 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.594	Length:	1647
Score:	521.00	Matches:	521
Percent Similarity:	94.90%	Conservative:	0
Best Local Similarity:	94.90%	Mismatches:	28
Query Match:	94.90%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AAV61686 (1-1647)

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Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db          1 GCGGTCGCTCCAGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCTCGCGGCGCCATC 60

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTGCGCCGGCAGTATAATCTATCAACATCTCCCCTCACCTCTTCCGTGGCCACCGGCACT 120

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              |||||||||||||||||||||||||||   |||   ||||||||||||||||||||||||
Db        121 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAAT 180

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 240

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTC 300

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 360

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 420

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 480

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAACACA 540

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 600

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
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```
Db        601 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 660

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db        661 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAG 720

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260

Db        721 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 780

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db        781 CTGTTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 840

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db        841 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCGGCCAATGGCGAGCCGACTGTTAAG 900

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320

Db        901 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 960

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db        961 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGG 1020

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1021 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1080

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1081 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1140

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1141 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1200

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420

Db       1201 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1260

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1261 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1320

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460

Db       1321 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1380

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480

Db       1381 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1440

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500

Db       1441 CCCGTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1500

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1501 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1560

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1561 CCTCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1620

Qy        541 ValLysValGlyLysThrArgGluLeu 549

Db       1621 ATGAAGGTGGGTAAAACTCGGGAGTTA 1647

RESULT 5
AAT27109
ID   AAT27109 standard; DNA; 1647 BP.
XX
AC   AAT27109;
XX
DT   16-OCT-2003  (revised)
DT   06-AUG-1996  (first entry)
XX
DE   Hepatitis E virus (Burma strain) 62K antigen DNA.
XX
KW   HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW   diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW   capsid; ds.
XX
OS   Hepatitis E virus; Burma strain.
XX
PN   WO9612807-A2.
XX
PD   02-MAY-1996.
XX
PF   23-OCT-1995;   95WO-US013703.
XX
PR   24-OCT-1994;   94US-00327952.
PR   13-OCT-1995;   95US-00542634.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fuerst TR,  Mcatee CP,  Yarbough PO,  Zhang Y;
XX
DR   WPI; 1996-230608/23.
DR   P-PSDB; AAR96090.
XX
PT   Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT   diagnostic reagents for determining HEV infection and in vaccines.
XX
PS   Disclosure; Page 72-73; 125pp; English.
XX
CC   A DNA sequence (AAT27109) codes for 62K antigen (AAR96091) comprising the
CC   C-terminal 549 amino acids of hepatitis E virus (HEV) Burma strain capsid
CC   protein (AAR96089). It is obtd. by PCR amplification of HEV Burma ORF-2
CC   (AAT27107) from pBET1 plasmid. The amplified fragment is inserted into
CC   vector pGEX for prodn. 62K in E. coli cells. Expression of full-length
CC   ORF-2 in Sf9 insect cells using a baculovirus system also results in
CC   prodn. of 62K antigen (see also AAR96101 and AAR96103). 62K represents an
CC   improved antigen, in comparison to bacterial expressed proteins, for use
CC   in HEV diagnostic assays, and also has excellent immunogenic properties.
CC   (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 1647 BP; 302 A; 533 C; 391 G; 421 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                0.602          Length:          1647
Score:                    520.00         Matches:         520
Percent Similarity:       94.72%         Conservative:    0
Best Local Similarity:    94.72%         Mismatches:      29
Query Match:              94.72%         Indels:          0
DB:                       1              Gaps:            0

US-09-769-066-16 (1-549) x AAT27109 (1-1647)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20

Db          1 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 60

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40

Db         61 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 120

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60

Db        121 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 180

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
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Db        181 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 240
Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
Db        241 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 300
Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
Db        301 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 360
Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
Db        361 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 420
Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
Db        421 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 480
Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
Db        481 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 540
Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
Db        541 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 600
Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
Db        601 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 660
Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
Db        661 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 720
Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
Db        721 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 780
Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
Db        781 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 840
Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
Db        841 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 900
Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
Db        901 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 960
Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
Db        961 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1020
Qy        341 ProThrProSerProAlaProSerArgProProSerValLeuArgAlaAsnAspValLeu 360
Db       1021 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1080
Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
Db       1081 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1140
Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
Db       1141 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1200
Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
Db       1201 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1260
Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
Db       1261 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1320
Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
Db       1321 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1380
Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
Db       1381 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1440
Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
Db       1441 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1500
Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
Db       1501 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1560
Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
Db       1561 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1620
Qy        541 ValLysValGlyLysThrArgGluLeu 549
Db       1621 ATGAAGGTGGGTAAAACTCGGGAGTTG 1647
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RESULT 6
AAQ47130
ID   AAQ47130 standard; DNA; 2100 BP.
XX
AC   AAQ47130;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   11-JAN-1994  (first entry)
XX
DE   HEV third and second ORFs.
XX
KW   Enterically transmitted non-A non-B hepatitis; ET-NANB; vaccine; ss.
XX
OS   Hepatitis E virus; Mexico strain.
XX
FH   Key             Location/Qualifiers
FT   CDS             5. .376
FT                   /*tag=  a
FT                   /label= ORF3
FT   CDS             46. .2100
FT                   /*tag=  b
FT                   /label= ORF2
FT   misc_RNA        275. .376
FT                   /*tag=  c
FT                   /label= 406.4-2
FT   misc_RNA        718. .2026
FT                   /*tag=  d
FT                   /label= C2
FT   misc_RNA        1045. .2026
FT                   /*tag=  e
FT                   /label= SG3
FT   misc_RNA        1882. .2026
FT                   /*tag=  f
FT                   /label= 406.3-2
XX
PN   WO9314116-A1.
XX
PD   22-JUL-1993.
XX
PF   15-JAN-1993;   93WO-US000459.
XX
PR   17-JAN-1992;   92US-00822335.
PR   01-MAY-1992;   92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
PA   (USSH ) US SEC DEPT HEALTH.
XX
```

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PI   Reyes GR,  Bradley DW,  Tam AW,  Carl M;
XX
DR   WPI; 1993-243144/30.
DR   P-PSDB; AAR38786, AAR38787.
XX
PT   New immunogenic hepatitis E virus (HEV) peptide(s) - are from the ORF1,
PT   ORF2 and ORF3 regions of HEV, useful as a vaccine against HEV infection.
XX
PS   Disclosure; Fig 7; 48pp; English.
XX
CC   Immunogenic hepatitis E virus (HEV) peptides are selected from the ORF1,
CC   ORF2 and ORF3 regions of HEV. The peptides can be used in vaccines to
CC   prevent infection by HEV. The antibodies can neutralise and block HEV
CC   infection and can be used to prevent or treat HEV infection. The peptides
CC   and antibodies can also be used as diagnostic reagents. (Updated on 25-
CC   MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS
CC   field)
XX
SQ   Sequence 2100 BP; 381 A; 659 C; 516 G; 544 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0.604          Length:          2100
Score:                  535.50         Matches:         546
Percent Similarity:     99.45%         Conservative:    0
Best Local Similarity:  99.45%         Mismatches:      2
Query Match:            97.54%         Indels:          1
DB:                     1              Gaps:            1

US-09-769-066-16 (1-549) x AAQ47130 (1-2100)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 438

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 498

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 558

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 618

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 678

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 738

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 798

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 858

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 918

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 978

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCAC---TCC 1035

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1036 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1095

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1155

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1215

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1275

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1335

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1395

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1396 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1455

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1515

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1516 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1575

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1576 CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1635

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1636 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1695

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1696 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1755

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1756 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1815

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1816 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1875

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1876 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1935

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1936 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1995

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1996 GTTAAGGTGGGTAAAACTCGGGAGTTG 2022

RESULT 7
AAQ46814
ID   AAQ46814 standard; DNA; 2100 BP.
XX
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```
AC   AAQ46814;
XX
DT   25-MAR-2003  (revised)
DT   14-FEB-1994  (first entry)
XX
DE   Mexico strain HEV ORF2 and ORF3.
XX
KW   Hepatitis E virus; vaccine; neutralising antibodies; infection; block;
KW   open reading frame; antibodies; ss.
XX
OS   Hepatitis E virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             5. .311
FT                   /*tag= a
FT                   /note= "ORF2"
FT   CDS             46. .2100
FT                   /*tag= b
FT                   /note= "ORF3"
XX
PN   WO9314208-A2.
XX
PD   22-JUL-1993.
XX
PF   19-JAN-1993;   93WO-US000475.
XX
PR   17-JAN-1992;   92US-00822335.
PR   20-APR-1992;   92US-00870985.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Reyes GR,  Bradley DW,  Twu J,  Purdy MA,  Tam AW,  Krawczynski KZ;
XX
DR   WPI; 1993-243223/30.
DR   P-PSDB; AAR39307, AAR39308.
XX
PT   Antigen and antibody vaccines against hepatitis E virus infection -
PT   contain peptide(s) derived from capsid protein C-terminal or antibodies
PT   against protein.
XX
PS   Disclosure; Fig 7; 43pp; English.
XX
CC   The sequence is that encoding Mexico strain hepatitis E virus (HEV) open
CC   reading frames ORF2 and ORF3. ORF2 encodes the putative capsid protein of
CC   the virus, this protein or peptide fragments of it may be used in a
CC   vaccine composition for immunising an individual against HEV. Antibodies
CC   raised against these peptides can also be used in such vaccines. (Updated
CC   on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 2100 BP; 381 A; 660 C; 515 G; 544 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:              0.611          Length:          2100
Score:                  534.50         Matches:         545
Percent Similarity:     99.27%         Conservative:    0
Best Local Similarity:  99.27%         Mismatches:      3
Query Match:            97.36%         Indels:          1
DB:                     1              Gaps:            1

US-09-769-066-16 (1-549) x AAQ46814 (1-2100)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 438

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 498

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 558

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 618

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 678

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCCATTACTTCCACTGAT 738

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCGCCTT 798

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAAGCC 858

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 918

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 978

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCAC---TCC 1035

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1036 GCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAA 1095

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 GATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACA 1155

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 TTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCT 1215

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 GGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAG 1275

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 CTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATC 1335

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 GATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGG 1395

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1396 CCCACCCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT 1455

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 TGGCTGTCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG 1515

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1516 GTTTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCC 1575

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1576 CGATCGCTTGACTGGTCCAAACTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAA 1635
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Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1636 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1695

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1696 ACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATT 1755

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1756 GAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGT 1815

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1816 CCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1875

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1876 GATACTTTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGC 1935

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1936 GCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAA 1995

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1996 GTTAAGGTGGGTAAAACTCGGGAGTTG 2022

RESULT 8
AAV61688
ID   AAV61688 standard; DNA; 1983 BP.
XX
AC   AAV61688;
XX
DT   03-DEC-1998  (first entry)
XX
DE   Hepatitis E virus hollow particle protein DNA #2.
XX
KW   Hollow particle protein; virus; antibody; detection; immunoassay;
KW   infection; ss.
XX
OS   Hepatitis virus.
XX
PN   JP10234383-A.
XX
PD   08-SEP-1998.
XX
PF   28-FEB-1997;   97JP-00062445.
XX
PR   28-FEB-1997;   97JP-00062445.
XX
PA   (DENK-) DENKA SEIKEN KK.
PA   (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
XX
DR   WPI; 1998-535037/46.
DR   P-PSDB; AAW76369.
XX
PT   Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids
PT   encoding it - useful for more accurate detection of HEV in samples, using
PT   immuno-assays and nucleic acid hybridisation.
XX
PS   Claim 13; Page 24-26; 29pp; Japanese.
XX
CC   This sequence encodes a Hepatitis E viral hollow particle protein. This
CC   polypeptide can be used to raise antibodies to detect HEV infection in
CC   samples, e.g. by immuno-assay based techniques, and the nucleic acid can
CC   be used for the same in nucleic acid hybridisation assays. The
CC   polypeptides and nucleic acids allow more accurate detection of HEV than
CC   previously possible
XX
SQ   Sequence 1983 BP; 342 A; 665 C; 485 G; 491 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:              0.692          Length:          1983
Score:                  521.00         Matches:         521
Percent Similarity:     94.90%         Conservative:    0
Best Local Similarity:  94.90%         Mismatches:      28
Query Match:            94.90%         Indels:          0
DB:                     1              Gaps:            0

US-09-769-066-16 (1-549) x AAV61688 (1-1983)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        334 GCGGTCGCTCCAGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCTCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||
Db        394 TTGCGCCGGCAGTATAATCTATCAACATCTCCCCTCACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||  |||  ||||||||||||||||||||||||||||
Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAACACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCCTATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||       ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAG 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||   ||||||      ||||||||||||||   ||||||||||||||||||||||
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CTGTTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCGGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293
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Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGACAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||  ||||||||||||||||||||||||||  |||      |||
Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              |||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||  |||||||||  ||||||||||||||  ||||||||||||||||||||||||
Db       1774 CCCGTCTCCATCTCTGCGGTTGCTGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||  |||||||||  ||||||||||||||||||||||||||||||||||||||||
Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 CCTCTTGGCCTCCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||
Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTA 1980
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RESULT 9
AAQ86592
ID AAQ86592 standard; DNA; 1984 BP.
XX
AC AAQ86592;
XX
DT 25-MAR-2003 (revised)
DT 28-SEP-1995 (first entry)
XX
DE Hepatitis E virus ORF2.
XX
KW HEV; ORF2; antigen; vaccine; immunogen; ss.
XX
OS Hepatitis E virus.
XX
FH Key Location/Qualifiers
FT CDS 1. .1983
FT /*tag= a
XX
PN WO9508632-A1.
XX
PD 30-MAR-1995.
XX
PF 23-SEP-1994; 94WO-AU000572.
XX
PR 24-SEP-1993; 93AU-00001423.
PR 15-DEC-1993; 93AU-00002964.
XX
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX
PI Anderson DA, Locarnini SA, Torresi J, Li F, Hui Z;
XX
DR WPI; 1995-139601/18.
DR P-PSDB; AAR70323.
XX
PT Antigens of hepatitis E virus (HEV) - selectively immuno:reactive to
PT convalescent and/or acute phase circulating antibodies to HEV.
XX
PS Disclosure; Page 39-41; 78pp; English.
XX
CC RNA from an HEV strain isolated in the Xinjiang region of China was
CC subjected to RT-PCR to obtain fragments corresp. to ORF2 (given in
CC AAQ86592) and ORF3 (AAQ86593) that encoded antigenic proteins (AAR70323-
CC 24, respectively). DNA fragments were manipulated into pGEX vectors for
CC production of GST fusion proteins in E. coli. Applications include HEV
CC infection diagnosis, therapy and vaccine development. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 1984 BP; 347 A; 666 C; 481 G; 490 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.692	Length:	1984
Score:	521.00	Matches:	521
Percent Similarity:	94.90%	Conservative:	0
Best Local Similarity:	94.90%	Mismatches:	28
Query Match:	94.90%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AAQ86592 (1-1984)

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Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        394 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              |||||||||||||||||||||||||  |||  ||||||||||||||||||||||||||
Db        454 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        874 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220

Db        934 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240

Db        994 CGTCGCGGTGCAGATGGGACTGCCGAGCTTACCACCACGGCTGCTACCCGCTTCATGAAG 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260

Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db       1114 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db       1174 GGTGGCCAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320

Db       1234 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db       1294 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1354 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1414 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1474 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420

Db       1534 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1594 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460

Db       1654 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480

Db       1714 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500

Db       1774 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCCGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1834 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1893

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1894 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 ValLysValGlyLysThrArgGluLeu 549

Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTA 1980
```

```
RESULT 10
ABL60053
ID   ABL60053 standard; DNA; 1990 BP.
XX
AC   ABL60053;
XX
DT   16-AUG-2002  (first entry)
XX
DE   Hepatitis E virus ORF-2 DNA #1.
XX
KW   Hepatitis E virus; ORF-2; HEV; virucide; immunisation; gene; ds.
XX
OS   Hepatitis E virus.
XX
PN   WO200240681-A1.
XX
PD   23-MAY-2002.
XX
PF   30-SEP-2001; 2001WO-CN001469.
XX
PR   30-SEP-2000; 2000CN-00130634.
XX
PA   (YANG-) YANG SHENG TANG CO LTD.
XX
PI   Xia N,  Zhang J,  Li S,  Ge S,  Gu Y,  He Z;
XX
DR   WPI; 2002-427096/45.
XX
PT   Polypeptide fragments of hepatitis E virus (HEV) for vaccine compositions
PT   and diagnosis in preventing and treating HEV infection.
XX
PS   Example 1; Page 82-83; 91pp; Chinese.
XX
CC   The sequence encodes hepatitis E virus (HEV) ORF-2 polypeptide. The
CC   invention relates to novel n-mer polypeptides comprising amino acids of
CC   ORF-2 of HEV where n = 2-180. The polypeptides of the invention have
CC   virucide activity. The polypeptide of HEV, its fragments, and chimeric
CC   proteins, are useful for vaccine compositions and diagnosis in preventing
CC   and treating HEV infection by immunisation, which may also be applied in
CC   the diagnosis of HEV infection
XX
SQ   Sequence 1990 BP; 348 A; 666 C; 481 G; 495 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0.694          Length:          1990
Score:                  521.00         Matches:         521
Percent Similarity:     94.90%         Conservative:    0
Best Local Similarity:  94.90%         Mismatches:      28
Query Match:            94.90%         Indels:          0
DB:                     1              Gaps:            0

US-09-769-066-16 (1-549) x ABL60053 (1-1990)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20

Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40

Db        394 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60

Db        454 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

Db        514 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        574 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 633
```

```
Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
Db        754 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
Db        814 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
Db        874 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
Db        934 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
Db        994 CGTCGCGGTGCAGATGGGACTGCCGAGCTTACCACCACGGCTGCTACCCGCTTCATGAAG 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
Db       1114 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
Db       1174 GGTGGCCAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
Db       1234 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
Db       1294 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
Db       1354 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
Db       1414 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
Db       1474 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
Db       1534 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
Db       1594 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
Db       1654 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
Db       1714 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
Db       1774 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCCGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
Db       1834 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1893

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
Db       1894 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 ValLysValGlyLysThrArgGluLeu 549
Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTA 1980
```

RESULT 11
ADB97808
ID ADB97808 standard; DNA; 1990 BP.
XX
AC ADB97808;
XX
DT 04-DEC-2003 (first entry)
XX
DE HEV ORF2 DNA #SEQ ID 2.
XX
KW Hepatitis E virus; HEV; virucide; vaccine; monoclonal antibody; NE2;
KW infection; ds.
XX
OS Hepatitis E virus.
XX
PN WO2003040187-A1.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-CN000797.
XX
PR 08-NOV-2001; 2001CN-00134643.
XX
PA (YANG-) YANG SHENG TANG CO LTD.
XX
PI Xia N, Zhang J, Gu Y, Li S, Ge S, He Z;
XX
DR WPI; 2003-441530/41.
XX
PT Hepatitis E virus monoclonal antibodies and their active fragments, for
PT use in diagnosis and developing remedies e.g. vaccines for preventing or
PT treating hepatitis E virus infection.
XX
PS Example 1; Page 131-133; 165pp; Chinese.
XX
CC The invention relates to a monoclonal antibody that binds specifically to
CC hepatitis E virus open-reading frame (ORF) 2. Also disclosed are
CC nucleotide sequences encoding the heavy-chain and/or light-chain variable
CC region of their degeneration sequences. The monoclonal antibody is
CC selected from anti-HEV monoclonal antibody 8C11 secreted by hybridoma
CC CCTCC-C200116, anti-HEV monoclonal antibody 13D8 secreted by hybridoma
CC CCTCC-C200114, anti-HEV monoclonal antibody 8H3 secreted by hybridoma
CC CCTCC-C200117, and anti-HEV monoclonal antibody 16D7 secreted by
CC hybridoma CCTCC-C200114. The monoclonal antibodies and their active
CC fragments are useful in diagnosis and developing remedies e.g. vaccines
CC for preventing or treating hepatitis E virus infection. From the whole
CC HEV gene obtained in patients, the HEV ORF fragment was prepared by using
CC the method of Aye et al. The polypeptide NE2 was then expressed and
CC isolated after biotechnological manipulations, which was characterised.
CC Its analogs were also produced for immunising mice and construction of
CC hybridomas. Tests were carried out to confirm usefulness of such
CC polypeptides and monoclonal antibodies. The current sequence represents
CC the HEV ORF2 encoding DNA.

```
XX
SQ   Sequence 1990 BP; 348 A; 666 C; 481 G; 495 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0.694          Length:          1990
Score:                  521.00         Matches:         521
Percent Similarity:     94.90%         Conservative:    0
Best Local Similarity:  94.90%         Mismatches:      28
Query Match:            94.90%         Indels:          0
DB:                     1              Gaps:            0

US-09-769-066-16 (1-549) x ADB97808 (1-1990)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              |||||||||||||||||||||||    ||||||||||||||||||||||||||||||||||
Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        394 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||    |||   ||||||||||||||||||||||||
Db        454 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGTCGCGGTGCAGATGGGACTGCCGAGCTTACCACCACGGCTGCTACCCGCTTCATGAAG 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||   ||||||      ||||||||||||||   ||||||||||||||||||||||
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGTGGCCAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db       1234 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||   ||||||||||||||||||||||||||||   |||       |||
Db       1534 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db       1654 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db       1714 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||   |||||||||   ||||||||||||||   ||||||||||||||||||||||
Db       1774 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCCGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||   |||||||||   ||||||||||||||||||||||||||||||||||||||||
Db       1834 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1893

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTA 1980

RESULT 12
AAT96959
ID   AAT96959 standard; DNA; 1983 BP.
XX
AC   AAT96959;
XX
DT   17-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   26-FEB-1998  (first entry)
XX
DE   Hepatitis E virus Burma strain ORF2.
XX
KW   Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
KW   diagnosis; HEV; ds.
XX
OS   Hepatitis E virus; - Burma strain.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1983
FT                   /*tag= a
FT                   /product= "ORF2_protein"
```

XX
PN US5686239-A.
XX
PD 11-NOV-1997.
XX
PF 09-MAY-1994; 94US-00240049.
XX
PR 17-JUN-1988; 88US-00208997.
PR 11-APR-1989; 89US-00336672.
PR 16-JUN-1989; 89US-00367486.
PR 13-OCT-1989; 89US-00420921.
PR 05-APR-1990; 90US-00505888.
PR 05-APR-1991; 91US-00681078.
PR 17-JAN-1992; 92US-00822335.
PR 20-APR-1992; 92US-00870985.
PR 01-MAY-1992; 92US-00876941.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Tam AW, Reyes GR, Yarbough PO;
XX
DR WPI; 1997-558132/51.
DR P-PSDB; AAW35826.
XX
PT Diagnosis of hepatitis E virus Burma and Mexico strain infection - by
PT immunoassay with hepatitis E virus peptide antigens.
XX
PS Disclosure; Col 23-24; 36pp; English.
XX
CC A method has been developed for detecting hepatitis E virus (HEV)
CC antibodies (Ab). The method comprises: (a) reacting a serum sample with a
CC HEV peptide antigen; and (b) examining the peptide for the presence of
CC bound Ab, where the presence of bound Ab indicates the presence of HEV
CC Ab. The present sequence encodes the protein from the open reading frame,
CC ORF2, from HEV Burma strain. The method can be used to diagnose infection
CC with the enterically transmitted non-A/non-B viral hepatitis agent HEV,
CC specifically the HEV Burma and Mexico strains. (Updated on 25-MAR-2003 to
CC correct PF field.) (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 1983 BP; 340 A; 665 C; 486 G; 492 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.7	Length:	1983
Score:	520.00	Matches:	520
Percent Similarity:	94.72%	Conservative:	0
Best Local Similarity:	94.72%	Mismatches:	29
Query Match:	94.72%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AAT96959 (1-1983)

```
Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||  |||  ||||||||||||||||||||||||||||
Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||  ||||||      ||||||||||||||   ||||||||||||||||||||||
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||  ||||||||||||||||||||||||  |||  |||  |||||||
Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||  |||
Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||  ||||||||||||  ||||||||||
Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773
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Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||   |||||||||   ||||||||||||||   ||||||||||||||||||||
Db       1774 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||   |||||||||   ||||||||||||||||||||||||||||||||||||||
Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||
Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTG 1980

RESULT 13
AAS01448
ID   AAS01448 standard; cDNA; 2054 BP.
XX
AC   AAS01448;
XX
DT   11-SEP-2003  (revised)
DT   18-JUL-2001  (first entry)
XX
DE   Hepatitis E virus (HEV) ORF2 cDNA.
XX
KW   Hepatitis E virus; HEV; E2; pE2; ORF2; immunoreactive viral peptide;
KW   antigenic activity; viral infection; ss.
XX
OS   Hepatitis E virus; Chinese strain D11092.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1983
FT                   /*tag=  a
FT                   /product= "Major HEV structural protein"
FT   misc_feature    1180. .1990
FT                   /*tag=  b
FT                   /note= "Corresponds to residues 1-810 of E2"
FT   mutation        replace(1810. .1812, CC)
FT                   /*tag=  c
FT                   /note= "Single base deletion present in E2"
XX
PN   WO200122916-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-IB001393.
XX
PR   30-SEP-1999;   99CA-02283538.
XX
PA   (UYHK-) UNIV HONG KONG.
XX
PI   Ng MH,  Im S,  Zhang J;
XX
DR   WPI; 2001-266109/27.
XX
PT   New immunoreactive peptide pE2, cloned from the genome of a Chinese
PT   strain of hepatitis E virus (HEV), for detecting and diagnosing HEV
PT   infection and for use as a vaccine for prevention of the viral infection
PT   in humans.
XX
PS   Disclosure; Fig 2A-2D; 101pp; English.
XX
CC   The present sequence for hepatitis E virus (HEV) ORF2 cDNA is used to
CC   clone a cDNA fragment E2 (AAS01434) which encodes for a novel peptide,
CC   pE2. During the cloning of the E2 fragment a single base deletion
CC   (presumed to be a PCR amplification error) at position 1811 of ORF2
CC   resulted in a frame shift causing the premature termination at a new stop
CC   codon at position 1820-1822, and giving rise to a smaller peptide, pE2.
CC   Peptide pE2 is a highly immunoreactive viral peptide which can be used in
CC   the development of diagnostic methods for the detection of HEV. Peptide
CC   pE2 which has antigenic activity is also useful as a vaccine for
CC   immunising an individual against infection from HEV and for determining
CC   the presence of HEV antibodies in a biological test sample such as human
CC   blood serum or plasma for detection and diagnosis of HEV infection. An
CC   antibody against pE2 is useful for detecting an HEV particle, in a
CC   biological test sample. The use of recombinant peptides such as pE2
CC   peptide have advantage over the prior art of using live intact virus
CC   particles by avoiding the potential risk of infectivity. The ORF3
CC   (AAS01449) of HEV Chinese strain D11092 is used to clone a cDNA fragment
CC   E3 (AAS01450) which encodes pE3 peptide. (Updated on 11-SEP-2003 to
CC   standardise OS field)
XX
SQ   Sequence 2054 BP; 355 A; 687 C; 491 G; 521 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0.712          Length:         2054
Score:                  521.00         Matches:        521
Percent Similarity:     94.90%         Conservative:   0
Best Local Similarity:  94.90%         Mismatches:     28
Query Match:            94.90%         Indels:         0
DB:                     1              Gaps:           0

US-09-769-066-16 (1-549) x AAS01448 (1-2054)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        394 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||   |||   ||||||||||||||||||||||||
Db        454 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||      ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
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Db        994 CGTCGCGGTGCAGATGGGACTGCCGAGCTTACCACCACGGCTGCTACCCGCTTCATGAAG 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
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Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280

Db       1114 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300

Db       1174 GGTGGCCAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320

Db       1234 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340

Db       1294 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360

Db       1354 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380

Db       1414 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400

Db       1474 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420

Db       1534 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440

Db       1594 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460

Db       1654 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480

Db       1714 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuGluGlu 500

Db       1774 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCACTCCGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520

Db       1834 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1893

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540

Db       1894 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 ValLysValGlyLysThrArgGluLeu 549

Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTA 1980

RESULT 14
AAT27107
ID   AAT27107 standard; DNA; 2049 BP.
XX
AC   AAT27107;
XX
DT   16-OCT-2003  (revised)
DT   06-AUG-1996  (first entry)
XX
DE   Hepatitis E virus (Burma strain) ORF-2.
XX
KW   HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW   diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
KW   capsid; ds.
XX
OS   Hepatitis E virus; Burma strain.
XX
PN   WO9612807-A2.
XX
PD   02-MAY-1996.
XX
PF   23-OCT-1995;   95WO-US013703.
XX
PR   24-OCT-1994;   94US-00327952.
PR   13-OCT-1995;   95US-00542634.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fuerst TR,  Mcatee CP,  Yarbough PO,  Zhang Y;
XX
DR   WPI; 1996-230608/23.
DR   P-PSDB; AAR96089.
XX
PT   Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT   diagnostic reagents for determining HEV infection and in vaccines.
XX
PS   Disclosure; Page 69-70; 125pp; English.
XX
CC   The hepatitis E virus (HEV) Burma strain ORF-2 (AAT27107) codes for the
CC   putative capsid protein (AAR96089). PCR amplification of ORF-2 allows
CC   prodn. of capsid protein or of C-terminal regions of the capsid protein
CC   (see also AAR96091, AAR96093 and AAR96095) and expression in Spodoptera
CC   frugiperda Sf9 insect cells using a baculovirus vector provides
CC   recombinant C-terminal regions (see also AAR96101 and AAR96103) useful as
CC   diagnostic reagents and in vaccines. The HEV Mexico strain ORF-2
CC   (AAT27108) may similarly be used. (Updated on 16-OCT-2003 to standardise
CC   OS field)
XX
SQ   Sequence 2049 BP; 344 A; 686 C; 496 G; 523 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0.719          Length:          2049
Score:                  520.00         Matches:         520
Percent Similarity:     94.72%         Conservative:    0
Best Local Similarity:  94.72%         Mismatches:      29
Query Match:            94.72%         Indels:          0
DB:                     1              Gaps:            0

US-09-769-066-16 (1-549) x AAT27107 (1-2049)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20

Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40

Db        394 TTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACCTCTTCCGTGGCCACCGGCACT 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60

Db        454 AACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80

Db        514 ACCCATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100

Db        574 ATCCGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120

Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT 693
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Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||    ||||||||||||||||||||
Db        814 ACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||       ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAG 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||    ||||||      ||||||||||||||    ||||||||||||||||||||
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACC 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||    ||||||||||||||||||||
Db       1234 TTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATT 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||    ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGG 1353

Qy        341 ProThrProSerProAlaProSerArgProProheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCA 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 GTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||   ||||||||||||||||||||||||||   |||      |||
Db       1534 CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db       1654 ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db       1714 GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||   |||||||||   ||||||||||||||||   ||||||||||||||||||||
Db       1774 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1954 ATGAAGGTGGGTAAAACTCGGGAGTTG 1980
```

RESULT 15
ABZ23919
ID ABZ23919 standard; DNA; 1980 BP.
XX
AC ABZ23919;
XX
DT 18-MAR-2003 (first entry)
XX
DE Swine HEV open reading frame (ORF) 2 protein encoding DNA.
XX
KW Swine; hepatitis E virus; HEV; open reading frame; ORF 2; virucide;
KW immunostimulant; vaccine; anti-viral; gene; ds.
XX
OS Swine hepatitis E virus.
XX
FH Key   Location/Qualifiers
FT CDS   1. .1980
FT   /*tag= a
FT   /product= "ORF2 protein"
FT   /partial
FT   /note= "the stop codon is not indicated"
XX
PN WO200289733-A2.
XX
PD 14-NOV-2002.
XX
PF 02-MAY-2002; 2002WO-US014100.
XX
PR 07-MAY-2001; 2001US-0289220P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Meng X, Purcell RH, Emerson SU;
XX
DR WPI; 2003-129157/12.
DR P-PSDB; ABB82786.
XX
PT New swine hepatitis E virus open-reading frame-2 protein and DNA encoding
PT the protein, useful for immunizing a mammal, producing antibodies and
PT detecting antibodies to hepatitis E virus in a biological sample.
XX
PS Disclosure; Fig 1B; 70pp; English.
XX
CC This DNA encodes a swine hepatitis E virus (HEV) open reading frame (ORF)
CC 2 protein. The protein can be expressed by standard recombinant
CC methodology. The ORF2 protein is useful for detecting antibodies to HEV
CC in a biological sample and for producing antibodies. The antibodies are
CC useful for detecting HEV in a biological sample, which is useful in
CC diagnosis of infection and disease caused by swine HEV, and for
CC monitoring the progression of such disease. The method is also useful for
CC monitoring the efficacy of therapeutic agents during the course of
CC treatment of HEV infection and disease in a mammal. The ORF2 protein can
CC be useful as diagnostic agent and as vaccine. The antibodies are useful
CC as anti-viral agent, and as a means for enhancing the immune response.
CC The ORF2 protein is sufficiently closely related to human HEV, and allows
CC evaluation as a potential source of infection in humans
XX

SQ Sequence 1980 BP; 356 A; 620 C; 484 G; 520 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.764	Length:	1980
Score:	513.00	Matches:	513
Percent Similarity:	93.61%	Conservative:	0
Best Local Similarity:	93.61%	Mismatches:	35
Query Match:	93.44%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x ABZ23919 (1-1980)

```
Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              |||||| ||||||  ||||||  ||||||||||||||||||||||||||||||||||||
Db        334 GCTGTATCACCGGCCCCCGACACAGCTCCTGTACCTGATGTTGACTCACGTGGTGCTATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CTGCGCCGGCAGTACAATCTGTCTACGTCCCCGCTCACGTCATCTGTCGCTGCTGGTACC 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        454 AACCTGGTTCTCTATGCCGCCCCGCTGAATCCTCTCTTGCCCCTCCAGGATGGCACCAAC 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||
Db        514 ACTCATATTATGGCTACTGAGGCGTCCAATTATGCTCAGTATCGGGTTGTTCGAGCTACG 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATCCGTTATCGCCCGCTGGTGCCAAATGCTGTTGGTGGCTATGCTATCTCTATTTCTTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCTCAAACTACAACCACCCCTACTTCAGTTGACATGAACTCTATTACCTCCACTGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTCAGGATTTTGGTTCAGCCCGGTATTGCCTCCGAGTTAGTCATCCCTAGTGAGCGCCTT 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        754 CATTACCGCAATCAAGGCTGGCGCTCTGTAGAGACCACGGGCGTGGCCGAGGAGGAAGCT 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ACCTCCGGTCTGGTAATGCTTTGCATTCACGGTTCTCCTGTTAACTCCTATACTAACACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCTTACACTGGTGCATTGGGGCTCCTTGATTTTGCATTAGAGCTTGAATTCAGAAATTTG 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||      ||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        934 ACACCCGGGAACACTAACACCCGTGTTTCCCGGTACACCAGCACAGCCCGCCATCGGCTG 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCCGCGGTGCTGATGGGACCGCAGAGCTTACCACCACAGCAGCCACACGTTTCATGAAG 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db       1054 GACTTGCATTTCACCGGCACGAACGGCGTTGGTGAGGTGGGTCGCGGTATAGCTCTAACA 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CTGTTTAACCTTGCTGATACGCTTCTTGGTGGTTTACCGACAGAATTGATTTCGTCGGCC 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGGGGCCAACTGTTTTACTCCCGCCCTGTCGTCTCGGCCAATGGCGAGCCGACGGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db       1234 TTATATACATCTGTTGAGAATGCGCAGCAGGACAAGGGCATTACCATCCCACACGATATA 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GATCTGGGTGATTCCCGTGTGGTTATTCAGGATTATGATAACCAGCACGAGCAAGACCGA 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCTACTCCGTCACCAGCCCCCTCTCGCCCTTTCTCAGTTCTTCGCGCCAATGATGTTCTG 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||  |||||||
Db       1414 TGGCTCTCCCTCACCGCCGCTGAGTACGATCAGACTACATATGGGTCGTCCACCAACCCT 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              |||  ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 ATGTATGTCTCCGATACGGTCACGCTAGTTAATGTGGCCACTGGTGCTCAGGCTGTTGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||  |||  |||
Db       1534 CGCTCTCTTGATTGGTCTAAAGTCACTCTGGATGGCCGCCCCCTCACTACCATTCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db       1594 TATTCAAAGACATTCTATGTTCTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGT 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 ACCACTAAGGCCGGCTACCCGTATAATTATAATACCACTGCTAGTGATCAAATTTTGATT 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db       1714 GAGAACGCGGCTGGCCACCGTGTTGCTATCTCTACCTATACCACTAGCTTGGGTGCCGGC 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              |||      |||||||||      ||||||||||||  ||||||||||||  ||||||||
Db       1774 CCTACCTCGATTTCCGCCGTTGGTGTGCTAGCCCCACACTCGGCTCTCGCCGTCCTTGAG 1833

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||  |||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db       1834 GATACTGTTGATTACCCTGCTCGTGCTCATACTTTTGATGATTTCTGCCCGGAGTGCCGC 1893

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db       1894 ACCCTTGGTTTGCAGGGTTGTGCATTCCAGTCTACTATTGCTGAGCTTCAGCGTCTTAAA 1953

Qy        541 ValLysValGlyLysThrArgGlu 548
              |||||||||||||||||||||||
Db       1954 ATGAAGGTAGGTAAAACCCGGGAG 1977
```

RESULT 16
ABL60054
ID ABL60054 standard; DNA; 1989 BP.
XX
AC ABL60054;
XX
DT 16-AUG-2002 (first entry)
XX
DE Hepatitis E virus ORF-2 DNA #2.
XX
KW Hepatitis E virus; ORF-2; HEV; virucide; immunisation; gene; ds.
XX
OS Hepatitis E virus.
XX
PN WO200240681-A1.
XX
PD 23-MAY-2002.
XX
PF 30-SEP-2001; 2001WO-CN001469.
XX
PR 30-SEP-2000; 2000CN-00130634.
XX

PA (YANG-) YANG SHENG TANG CO LTD.
XX
PI Xia N, Zhang J, Li S, Ge S, Gu Y, He Z;
XX
DR WPI; 2002-427096/45.
XX
PT Polypeptide fragments of hepatitis E virus (HEV) for vaccine compositions
PT and diagnosis in preventing and treating HEV infection.
XX
PS Example 1; Page 83-84; 91pp; Chinese.
XX
CC The sequence encodes hepatitis E virus (HEV) ORF-2 polypeptide. The
CC invention relates to novel n-mer polypeptides comprising amino acids of
CC ORF-2 of HEV where n = 2-180. The polypeptides of the invention have
CC virucide activity. The polypeptide of HEV, its fragments, and chimeric
CC proteins, are useful for vaccine compositions and diagnosis in preventing
CC and treating HEV infection by immunisation, which may also be applied in
CC the diagnosis of HEV infection
XX
SQ Sequence 1989 BP; 347 A; 666 C; 481 G; 495 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.817	Length:	1989
Score:	508.00	Matches:	521
Percent Similarity:	94.90%	Conservative:	0
Best Local Similarity:	94.90%	Mismatches:	28
Query Match:	92.53%	Indels:	1
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x ABL60054 (1-1989)

```
Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              |||||||||||||||||||||||||||  |||  ||||||||||||||||||||||||||||
Db        454 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGTCGCGGTGCAGATGGGACTGCCGAGCTTACCACCACGGCTGCTACCCGCTTCATGAAG 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||  ||||||  ||||||||||||||||  ||||||||||||||||||||||||||||
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGTGGCCAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db       1234 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||  ||||||||||||||||||||||||||||  |||  |||
Db       1534 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1593

Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db       1654 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db       1714 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||  ||||||||||  ||||||||||||||||  ||||||||||||||||||||||||
Db       1774 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCC-TCCGCGCTAGCATTGCTTGAG 1832

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||  ||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db       1833 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1892

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1893 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1952

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||||
Db       1953 ATGAAGGTGGGTAAAACTCGGGAGTTA 1979
```

RESULT 17
ADB97809
ID ADB97809 standard; DNA; 1989 BP.

XX
AC ADB97809;
XX
DT 04-DEC-2003 (first entry)
XX
DE HEV related DNA #SEQ ID 3.
XX
KW Hepatitis E virus; HEV; virucide; vaccine; monoclonal antibody; NE2;
KW infection; ds.
XX
OS Unidentified.
XX
PN WO2003040187-A1.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-CN000797.
XX
PR 08-NOV-2001; 2001CN-00134643.
XX
PA (YANG-) YANG SHENG TANG CO LTD.
XX
PI Xia N, Zhang J, Gu Y, Li S, Ge S, He Z;
XX
DR WPI; 2003-441530/41.
XX
PT Hepatitis E virus monoclonal antibodies and their active fragments, for
PT use in diagnosis and developing remedies e.g. vaccines for preventing or
PT treating hepatitis E virus infection.
XX
PS Example 1; Page 133-135; 165pp; Chinese.
XX
CC The invention relates to a monoclonal antibody that binds specifically to
CC hepatitis E virus open-reading frame (ORF) 2. Also disclosed are
CC nucleotide sequences encoding the heavy-chain and/or light-chain variable
CC region of their degeneration sequences. The monoclonal antibody is
CC selected from anti-HEV monoclonal antibody 8C11 secreted by hybridoma
CC CCTCC-C200116, anti-HEV monoclonal antibody 13D8 secreted by hybridoma
CC CCTCC-C200114, anti-HEV monoclonal antibody 8H3 secreted by hybridoma
CC CCTCC-C200117, and anti-HEV monoclonal antibody 16D7 secreted by
CC hybridoma CCTCC-C200114. The monoclonal antibodies and their active
CC fragments are useful in diagnosis and developing remedies e.g. vaccines
CC for preventing or treating hepatitis E virus infection. From the whole
CC HEV gene obtained in patients, the HEV ORF fragment was prepared by using
CC the method of Aye et al. The polypeptide NE2 was then expressed and
CC isolated after biotechnological manipulations, which was characterised.
CC Its analogs were also produced for immunising mice and construction of
CC hybridomas. Tests were carried out to confirm usefulness of such
CC polypeptides and monoclonal antibodies. The current sequence represents a
CC HEV related DNA.
XX
SQ Sequence 1989 BP; 347 A; 666 C; 481 G; 495 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.817	Length:	1989
Score:	508.00	Matches:	521
Percent Similarity:	94.90%	Conservative:	0
Best Local Similarity:	94.90%	Mismatches:	28
Query Match:	92.53%	Indels:	1
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x ADB97809 (1-1989)

```
Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        334 GCGGTCGCTCCGGCCCATGACACCCCGCCAGTGCCTGATGTTGACTCCCGCGGCGCCATC 393

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CTGCGCCGGCAGTATAACCTATCAACATCTCCCCTTACTTCTTCCGTGGCCACCGGTACA 453

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||  |||  ||||||||||||||||||||||||||
Db        454 AACTTGGTTCTATACGCCGCTCCTCTTAGCCCACTTCTACCCCTCCAGGACGGCACCAAT 513

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 ACTCATATAATGGCCACAGAAGCTTCTAATTATGCCCAGTACCGGGTTGCTCGTGCCACA 573

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATTCGCTACCGCCCGCTGGTCCCCAACGCTGTTGGTGGCTACGCCATCTCCATCTCGTTC 633

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGGCCACAGACCACCACCACCCCGACGTCCGTTGACATGAATTCAATAACCTCGACGGAT 693

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTA 753

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTACCGTAACCAAGGTTGGCGCTCTGTTGAGACCTCCGGGGTGGCGGAGGAGGAGGCC 813

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ACCTCTGGTCTTGTTATGCTCTGCATACATGGCTCACCTGTAAATTCTTATACTAATACA 873

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 CCTTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTCGAACTTGAGTTCCGCAACCTC 933

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ACCCCCGGTAATACCAACACGCGGGTCTCCCGTTACTCCAGCACTGCCCGTCACCGCCTT 993

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGTCGCGGTGCAGATGGGACTGCCGAGCTTACCACCACGGCTGCTACCCGCTTCATGAAG 1053

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||   ||||||      ||||||||||||||   ||||||||||||||||||||
Db       1054 GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGTGGGATAGCGCTTACC 1113

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 CTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATTTCGTCGGCT 1173

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 GGTGGCCAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAG 1233

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db       1234 CTTTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATC 1293

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArg 340
              ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GACCTCGGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGA 1353

Qy        341 ProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 CCGACACCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTT 1413

Qy        361 TrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPro 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 TGGCTTTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCA 1473

Qy        381 ValTyrIleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAla 400
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 GTCTATGTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCC 1533

Qy        401 ArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGln 420
              ||||||||||||||  ||||||||||||||||||||||||||  |||      |||
Db       1534 CGGTCACTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAG 1593
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Qy        421 TyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TATTCAAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGT 1653

Qy        441 ThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIle 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db       1654 ACTACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTT 1713

Qy        461 GluAsnAlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGly 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 GAGAATGCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773

Qy        481 ProValAlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGlu 500
              ||||||   |||||||||   ||||||||||||||||   ||||||||||||||||||||
Db       1774 CCCGTCTCTATTTCCGCGGTTGCTGTTTTAGCCCCCCC-TCCGCGCTAGCATTGCTTGAG 1832

Qy        501 AspThrPheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArg 520
              ||||||   |||||||||   ||||||||||||||||||||||||||||||||||||||||
Db       1833 GATACCATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGC 1892

Qy        521 AlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1893 CCCCTTGGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1952

Qy        541 ValLysValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||||||
Db       1953 ATGAAGGTGGGTAAAACTCGGGAGTTA 1979
```

RESULT 18
AAQ27436
ID AAQ27436 standard; DNA; 1643 BP.
XX
AC AAQ27436;
XX
DT 27-AUG-2003 (revised)
DT 05-FEB-1993 (first entry)
XX
DE DNA encoding epidemic NANBH virus antigen peptide.
XX
KW NANBH; non-A non-B hepatitis; immunoassay; ss.
XX
OS Non-A.
OS non-B hepatitis virus.
XX
FH Key Location/Qualifiers
FT CDS 3. .1643
FT /*tag= a
XX
PN JP04200388-A.
XX
PD 21-JUL-1992.
XX
PF 29-NOV-1990; 90JP-00334835.
XX
PR 29-NOV-1990; 90JP-00334835.
XX
PA (KAGA) KAGAKU OYOBI KESSEI RYOHO.
XX
DR WPI; 1992-290153/35.
DR P-PSDB; AAR26189.
XX
PT Epidemic non-A, non-B hepatitis virus antigen peptide (I) - and a nucleic
PT acid (II) fragment coding it.
XX
PS Claim 3; Fig 1; 15pp; Japanese.
XX
CC The sequence is that encoding an epidemic non-A, non-B hepatitis (NANBH)
CC virus antigen peptide. The peptide is useful for the detection of NANBH
CC virus by immunoassay of the antibody relates to epidemic NANBH virus in
CC which the peptide is used as an antigen. (Updated on 27-AUG-2003 to
CC correct OS field.)
XX

SQ Sequence 1643 BP; 297 A; 522 C; 382 G; 439 T; 0 U; 3 Other;

Alignment Scores:

Pred. No.:	1.26	Length:	1643
Score:	460.50	Matches:	484
Percent Similarity:	91.67%	Conservative:	0
Best Local Similarity:	91.67%	Mismatches:	43
Query Match:	83.88%	Indels:	2
DB:	1	Gaps:	1

US-09-769-066-16 (1-549) x AAQ27436 (1-1643)

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Qy         22 ArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThrAsn 41
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db          3 CGCCGGCAGTATAATCTATCAACATCTCCCCTCACTTCTTCCGTGGCCACCGGCACTAAC 62

Qy         42 LeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsnThr 61
              ||||||||||||||||||||||||   |||   |||||||||||||||||||||||||||
Db         63 CTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTCTTACCTCTTCAGGACGGCACCAATACC 122

Qy         62 HisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThrIle 81
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||||
Db        123 CATATAATGGCCACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGTCCGTGCCACAATC 182

Qy         82 ArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPheTrp 101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 CGTTACCGCCCGCTGGTCCCCAATGCTGTCGGCGGTTATGCCATCTCCATCTCATTCTGG 242

Qy        102 ProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAspVal 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 CCACAGACCACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGATGTT 302

Qy        122 ArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeuHis 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACAC 362

Qy        142 TyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAlaThr 161
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 TATCGTAACCAAGGCTGGCGCTCCGTCGAGACCTCTGGGGTGGCTGAGGAGGAGGCTACC 422

Qy        162 SerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThrPro 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 TCTGGTCTTGTTATGCTTTGCATACATGGCTCACCCGTAAATTCCTATACTAACACACCC 482

Qy        182 TyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeuThr 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 TATACCGGTGCCCTCGGGCTGCTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTTACC 542

Qy        202 ThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeuArg 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGT 602

Qy        222 ArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAsp 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 CGCGGTGCGGACGGGACTGCCGAGCTCACCACCACGGCCGCTACCCGCTTTATGAAGGAC 662

Qy        242 LeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeu 261
              |||   ||||||      ||||||||||||||   ||||||||||||||||||||||||
Db        663 CTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTG 722

Qy        262 LeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGly 281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 TTTAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGT 782

Qy        282 GlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeu 301
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        783 GGCCAGCTGTTCTACTCCCGTCCCGTCGTCTCGGCCCATGGCGAGCCGACTGTTAAGTTG 842

Qy        302 TyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAsp 321
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        843 TATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGAC 902

Qy        322 LeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgPro 341
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Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGCACAACA 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATTGAAAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGTCCGGTC 780

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAGGATACT 840

Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGCGCTTTA 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||
Db        961 GTGGGTAAAACTCGGGAGTTG 981

RESULT 20
AAT96966
ID   AAT96966 standard; DNA; 984 BP.
XX
AC   AAT96966;
XX
DT   17-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   26-FEB-1998  (first entry)
XX
DE   Hepatitis E virus Mexico strain peptide antigen SG3 encoding DNA.
XX
KW   Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
KW   diagnosis; HEV; ds.
XX
OS   Hepatitis E virus; - Mexico strain.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag=  a
FT                   /product= "Peptide_antigen_SG3"
XX
PN   US5686239-A.
XX
PD   11-NOV-1997.
XX
PF   09-MAY-1994;   94US-00240049.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   17-JAN-1992;   92US-00822335.
PR   20-APR-1992;   92US-00870985.
PR   01-MAY-1992;   92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Tam AW,  Reyes GR,  Yarbough PO;
XX
DR   WPI; 1997-558132/51.
DR   P-PSDB; AAW35821.
XX
PT   Diagnosis of hepatitis E virus Burma and Mexico strain infection - by
PT   immunoassay with hepatitis E virus peptide antigens.
XX
PS   Disclosure; Col 31-32; 36pp; English.
XX
CC   A method has been developed for detecting hepatitis E virus (HEV)
CC   antibodies (Ab). The method comprises: (a) reacting a serum sample with a
CC   HEV peptide antigen; and (b) examining the peptide for the presence of
CC   bound Ab, where the presence of bound Ab indicates the presence of HEV
CC   Ab. The present sequence encodes a specifically claimed HEV peptide
CC   antigen. The method can be used to diagnose infection with the
CC   enterically transmitted non-A/non-B viral hepatitis agent HEV,
CC   specifically the HEV Burma and Mexico strains. (Updated on 25-MAR-2003 to
CC   correct PF field.) (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ   Sequence 984 BP; 192 A; 282 C; 264 G; 246 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                4.41          Length:          984
Score:                    327.00        Matches:         327
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              59.56%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x AAT96966 (1-984)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGCCGACGGGACTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAAGATCTC 60

Qy        243 HisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeu 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAACATTACTT 120

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATTTCGTCGGCTGGCGGG 180

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTAT 240

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCACGATATCGATCTT 300

Qy        323 GlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGGCCCACC 360

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTTTGGCTG 420

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTAT 480

Qy        383 IleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCCCGATCG 540

Qy        403 LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTTGACTGGTCCAAAGTCACCCTCGACGGGCGGCCCCTCCCGACTGTTGAGCAATATTCC 600

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGCACAACA 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATTGAAAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGGTCCGGTC 780

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAGGATACT 840

Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTTGATTATCCGGGGCGGGCGCACACATTTGATGACTTCTGCCCTGAATGCCGCGCTTTA 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLys 542
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549
                |||||||||||||||||||||
Db        961 GTGGGTAAAACTCGGGAGTTG 981

RESULT 21
AAZ00231
ID   AAZ00231 standard; DNA; 1020 BP.
XX
AC   AAZ00231;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Nucleic acid sequence of HEV clone us2-1019.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 5; Page 192; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a HEV US subtype specific sequence obtained
CC   by PCR amplification
XX
SQ   Sequence 1020 BP; 204 A; 292 C; 246 G; 276 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.:              4.77          Length:        1020
```

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Score:                  323.00        Matches:       323
Percent Similarity:     95.85%        Conservative:  0
Best Local Similarity:  95.85%        Mismatches:    14
Query Match:            58.83%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AAZ00231 (1-1020)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||  ||||||  ||||||  ||||||||||||||||||||||||||||||||||||
Db          9 GCCGTGTCACCGGCTCCTGACACAGCCCCTGTACCTGATGTTGACTCACGTGGTGCTATT 68

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 CTGCGCCGGCAGTACAATTTGTCCACGTCCCCGCTCACGTCATCTGTCGCTTCGGGTACT 128

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        129 AATTTGGTCCTCTATGCTGCCCCGCTGAATCCCCTCTTGCCTCTCCAGGATGGTACCAAC 188

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||
Db        189 ACTCATATTATGGCTACTGAGGCATCCAATTATGCCCAGTATCGGGTTGTTCGAGCTACA 248

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 ATCCGTTATCGCCCGCTGGTGCCGAATGCCGTTGGTGGCTATGCCATTTCCATTTCTTTC 308

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TGGCCCCAAACTACAACTACCCCTACTTCTGTCGATATGAATTCTATTACTTCCACYGAT 368

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GTTAGGATTTTGGTTCAGCCCGGTATTGCCTCCGAGCTAGTCATCCCCAGTGAGCGCCTT 428

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        429 CATTACCGTAATCAAGGCTGGCGCTCTGTTGAGACCACGGGTGTGGCTGAGGAGGAGGCT 488

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 ACTTCCGGTCTGGTAATGCTTTGCATTCATGGCTCTCCTGTTAATTCCTACACTAATACA 548

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 CCTTACACTGGTGCGCTGGGGCTTCTTGATTTTGCACTAGAGCTTGAATTTAGGAATTTG 608

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||  ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        609 ACACCCGGGAACACCAACACCCGTGTTTCCCGGTATACCAGCACAGCCCGCCACCGGCTG 668

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CGCCGTGGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCCACACGTTTCATGAAG 728

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||  |||  ||||||||||||||||||||||||||||||||||||||||||||
Db        729 GACCTGCACTTCGCTGGCACGAATGGCGTTGGTGAGGTGGGTCGTGGTATCGCCCTGACA 788

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 CTGTTCAATCTCGCTGATACGCTTCTCGGCGGTTTACCGACAGAATTGATTTCGTCGGCT 848

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLys 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 GGGGGCCAACTGTTTTACTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAG 908

Qy        301 LeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIle 320
              ||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        909 TTATATACATCTGTTGAGAATGCGCAGCAAGACAAGGGCATCACCATTCCACATGATATA 968

Qy        321 AspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 GACCTGGGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCAYGAA 1019

RESULT 22
AAT27111
ID   AAT27111 standard; DNA; 984 BP.
XX
AC   AAT27111;
XX
DT   16-OCT-2003  (revised)
DT   06-AUG-1996  (first entry)
XX
DE   Hepatitis E virus (Burma strain) SG3 antigen DNA.
XX
KW   HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine;
KW   diagnosis; antigen; ds.
XX
OS   Hepatitis E virus; Burma strain.
XX
PN   WO9612807-A2.
XX
PD   02-MAY-1996.
XX
PF   23-OCT-1995;   95WO-US013703.
XX
PR   24-OCT-1994;   94US-00327952.
PR   13-OCT-1995;   95US-00542634.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Fuerst TR,  Mcatee CP,  Yarbough PO,  Zhang Y;
XX
DR   WPI; 1996-230608/23.
DR   P-PSDB; AAR96093.
XX
PT   Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as
PT   diagnostic reagents for determining HEV infection and in vaccines.
XX
PS   Disclosure; Page 74-75; 125pp; English.
XX
CC   A DNA sequence (AAT27111) codes for SG3 antigen (AAR96093) comprising the
CC   C-terminal 327 amino acids of hepatitis E virus (HEV) Burma strain capsid
CC   protein (AAR96089). It is obtd. by PCR amplification of pBET1 contg. the
CC   HEV ORF-2 (AAT27107) and ORF-3 (AAT27115). The amplified fragment is
CC   inserted into pBluescript and the cloned insert is ligated into vector
CC   pGEX for prodn. of SG3 in E. coli cells SG3 shows low antigenicity
CC   compared with 62K antigen (see also AAR96091-92 and AAR96101-04) from HEV
CC   Burma and Mexico strain capsid proteins, produced using a baculovirus
CC   expression system. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 984 BP; 180 A; 300 C; 246 G; 258 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              5.78          Length:         984
Score:                  305.00        Matches:        305
Percent Similarity:     93.27%        Conservative:   0
Best Local Similarity:  93.27%        Mismatches:     22
Query Match:            55.56%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AAT27111 (1-984)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTC 60

Qy        243 HisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeu 262
              ||||||     ||||||||||||||   ||||||||||||||||||||||
Db         61 TATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTC 120

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGC 180

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTAT 240

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu 322
              |||||||||||||||||||||||||||||||   |||||||||||||||||||||||
Db        241 ACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTC 300

Qy        323 GlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGGCCGACG 360

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTC 420

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTTAT 480

Qy        383 IleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCG 540

Qy        403 LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer 422
              ||||||||   ||||||||||||||||||||||||||   |||       |||||||||
Db        541 CTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAGTACTCG 600

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACAACT 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||   |||   ||||||
Db        661 AAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        721 GCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTC 780

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502
              |||||||||   ||||||||||||||||   |||||||||||||||||||||||||||||
Db        781 TCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACC 840

Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||   |||
Db        841 TTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCCTT 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        901 GGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||
Db        961 GTGGGTAAAACTCGGGAGTTG 981

RESULT 23
AAT96965
ID   AAT96965 standard; DNA; 984 BP.
XX
AC   AAT96965;
XX
DT   17-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   26-FEB-1998  (first entry)
XX
DE   Hepatitis E virus Burma strain peptide antigen SG3 encoding DNA.
XX
KW   Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
KW   diagnosis; HEV; ds.
XX
OS   Hepatitis E virus; - Burma strain.
```

```
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .984
FT                   /*tag=  a
FT                   /product= "Peptide_antigen_SG3"
XX
PN   US5686239-A.
XX
PD   11-NOV-1997.
XX
PF   09-MAY-1994;    94US-00240049.
XX
PR   17-JUN-1988;    88US-00208997.
PR   11-APR-1989;    89US-00336672.
PR   16-JUN-1989;    89US-00367486.
PR   13-OCT-1989;    89US-00420921.
PR   05-APR-1990;    90US-00505888.
PR   05-APR-1991;    91US-00681078.
PR   17-JAN-1992;    92US-00822335.
PR   20-APR-1992;    92US-00870985.
PR   01-MAY-1992;    92US-00876941.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Tam AW,  Reyes GR,  Yarbough PO;
XX
DR   WPI; 1997-558132/51.
DR   P-PSDB; AAW35820.
XX
PT   Diagnosis of hepatitis E virus Burma and Mexico strain infection - by
PT   immunoassay with hepatitis E virus peptide antigens.
XX
PS   Disclosure; Col 29-32; 36pp; English.
XX
CC   A method has been developed for detecting hepatitis E virus (HEV)
CC   antibodies (Ab). The method comprises: (a) reacting a serum sample with a
CC   HEV peptide antigen; and (b) examining the peptide for the presence of
CC   bound Ab, where the presence of bound Ab indicates the presence of HEV
CC   Ab. The present sequence encodes a specifically claimed HEV peptide
CC   antigen. The method can be used to diagnose infection with the
CC   enterically transmitted non-A/non-B viral hepatitis agent HEV,
CC   specifically the HEV Burma and Mexico strains. (Updated on 25-MAR-2003 to
CC   correct PF field.) (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ   Sequence 984 BP; 180 A; 300 C; 246 G; 258 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                5.78          Length:          984
Score:                    305.00        Matches:         305
Percent Similarity:       93.27%        Conservative:    0
Best Local Similarity:    93.27%        Mismatches:      22
Query Match:              55.56%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x AAT96965 (1-984)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGTGCGGACGGGACTGCCGAGCTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTC 60

Qy        243 HisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeu 262
                 ||||||      ||||||||||||||||   ||||||||||||||||||||||||
Db         61 TATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTC 120

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGC 180

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTAT 240

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        241 ACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTC 300

Qy        323 GlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGGCCGACG 360

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTC 420

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTTAT 480

Qy        383 IleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCG 540

Qy        403 LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer 422
              ||||||||  ||||||||||||||||||||||||||  |||      |||||||||
Db        541 CTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCATCCAGCAGTACTCG 600

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACAACT 660

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAAT 720

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTC 780

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502
              |||||||||  ||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        781 TCCATTTCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACC 840

Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCCTT 900

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAG 960

Qy        543 ValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||
Db        961 GTGGGTAAAACTCGGGAGTTG 981

RESULT 24
AAZ00279
ID   AAZ00279 standard; DNA; 1026 BP.
XX
AC   AAZ00279;
XX
DT   12-OCT-1999  (first entry)
XX
DE   HEV US and CMP-KDO synthetase (CKS) fusion protein cksorf2m-2 DNA.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
```

```
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
DR   P-PSDB; AAY31400.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 10; Page 233-234; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a DNA encoding a HEV US and CKS fusion
CC   protein
XX
SQ   Sequence 1026 BP; 215 A; 285 C; 248 G; 278 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              6.35          Length:          1026
Score:                  300.00        Matches:         300
Percent Similarity:     92.02%        Conservative:    0
Best Local Similarity:  92.02%        Mismatches:      26
Query Match:            54.64%        Indels:          0
DB:                     1             Gaps:            0

US-09-769-066-16 (1-549) x AAZ00279 (1-1026)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCCACACGTTTCATGAAGGACCTG 69

Qy        243 HisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeu 262
              ||||||   |||   ||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CACTTCGCTGGCACGAATGGCGTTGGTGAGGTGGGTCGTGGTATCGCCCTGACACTGTTC 129

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 AATCTCGCTGATACGCTTCTCGGCGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGC 189

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CAACTGTTTTACTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATAT 249

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||      ||||||||||||||||||||
Db        250 ACATCTGTTGAGAATGCGCAGCAAGACAAGGGCATCACCATTCCACATGATATAGACCTG 309

Qy        323 GlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCATGAGCAAGACCGACCTACT 369

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CCGTCACCTGCCCCCTCTCGCCCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTT 429

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||   ||||||||||||||||   |||   |||
Db        430 TCCCTCACTGCCGCTGAGTATGACCAGACTACGTATGGGTCGTCCACCAACCCTATGTAT 489

Qy        383 IleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
                  ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GTCTCTGACACAGTTACGCTTGTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCC 549

Qy        403 LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 CTTGATTGGTCTAAAGTTACTCTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCT 609

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 AAGACATTTTATGTTCTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACT 669

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAGGCCGGCTACCCTTACAATTATAATACTACCGCTAGTGACCAAATTTTGATTGAGAAT 729

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        730 GCGGCCGGCCACCGTGTCGCTATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACC 789

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502
                  |||||||||      ||||||||||||   ||||||||||||   ||||||||||||
Db        790 TCGATCTCTGCGGTCGGCGTACTGGCTCCACACTCTGCCCTTGCCGTTCTTGAGGATACT 849

Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522
                ||||||||||   ||||||||||||||||||||||||||||||||||||||   |||
Db        850 ATTGATTACCCCGCCCGTGCCCATACTTTTGATGATTTTTGCCCGGAGTGCCGTACCCTA 909

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLys 542
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||   |||
Db        910 GGTTTGCAGGGTTGTGCATTCCAGTCTACTATTGCTGAGCTCCAGCGTTTAAAAATGAAG 969

Qy        543 ValGlyLysThrArgGlu 548
              ||||||||||||||||
Db        970 GTAGGTAAAACCCGGGAG 987

RESULT 25
AAZ00282
ID   AAZ00282 standard; DNA; 960 BP.
XX
AC   AAZ00282;
XX
DT   12-OCT-1999  (first entry)
XX
DE   HEV US recombinant protein plorf2-2.6 DNA.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
DR   P-PSDB; AAY31401, AAY31403.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 10; Page 235-236; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
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CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a DNA encoding a recombinant HEV protein
XX
SQ   Sequence 960 BP; 188 A; 274 C; 230 G; 268 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.64          Length:          960
Score:                    292.00        Matches:         292
Percent Similarity:       92.11%        Conservative:    0
Best Local Similarity:    92.11%        Mismatches:      25
Query Match:              53.19%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x AAZ00282 (1-960)

Qy        223 GlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLysAspLeu 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GGTGCTGATGGGACTGCTGAGCTTACTACCACAGCAGCCACACGTTTCATGAAGGACCTG 69

Qy        243 HisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThrLeuLeu 262
              ||||||   |||   ||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CACTTCGCTGGCACGAATGGCGTTGGTGAGGTGGGTCGTGGTATCGCCCTGACACTGTTC 129

Qy        263 AsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGly 282
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 AATCTCGCTGATACGCTTCTCGGCGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGC 189

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CAACTGTTTTACTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATAT 249

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||      ||||||||||||||||||||||
Db        250 ACATCTGTTGAGAATGCGCAGCAAGACAAGGGCATCACCATTCCACATGATATAGACCTG 309

Qy        323 GlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCATGAGCAAGACCGACCTACT 369

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 CCGTCACCTGCCCCCTCTCGCCCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTT 429

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||   ||||||||||||||||   |||   |||
Db        430 TCCCTCACTGCCGCTGAGTATGACCAGACTACGTATGGGTCGTCCACCAACCCTATGTAT 489

Qy        383 IleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
                  ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GTCTCTGACACAGTTACGCTTGTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCC 549

Qy        403 LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer 422
              ||||||||||||||||||||||||||||||||||||   |||       |||||||||
Db        550 CTTGATTGGTCTAAAGTTACTCTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCT 609

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 AAGACATTTTATGTTCTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACT 669

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AAGGCCGGCTACCCTTACAATTATAATACTACCGCTAGTGACCAAATTTTGATTGAGAAT 729

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        730 GCGGCCGGCCACCGTGTCGCTATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACC 789

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502
                  |||||||||      ||||||||||||   ||||||||||||   ||||||||||||
Db        790 TCGATCTCTGCGGTCGGCGTACTGGCTCCACACTCTGCCCTTGCCGTTCTTGAGGATACT 849
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Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522
                  |||||||||   ||||||||||||||||||||||||||||||||||||||   |||
Db        850 ATTGATTACCCCGCCCGTGCCCATACTTTTGATGATTTTTGCCCGGAGTGCCGTACCCTA 909

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeu 539
              ||||||||||||||||||||||||||||   ||||||||||||||||||
Db        910 GGTTTGCAGGGTTGTGCATTCCAGTCTACTATTGCTGAGCTCCAGCGTTTA 960

RESULT 26
AAZ00129
ID   AAZ00129 standard; DNA; 899 BP.
XX
AC   AAZ00129;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Nucleic acid sequence of HEV clone df-orf2/3.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 3; Page 144-145; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a HEV US subtype specific sequence obtained
CC   by PCR amplification
XX
SQ   Sequence 899 BP; 176 A; 253 C; 207 G; 263 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                6.86          Length:          899
Score:                    285.00        Matches:         285
Percent Similarity:       95.96%        Conservative:    0
Best Local Similarity:    95.96%        Mismatches:      12
Query Match:              51.91%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x AAZ00129 (1-899)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              |||      ||||||   ||||||   ||||||||||||||||||||||||||||||||||||
Db          8 GCCATATCACCAGCCCCTGATACAGCTCCTGTACCTGATGTTGACTCACGTGGTGCTATT 67

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 TTGCGCCGGCAGTACAATTTGTCTACGTCCCCGCTTACATCATCTGTTGCTTCTGGTACT 127
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Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        128 AATCTGGTTCTCTATGCTGCCCCGCTGAACCCTCTCTTGCCTCTTCAGGATGGCACCAAC 187

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        188 ACTCATATTATGGCTACTGAGGCATCTAATTACGCCCAGTATCGGGTTGTTCGGGCTACG 247

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 ATTCGTTATCGCCCGTTGGTGCCAAATGCTGTTGGTGGTTATGCTATCTCTATTTCTTTC 307

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 TGGCCTCAAACTACAACTACCCCTACTTCTGTTGACATGAATTCTATCACTTCTACTGAT 367

Qy        121 ValArgIleLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 GTCAGGATCTTGGTCCAGCCCGGTATAGCCTCCGAGTTAGTCATCCCTAGTGAACGCCTT 427

Qy        141 HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlaGluGluGluAla 160
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        428 CACTACCGCAACCAAGGCTGGCGCTCTGTTGAGACCACGGGTGTGGCCGAAGAGGAGGCT 487

Qy        161 ThrSerGlyLeuValMetLeuCysIleHisGlySerProValAsnSerTyrThrAsnThr 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 ACCTCCGGTCTGGTAATGCTTTGTATTCATGGCTCCCCTGTTAACTCCTACACTAATACA 547

Qy        181 ProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPheArgAsnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 CCTTACACCGGTGCATTGGGGCTTCTTGATTTTGCATTAGAACTTGAATTTAGAAATTTG 607

Qy        201 ThrThrCysAsnThrAsnThrArgValSerArgTyrSerSerThrAlaArgHisArgLeu 220
              |||      ||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        608 ACACCCGGGAACACTAACACCCGTGTTTCCCGGTATACTAGCACAGCCCGCCACCGGCTG 667

Qy        221 ArgArgGlyAlaAspGlyThrAlaGluLeuThrThrThrAlaAlaThrArgPheMetLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CGCCGCGGTGCTGATGGGACCGCTGAGCTCACCACCACAGCAGCCACACGCTTCATGAAG 727

Qy        241 AspLeuHisPheThrGlyLeuAsnGlyValGlyGluValGlyArgGlyIleAlaLeuThr 260
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        728 GATTTGCATTTTACTGGTACGAACGGCGTTGGTGAGGTGGGTCGTGGTATTGCCCTGACT 787

Qy        261 LeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIleSerSerAla 280
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CTGTTTAATCTTGCTGATACGCTTCTTGGTGGTTTACCGACAGAATTGATTTCGTCGGCT 847

Qy        281 GlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 GGGGGTCAACTGTTTTACTCCCGCCCTGTTGTCTCAGCCAATGGCGAGCCA 898

RESULT 27
AAZ00193
ID   AAZ00193 standard; DNA; 960 BP.
XX
AC   AAZ00193;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Nucleic acid sequence of HEV clone 3p RACE.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 3; Page 160; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a HEV US subtype specific sequence obtained
CC   by PCR amplification
XX
SQ   Sequence 960 BP; 198 A; 262 C; 213 G; 283 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.:                10.2          Length:          960
Score:                    256.00        Matches:         256
Percent Similarity:       91.10%        Conservative:    0
Best Local Similarity:    91.10%        Mismatches:      25
Query Match:              46.63%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x AAZ00193 (1-960)

Qy        268 LeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSer 287
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CTTCTTGGTGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGTCAACTGTTTTACTCC 62

Qy        288 ArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsn 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGCCCTGTTGTCTCGGCCAATGGCGAGCCAACAGTAAAGTTATACACATCTGTTGAGAAT 122

Qy        308 AlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeuGlyAspSerArgVal 327
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        123 GCGCAGCAAGACAAGGGCATCACCATTCCACACGACATAGATTTAGGTGACTCCCGTGTG 182

Qy        328 ValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaPro 347
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GTTATCCAGGATTATGATAACCAGCACGAACAAGATCGACCTACCCCGTCACCTGCCCCC 242

Qy        348 SerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAla 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 TCCCGCCCTTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTCTCTCTCACTGCCGCT 302

Qy        368 GluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrIleSerAspSerVal 387
              ||||||   |||   ||||||||||||||||||   |||   |||   ||||||   |||
Db        303 GAGTACGRCCAGACCACGTATGGGTCGTCCACCAACCCTATGTATGTCTCTGATACAGTC 362

Qy        388 ThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLys 407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 ACGCTTGTTAATGTAGCCACTGGTGCTCAGGCTGTTGCCCGCTCTCTTGACTGGTCTAAA 422

Qy        408 ValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheVal 427
              ||||||||||||||||||||||   |||       ||||||||||   |||   |||
Db        423 GTTACTCTGGATGGTCGCCCTCTTACTACCATTCAGCAGTATTCTAAGAAATTTTATGTT 482

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 CTCCCGCTTCGSGGGAAGCTGTCCTTTTGGGAGGCTGGTACGACCAAGGCCGGCTACCCG 542
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Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArg 467
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 TATAATTATAATACCACTGCTAGTGACCAAATTTTGATTGAGAACGCGGCCGGTCACCGT 602

Qy        468 ValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAla 487
              |||||||||||||||||||||||||   ||||||||||||||||      |||||||||
Db        603 GTCGCCATTTCTACTTATACCACTAGTTTGGGTGCCGGCCCTACCTCGATYTCTGCGGTC 662

Qy        488 AlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGly 507
                  ||||||||||||  ||||||||||||  ||||||||||||  |||||||||
Db        663 GGTGTACTAGCTCCACATTCGGCCCTTGCTGTTCTCGAGGATACTGTTGATTATCCTGCT 722

Qy        508 ArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCys 527
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 CGTGCCCATACTTTTGATGATTTCTGCCCGGAGTGTCGCACCCTTGGTCTGCAGGGTTGT 782

Qy        528 AlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLysValGlyLysThrArg 547
              ||||||||||||||||  ||||||||||||||||||||  ||||||||||||||||||||
Db        783 GCATTCCAATCTACTATTGCTGAACTTCAGCGTCTTAAAATGAAGGTAGGTAAAACCCGG 842

Qy        548 Glu 548
              |||
Db        843 GAG 845
```

RESULT 28
AAZ00277
ID AAZ00277 standard; DNA; 920 BP.
XX
AC AAZ00277;
XX
DT 12-OCT-1999 (first entry)
XX
DE Nucleic acid sequence of HEV clone z12-3p.con.
XX
KW Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW vaccine; passive immunisation; ss.
XX
OS Hepatitis E virus.
XX
PN WO9919732-A1.
XX
PD 22-APR-1999.
XX
PF 15-OCT-1998; 98WO-US021941.
XX
PR 15-OCT-1997; 97US-0061199P.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Schlauder GG, Erker JC, Desai SM, Dawson GJ, Mushahwar IK;
XX
DR WPI; 1999-288017/24.
XX
PT Detection of United States isolates of hepatitis E virus.
XX
PS Example 13; Page 230; 260pp; English.
XX
CC The invention provides a method for detecting a US (sub)type hepatitis E
CC virus (US-HEV), or its naturally occurring variants in a sample by
CC treatment with a binding partner specific for a marker of the virus, and
CC then detecting any complex formed. The method is used to diagnose
CC infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC are useful in vaccines or for passive immunisation. The polypeptides are
CC also used to raise specific antibodies (useful as immunoassay reagents).
CC Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC usual hybridisation and amplification assays for detecting infection. The
CC present sequence represents a HEV US subtype specific sequence obtained
CC by PCR amplification
XX
SQ Sequence 920 BP; 198 A; 254 C; 207 G; 261 T; 0 U; 0 Other;

```
Alignment Scores:
Pred. No.:              10.6          Length:          920
Score:                  250.00        Matches:         250
Percent Similarity:     90.91%        Conservative:    0
Best Local Similarity:  90.91%        Mismatches:      25
Query Match:            45.54%        Indels:          0
DB:                     1             Gaps:            0

US-09-769-066-16 (1-549) x AAZ00277 (1-920)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTAATTTCGTCGGCTGGGGGTCAACTGTTCTACTCCCGCCCTGTCGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTCAAGTTATACACATCTGTTGAGAATGCACAGCAGGATAAGGGG 121

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ATAGCTATTCCACATGACATAGATTTGGGCGACTCTCGTTTGGTAATCCAGGATTACGAT 181

Qy        334 AsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgProPheServVal 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AATCAGCACGAGCAGGACCGGCCCACCCCTTCGCCCGCCCCGTCTCGTCCTTTCTCGGTC 241

Qy        354 LeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThr 373
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||  |||
Db        242 CTCCGCGCTAATGATGCTTTGTGGCTTTCTCTTACCGCTGCTGAGTATGACCAGACTACA 301

Qy        374 TyrGlySerSerThrGlyProValTyrIleSerAspSerValThrLeuValAsnValAla 393
              ||||||||||||||||  |||  |||  ||||||  ||||||  ||||||||||||||
Db        302 TATGGGTCGTCCACCAACCCGATGTATGTCTCAGACACTGTTACATTTGTCAATGTGGCC 361

Qy        394 ThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeuAspGlyArg 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 ACAGGGGCTCAGGCTGTCGCCCGTTCTCTTGATTGGTCTAAAGTTACCCTGGACGGCCGC 421

Qy        414 ProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuProLeuArgGlyLys 433
              ||||||  |||      ||||||||||||||||||  ||||||||||||||||||||||
Db        422 CCTCTTACTACCATCCAGCAGTACTCTAAGACATTTTATGTTCTCCCACTTCGCGGGAAG 481

Qy        434 LeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThr 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 TTATCTTTTTGGGAGGCTGGCACAACTAAAGCCGGTTACCCTTATAATTATAACACAACT 541

Qy        454 AlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAlaIleSerThrTyr 473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 GCTAGTGACCAGATTCTGATTGAAAACGCGGCTGGCCATCGTGTCGCTATATCTACTTAT 601

Qy        474 ThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArg 493
              ||||||  ||||||||||||||||||      ||||||      ||||||||||||
Db        602 ACTACTAGCCTGGGCGCCGGCCCTGTGTCAGTTTCTGCGGTTGGTGTGTTAGCCCCACAC 661

Qy        494 SerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHisThrPheAsp 513
              |||  ||||||  ||||||||||||  ||||||||  ||||||||||||||||||||
Db        662 TCGAGCCTTGCTATTCTTGAAGACACTGTTGACTATCCGGCCCGTGCTCACACTTTTGAT 721

Qy        514 AspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGlnSerThrVal 533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GACTTCTGTCCGGAATGCCGTGCCCTGGGTCTGCAGGGGTGTGCTTTTCAATCTACTATC 781

Qy        534 AlaGluLeuGlnArgLeuLysValLysValGlyLysThrArgGlu 548
              ||||||||||||||||||  ||||||||||||||||||||||||
Db        782 GCTGAGCTCCAGCGTCTTAAAATGAAGGTAGGCAAAACCCGGGAG 826
```

RESULT 29
AAS01434
ID AAS01434 standard; cDNA; 810 BP.
XX
AC AAS01434;
XX
DT 18-JUL-2001 (first entry)

```
XX
DE   Hepatitis E virus (HEV) E2 cDNA fragment derived from ORF2.
XX
KW   Hepatitis E virus; HEV; E2; pE2; ORF2; immunoreactive viral peptide;
KW   antigenic activity; viral infection; mutant; ss.
XX
OS   Hepatitis E virus; Chinese strain D11092.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .810
FT                   /*tag=  b
FT                   /note= "Corresponds to residues 1180-1990 of ORF2"
FT   CDS             1. .642
FT                   /*tag=  a
FT                   /partial
FT                   /product= "pE2 peptide"
FT                   /note= "Specifically claimed. This sequence lacks a start
FT                   codon"
FT   mutation        replace(631. .632, CAC)
FT                   /*tag=  c
XX
PN   WO200122916-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-IB001393.
XX
PR   30-SEP-1999;   99CA-02283538.
XX
PA   (UYHK-) UNIV HONG KONG.
XX
PI   Ng MH,  Im S,  Zhang J;
XX
DR   WPI; 2001-266109/27.
DR   P-PSDB; AAU00496.
XX
PT   New immunoreactive peptide pE2, cloned from the genome of a Chinese
PT   strain of hepatitis E virus (HEV), for detecting and diagnosing HEV
PT   infection and for use as a vaccine for prevention of the viral infection
PT   in humans.
XX
PS   Claim 5; Fig 2B-2D; 101pp; English.
XX
CC   The present sequence for hepatitis E virus (HEV) E2 cDNA fragment encodes
CC   for a novel peptide, pE2 which is cloned from ORF2 (AAS01448) of the HEV
CC   Chinese strain D11092 genome. During the cloning of the E2 fragment a
CC   single base deletion (presumed to be a PCR amplification error) at
CC   position 1811 of ORF2 resulted in a frame shift causing the premature
CC   termination at a new stop codon at position 1820-1822, and giving rise to
CC   a smaller peptide, pE2. Peptide pE2 is a highly immunoreactive viral
CC   peptide which can be used in the development of diagnostic methods for
CC   the detection of HEV. Peptide pE2 which has antigenic activity is also
CC   useful as a vaccine for immunising an individual against infection from
CC   HEV and for determining the presence of HEV antibodies in a biological
CC   test sample such as human blood serum or plasma for detection and
CC   diagnosis of HEV infection. An antibody against pE2 is useful for
CC   detecting an HEV particle, in a biological test sample. The use of
CC   recombinant peptides such as pE2 peptide have advantage over the prior
CC   art of using live intact virus particles by avoiding the potential risk
CC   of infectivity. The ORF3 (AAS01449) of HEV Chinese strain D11092 is used
CC   to clone a cDNA fragment E3 (AAS001450) which encodes pE3 peptide
XX
SQ   Sequence 810 BP; 150 A; 249 C; 192 G; 219 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              11.3          Length:         810
Score:                  237.00        Matches:        250
Percent Similarity:     93.63%        Conservative:   0
Best Local Similarity:  93.63%        Mismatches:     17
Query Match:            43.17%        Indels:         1
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AAS01434 (1-810)

Qy        283 GlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluProThrValLysLeuTyr 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCTGTTCTACTCTCGTCCCGTCGTCTCAGCCAATGGCGAGCCGACTGTTAAGCTTTAT 60

Qy        303 ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu 322
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db         61 ACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCGCATGACATCGACCTC 120

Qy        323 GlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThr 342
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGGAGTCTCGTGTAGTTATTCAGGATTATGACAACCAACATGAGCAGGACCGACCGACA 180

Qy        343 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTTCCCCAGCCCCATCGCGCCCTTTTTCTGTCCTCCGAGCTAATGATGTGCTTTGGCTT 240

Qy        363 SerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyr 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTCTCACCGCTGCCGAGTATGACCAGTCCACTTACGGCTCTTCGACCGGCCCAGTCTAT 300

Qy        383 IleSerAspSerValThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSer 402
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTCTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCGGTCA 360

Qy        403 LeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSer 422
              |||||||||  |||||||||||||||||||||||||||  |||  |||||||||
Db        361 CTCGACTGGACCAAGGTCACACTTGATGGTCGCCCCCTTTCCACCATCCAGCAGTATTCA 420

Qy        423 LysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThr 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGTACTACT 480

Qy        443 LysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsn 462
              ||||||||||||||||||||||||||||||||||||||||||||||  |||   ||||||
Db        481 AAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGTGACCAACTGCTCGTTGAGAAT 540

Qy        463 AlaAlaGlyHisArgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProVal 482
              ||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        541 GCCGCTGGGCATCGGGTTGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTC 600

Qy        483 AlaIleSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThr 502
                  |||||||||  ||||||||||||||  ||||||||||||||||||||||||||||||
Db        601 TCTATTTCCGCGGTTGCTGTTTTAGCCCCCCC-TCCGCGCTAGCATTGCTTGAGGATACC 659

Qy        503 PheAspTyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysArgAlaLeu 522
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||  |||
Db        660 ATGGACTACCCTGCCCGCGCCCATACTTTCGATGACTTCTGCCCGGAGTGCCGCCCCCTT 719

Qy        523 GlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLysValLys 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        720 GGCCTCCAGGGCTGTGCTTTTCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAG 779

Qy        543 ValGlyLysThrArgGluLeu 549
              |||||||||||||||||||||
Db        780 GTGGGTAAAACTCGGGAGTTA 800

RESULT 30
AAZ00255
ID   AAZ00255 standard; DNA; 901 BP.
XX
AC   AAZ00255;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Nucleic acid sequence of HEV clone us2-3p.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
```

PN WO9919732-A1.
XX
PD 22-APR-1999.
XX
PF 15-OCT-1998; 98WO-US021941.
XX
PR 15-OCT-1997; 97US-0061199P.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Schlauder GG, Erker JC, Desai SM, Dawson GJ, Mushahwar IK;
XX
DR WPI; 1999-288017/24.
XX
PT Detection of United States isolates of hepatitis E virus.
XX
PS Example 5; Page 198-199; 260pp; English.
XX
CC The invention provides a method for detecting a US (sub)type hepatitis E
CC virus (US-HEV), or its naturally occurring variants in a sample by
CC treatment with a binding partner specific for a marker of the virus, and
CC then detecting any complex formed. The method is used to diagnose
CC infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC are useful in vaccines or for passive immunisation. The polypeptides are
CC also used to raise specific antibodies (useful as immunoassay reagents).
CC Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC usual hybridisation and amplification assays for detecting infection. The
CC present sequence represents a HEV US subtype specific sequence obtained
CC by PCR amplification
XX
SQ Sequence 901 BP; 198 A; 250 C; 195 G; 257 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	12.4	Length:	901
Score:	236.00	Matches:	236
Percent Similarity:	91.12%	Conservative:	0
Best Local Similarity:	91.12%	Mismatches:	23
Query Match:	42.99%	Indels:	0
DB:	1	Gaps:	0

US-09-769-066-16 (1-549) x AAZ00255 (1-901)

```
Qy        290 ValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGln 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATATACATCTGTTGAGAATGCGCAG 60

Qy        310 GlnAspLysGlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIle 329
              ||||||||||||      ||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAGACAAGGGCATCACCATTCCACATGATATAGACCTGGGTGACTCCCGTGTGGTTATC 120

Qy        330 GlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArg 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGGATTATGATAACCAGCAYGAGCAAGACCGACCTACTCCGTCACCTGCCCCCTCTCGC 180

Qy        350 ProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyr 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTTTCCCTCACTGCCGCTGAGTAT 240

Qy        370 AspGlnSerThrTyrGlySerSerThrGlyProValTyrIleSerAspSerValThrLeu 389
              ||||||   ||||||||||||||||||   |||   |||   ||||||   |||||||||
Db        241 GACCAGACTACGTATGGGTCGTCCACCAACCCTATGTATGTCTCTGACACAGTTACGCTT 300

Qy        390 ValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThr 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCCCTTGATTGGTCTAAAGTTACT 360

Qy        410 LeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuPro 429
              ||||||||||||||||||   |||      ||||||||||||||||   |||||||||
Db        361 CTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCTAAGACATTTTATGTTCTCCCG 420

Qy        430 LeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsn 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        421 CTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACTAAGGCCGGCTACCCTTACAAT 480

Qy        450 TyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAla 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TATAATACTACCGCTAGTGACCAAATTTTGATTGAGAATGCGGCCGGCCACCGTGTCGCT 540

Qy        470 IleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaVal 489
              ||||||||||||||||||   ||||||||||||||||   |||||||||      |||
Db        541 ATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACCTCGATCTCTGCGGTCGGCGTA 600

Qy        490 LeuAlaProArgSerAlaLeuAlaLeuGluAspThrPheAspTyrProGlyArgAla 509
              ||||||||   ||||||||||||   ||||||||||||   |||||||||   ||||||
Db        601 CTGGCTCCACACTCTGCCCTTGCCGTTCTTGAGGATACTATTGATTACCCCGCCCGTGCC 660

Qy        510 HisThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPhe 529
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        661 CATACTTTTGATGATTTTTGCCCGGAGTGCCGTACCCTAGGTTTGCAGGGTTGTGCATTC 720

Qy        530 GlnSerThrValAlaGluLeuGlnArgLeuLysValLysValGlyLysThrArgGlu 548
              ||||||||   ||||||||||||||||||||   ||||||||||||||||||||
Db        721 CAGTCTACTATTGCTGAGCTCCAGCGTTTAAAAATGAAGGTAGGTAAAACCCGGGAG 777
```

RESULT 31
AAZ00276
ID AAZ00276 standard; DNA; 890 BP.
XX
AC AAZ00276;
XX
DT 12-OCT-1999 (first entry)
XX
DE Nucleic acid sequence of HEV clone z12-3p.race.
XX
KW Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW vaccine; passive immunisation; ss.
XX
OS Hepatitis E virus.
XX
PN WO9919732-A1.
XX
PD 22-APR-1999.
XX
PF 15-OCT-1998; 98WO-US021941.
XX
PR 15-OCT-1997; 97US-0061199P.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Schlauder GG, Erker JC, Desai SM, Dawson GJ, Mushahwar IK;
XX
DR WPI; 1999-288017/24.
XX
PT Detection of United States isolates of hepatitis E virus.
XX
PS Example 13; Page 229-230; 260pp; English.
XX
CC The invention provides a method for detecting a US (sub)type hepatitis E
CC virus (US-HEV), or its naturally occurring variants in a sample by
CC treatment with a binding partner specific for a marker of the virus, and
CC then detecting any complex formed. The method is used to diagnose
CC infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC are useful in vaccines or for passive immunisation. The polypeptides are
CC also used to raise specific antibodies (useful as immunoassay reagents).
CC Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC usual hybridisation and amplification assays for detecting infection. The
CC present sequence represents a HEV US subtype specific sequence obtained
CC by PCR amplification
XX
SQ Sequence 890 BP; 190 A; 246 C; 203 G; 251 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	12.5	Length:	890
Score:	234.00	Matches:	234

```
Percent Similarity:     90.35%          Conservative:  0
Best Local Similarity:  90.35%          Mismatches:    25
Query Match:            42.62%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-16 (1-549) x AAZ00276 (1-890)

Qy        290 ValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGln 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCGTCTCGGCCAATGGCGAGCCGACTGTCAAGTTATACACATCTGTTGAGAATGCACAG 60

Qy        310 GlnAspLysGlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIle 329
              |||||||||||   |||||||||||||||||||||||||||||||||||   ||||||
Db         61 CAGGATAAGGGGATAGCTATTCCACATGACATAGATTTGGGCGACTCTCGTTTGGTAATC 120

Qy        330 GlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArg 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGGATTACGATAATCAGCACGAGCAGGACCGGCCCACCCCTTCGCCCGCCCCGTCTCGT 180

Qy        350 ProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyr 369
              ||||||||||||||||||||||||||   |||||||||||||||||||||||||||||||
Db        181 CCTTTCTCGGTCCTCCGCGCTAATGATGCTTTGTGGCTTTCTCTTACCGCTGCTGAGTAT 240

Qy        370 AspGlnSerThrTyrGlySerSerThrGlyProValTyrIleSerAspSerValThrLeu 389
              ||||||   ||||||||||||||||||   |||   |||   ||||||   ||||||
Db        241 GACCAGACTACATATGGGTCGTCCACCAACCCGATGTATGTCTCAGACACTGTTACATTT 300

Qy        390 ValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThr 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTCAATGTGGCCACAGGGGCTCAGGCTGTCGCCCGTTCTCTTGATTGGTCTAAAGTTACC 360

Qy        410 LeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuPro 429
              ||||||||||||||||||   |||       ||||||||||||||||||   |||||||||
Db        361 CTGGACGGCCGCCCTCTTACTACCATCCAGCAGTACTCTAAGACATTTTATGTTCTCCCA 420

Qy        430 LeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsn 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTTCGCGGGAAGTTATCTTTTTGGGAGGCTGGCACAACTAAAGCCGGTTACCCTTATAAT 480

Qy        450 TyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArgValAla 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TATAACACAACTGCTAGTGACCAGATTCTGATTGAAAACGCGGCTGGCCATCGTGTCGCT 540

Qy        470 IleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaVal 489
              ||||||||||||||||||   ||||||||||||||||||       ||||||       |||
Db        541 ATATCTACTTATACTACTAGCCTGGGCGCCGGCCCTGTGTCAGTTTCTGCGGTTGGTGTG 600

Qy        490 LeuAlaProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAla 509
              |||||||||   |||   ||||||   ||||||||||||   |||||||||   ||||||
Db        601 TTAGCCCCACACTCGAGCCTTGCTATTCTTGAAGACACTGTTGACTATCCGGCCCGTGCT 660

Qy        510 HisThrPheAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPhe 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACACTTTTGATGACTTCTGTCCGGAATGCCGTGCCCTGGGTCTGCAGGGGTGTGCTTTT 720

Qy        530 GlnSerThrValAlaGluLeuGlnArgLeuLysValLysValGlyLysThrArgGlu 548
              |||||||||   ||||||||||||||||||   ||||||||||||||||||||
Db        721 CAATCTACTATCGCTGAGCTCCAGCGTCTTAAAATGAAGGTAGGCAAAACCCGGGAG 777

RESULT 32
AAZ00212
ID   AAZ00212 standard; DNA; 678 BP.
XX
AC   AAZ00212;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Nucleic acid sequence of HEV clone us2-667.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 5; Page 187; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a HEV US subtype specific sequence obtained
CC   by PCR amplification
XX
SQ   Sequence 678 BP; 138 A; 197 C; 155 G; 187 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:              13.7            Length:        678
Score:                  209.00          Matches:       209
Percent Similarity:     92.89%          Conservative:  0
Best Local Similarity:  92.89%          Mismatches:    16
Query Match:            38.07%          Indels:        0
DB:                     1               Gaps:          0

US-09-769-066-16 (1-549) x AAZ00212 (1-678)

Qy        268 LeuLeuGlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSer 287
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CTTCTTGGTGGTTTACCGACAGAATTGATTTCGTCGGCTGGGGGCCAACTGTTTTACTCC 62

Qy        288 ArgProValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsn 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGCCCGGTTGTCTCAGCCAATGGCGAGCCAACAGTAAAGTTATATACATCTGTTGAGAAT 122

Qy        308 AlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeuGlyAspSerArgVal 327
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        123 GCGCAGCAAGACAAGGGCATCACCATTCCACATGATATAGACCTGGGTGACTCCCGTGTG 182

Qy        328 ValIleGlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaPro 347
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GTTATCCAGGATTATGATAACCAGCAYGAGCAAGACCGACCTACTCCGTCACCTGCCCCC 242

Qy        348 SerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAla 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 TCTCGCCCCTTCTCAGTTCTTCGTGCCAATGATGTTTTGTGGCTTTCCCTCACTGCCGCT 302

Qy        368 GluTyrAspGlnSerThrTyrGlySerSerThrGlyProValTyrIleSerAspSerVal 387
              ||||||||||||   ||||||||||||||||||   |||   |||   ||||||   |||
Db        303 GAGTATGACCAGACTACGTATGGGTCGTCCACCAACCCTATGTATGTCTCTGACACAGTT 362

Qy        388 ThrLeuValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLys 407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 ACGCTTGTTAATGTGGCTACTGGTGCTCAGGCTGTTGCCCGCTCCCTTGATTGGTCTAAA 422

Qy        408 ValThrLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheVal 427
```

```
Db        423 GTTACTCTGGACGGCCGCCCCCTTACTACCATTCAGCAGTATTCTAAGACATTTTATGTT 482

Qy        428 LeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrPro 447

Db        483 CTCCCGCTCCGCGGGAAGCTGTCCTTTTGGGAGGCTGGCACGACTAAGGCCGGCTACCCT 542

Qy        448 TyrAsnTyrAsnThrThrAlaSerAspGlnIleLeuIleGluAsnAlaAlaGlyHisArg 467

Db        543 TACAATTATAATACTACCGCTAGTGACCAAATTTTGATTGAGAATGCGGCCGGCCACCGT 602

Qy        468 ValAlaIleSerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAla 487

Db        603 GTCGCTATTTCCACCTATACCACTAGCTTAGGTGCCGGTCCTACCTCGATCTCTGCGGTC 662

Qy        488 AlaValLeuAlaPro 492

Db        663 GGTGTACTAGCTCCA 677
```

RESULT 33
AAZ00310
ID AAZ00310 standard; DNA; 250 BP.
XX
AC AAZ00310;
XX
DT 12-OCT-1999 (first entry)
XX
DE Conserved Nucleic acid sequence derived from HEV.
XX
KW Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW vaccine; passive immunisation; ss.
XX
OS Hepatitis E virus.
XX
PN WO9919732-A1.
XX
PD 22-APR-1999.
XX
PF 15-OCT-1998; 98WO-US021941.
XX
PR 15-OCT-1997; 97US-0061199P.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Schlauder GG, Erker JC, Desai SM, Dawson GJ, Mushahwar IK;
XX
DR WPI; 1999-288017/24.
XX
PT Detection of United States isolates of hepatitis E virus.
XX
PS Example 11; Page 9B; 260pp; English.
XX
CC The invention provides a method for detecting a US (sub)type hepatitis E
CC virus (US-HEV), or its naturally occurring variants in a sample by
CC treatment with a binding partner specific for a marker of the virus, and
CC then detecting any complex formed. The method is used to diagnose
CC infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC are useful in vaccines or for passive immunisation. The polypeptides are
CC also used to raise specific antibodies (useful as immunoassay reagents).
CC Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC usual hybridisation and amplification assays for detecting infection.
CC Sequences AAZ00300-312 represent conserved nucleic acid sequences from
CC various strains of HEV
XX
SQ Sequence 250 BP; 56 A; 66 C; 65 G; 63 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	27.2	Length:	250
Score:	83.00	Matches:	83
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	15.12%	Indels:	0

```
DB:                 1            Gaps:          0

US-09-769-066-16 (1-549) x AAZ00310 (1-250)

Qy        258 AlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277

Db          2 GCTCTAACATTACTTAACCTTGCTGACACGCTCCTCGGCGGGCTCCCGACAGAATTAATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297

Db         62 TCGTCGGCTGGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCA 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIlePro 317

Db        122 ACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCC 181

Qy        318 HisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337

Db        182 CACGATATCGATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAG 241

Qy        338 GlnAspArg 340

Db        242 CAGGATCGG 250
```

RESULT 34
AAZ00309
ID AAZ00309 standard; DNA; 250 BP.
XX
AC AAZ00309;
XX
DT 12-OCT-1999 (first entry)
XX
DE Conserved Nucleic acid sequence derived from HEV.
XX
KW Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW vaccine; passive immunisation; ss.
XX
OS Hepatitis E virus.
XX
PN WO9919732-A1.
XX
PD 22-APR-1999.
XX
PF 15-OCT-1998; 98WO-US021941.
XX
PR 15-OCT-1997; 97US-0061199P.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Schlauder GG, Erker JC, Desai SM, Dawson GJ, Mushahwar IK;
XX
DR WPI; 1999-288017/24.
XX
PT Detection of United States isolates of hepatitis E virus.
XX
PS Example 11; Page 9B; 260pp; English.
XX
CC The invention provides a method for detecting a US (sub)type hepatitis E
CC virus (US-HEV), or its naturally occurring variants in a sample by
CC treatment with a binding partner specific for a marker of the virus, and
CC then detecting any complex formed. The method is used to diagnose
CC infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC are useful in vaccines or for passive immunisation. The polypeptides are
CC also used to raise specific antibodies (useful as immunoassay reagents).
CC Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC usual hybridisation and amplification assays for detecting infection.
CC Sequences AAZ00300-312 represent conserved nucleic acid sequences from
CC various strains of HEV
XX
SQ Sequence 250 BP; 57 A; 65 C; 62 G; 66 T; 0 U; 0 Other;

Alignment Scores:

```
Pred. No.:              28.1          Length:        250
Score:                  80.00         Matches:       80
Percent Similarity:     96.39%        Conservative:  0
Best Local Similarity:  96.39%        Mismatches:    3
Query Match:            14.57%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AAZ00309 (1-250)

Qy        258 AlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        122 ACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCG 181

Qy        318 HisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        182 CATGACATTGACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACATGAA 241

Qy        338 GlnAspArg 340
              |||||||||
Db        242 CAAGATCGG 250

RESULT 35
AAZ00307
ID   AAZ00307 standard; DNA; 250 BP.
XX
AC   AAZ00307;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Conserved Nucleic acid sequence derived from HEV.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 11; Page 9B; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection.
CC   Sequences AAZ00300-312 represent conserved nucleic acid sequences from
CC   various strains of HEV
XX
SQ   Sequence 250 BP; 56 A; 68 C; 64 G; 62 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              28.1          Length:        250
Score:                  80.00         Matches:       80
Percent Similarity:     96.39%        Conservative:  0
Best Local Similarity:  96.39%        Mismatches:    3
Query Match:            14.57%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AAZ00307 (1-250)

Qy        258 AlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGCTTACCCTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGTGGCCAGCTGTTCTACTCTCGCCCCGTCGTCTCAGCCAATGGCGAGCCG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        122 ACTGTTAAGCTGTATACATCTGTGGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCG 181

Qy        318 HisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        182 CATGACATCGACCTCGGGGAATCCCGTGTAGTTATTCAGGATTATGACAACCAACATGAG 241

Qy        338 GlnAspArg 340
              |||||||||
Db        242 CAGGACCGA 250

RESULT 36
AAZ00308
ID   AAZ00308 standard; DNA; 250 BP.
XX
AC   AAZ00308;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Conserved Nucleic acid sequence derived from HEV.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 11; Page 9B; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
```

```
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection.
CC   Sequences AAZ00300-312 represent conserved nucleic acid sequences from
CC   various strains of HEV
XX
SQ   Sequence 250 BP; 56 A; 67 C; 64 G; 63 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              28.1          Length:          250
Score:                  80.00         Matches:         80
Percent Similarity:     96.39%        Conservative:    0
Best Local Similarity:  96.39%        Mismatches:      3
Query Match:            14.57%        Indels:          0
DB:                     1             Gaps:            0

US-09-769-066-16 (1-549) x AAZ00308 (1-250)

Qy        258 AlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCGCTTACCCTGTTTAACCTTGCTGACACCCTGCTTGGCGGTCTACCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGTGGCCAGCTGTTCTACTCTCGCCCCGTCGTCTCAGCCAATGGCGAGCCG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIlePro 317
              ||||||||||||||||||||||||||||||||||||||||||||||||    |||||||||
Db        122 ACTGTTAAGCTGTATACATCTGTAGAGAATGCTCAGCAGGATAAGGGTATTGCAATCCCG 181

Qy        318 HisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        182 CATGACATCGACCTCGGGGAATCTCGAGTTGTTATTCAGGATTATGACAACCAACATGAG 241

Qy        338 GlnAspArg 340
              |||||||||
Db        242 CAGGACCGG 250

RESULT 37
AAZ00290
ID   AAZ00290 standard; DNA; 197 BP.
XX
AC   AAZ00290;
XX
DT   12-OCT-1999  (first entry)
XX
DE   HEV isolate 1440o2.seq ORF1 DNA sequence.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
DR   P-PSDB; AAY31407.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 14; Page 246; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a HEV US subtype specific sequence obtained
CC   by PCR amplification
XX
SQ   Sequence 197 BP; 54 A; 44 C; 47 G; 48 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.:              28.2          Length:          197
Score:                  64.00         Matches:         64
Percent Similarity:     98.46%        Conservative:    0
Best Local Similarity:  98.46%        Mismatches:      1
Query Match:            11.66%        Indels:          0
DB:                     1             Gaps:            0

US-09-769-066-16 (1-549) x AAZ00290 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTRATTTCGTCGGCTGGAGGTCAACTGTTCTACTCCCGCCCGGTTGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTTAAGTTATACACCTCTGTCGAGAATGCACAGCAGGATAAGGGC 121

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ATTGCTATACCACATGATATAGACTTAGGGGATTCCCGTGTGGTTATACAAGATTATGAY 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCARCAYGAACAA 196

RESULT 38
AAZ00292
ID   AAZ00292 standard; DNA; 197 BP.
XX
AC   AAZ00292;
XX
DT   12-OCT-1999  (first entry)
XX
DE   HEV isolate 2015o2.seq ORF1 DNA sequence.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
DR   P-PSDB; AAY31409.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
```

```
PS   Example 14; Page 248; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a HEV US subtype specific sequence obtained
CC   by PCR amplification
XX
SQ   Sequence 197 BP; 53 A; 50 C; 47 G; 43 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.:              28.2          Length:         197
Score:                  64.00         Matches:        64
Percent Similarity:     98.46%        Conservative:   0
Best Local Similarity:  98.46%        Mismatches:     1
Query Match:            11.66%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AAZ00292 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTRATTTCGTCGGCTGGAGGCCAGCTCTTCTACTCCCGCCCAGTCGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTTAAATTGTATACATCCGTCGAGAATGCGCAGCAGGACAAGGGC 121

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ATTGCCATACCACATGATATAGATCTAGGAGATTCCCGCGTGGTTATCCAGGATTATGAY 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCARCAYGAACAA 196

RESULT 39
AAZ00272
ID   AAZ00272 standard; DNA; 197 BP.
XX
AC   AAZ00272;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Nucleic acid sequence of HEV isolate z12-orf2.con.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 13; Page 228-229; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a HEV US subtype specific sequence obtained
CC   by PCR amplification
XX
SQ   Sequence 197 BP; 54 A; 46 C; 48 G; 49 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              28.5          Length:         197
Score:                  63.00         Matches:        63
Percent Similarity:     96.92%        Conservative:   0
Best Local Similarity:  96.92%        Mismatches:     2
Query Match:            11.48%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AAZ00272 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTAATTTCGTCGGCTGGGGGTCAACTGTTCTACTCCCGCCCTGTCGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCGACTGTCAAGTTATACACATCTGTTGAGAATGCACAGCAGGATAAGGGG 121

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ATAGCTATTCCACATGACATAGATTTGGGCGACTCTCGTTTGGTAATCCAGGATTATGAT 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCAACACGAACAA 196

RESULT 40
AAZ00253
ID   AAZ00253 standard; DNA; 197 BP.
XX
AC   AAZ00253;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Nucleic acid sequence of HEV clone us2-orf2.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
XX
```

```
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 5; Page 198; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection. The
CC   present sequence represents a HEV US subtype specific sequence obtained
CC   by PCR amplification
XX
SQ   Sequence 197 BP; 53 A; 47 C; 50 G; 46 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:                28.5          Length:          197
Score:                    63.00         Matches:         63
Percent Similarity:       96.92%        Conservative:    0
Best Local Similarity:    96.92%        Mismatches:      2
Query Match:              11.48%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x AAZ00253 (1-197)

Qy        274 ThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAla 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGAATTGATTTCGTCGGCTGGGGGCCAACTGTTTTACTCCCGCCCGGTTGTCTCAGCC 61

Qy        294 AsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGly 313
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AATGGCGAGCCAACAGTAAAGTTATATACATCTGTTGAGAATGCGCAGCAAGACAAGGGC 121

Qy        314 ValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAsp 333
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ATCACCATTCCACATGATATAGACCTGGGTGACTCCCGTGTGGTTATCCAGGATTATGAT 181

Qy        334 AsnGlnHisGluGln 338
              |||||||||||||||
Db        182 AACCAGCAYGAGCAA 196

RESULT 41
ADD24381
ID   ADD24381 standard; cDNA; 450 BP.
XX
AC   ADD24381;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Hepatitis E virus epitope 406.4-2 cDNA.
XX
KW   ss; gene; non-A/non-B viral hepatitis; ET-NANB; HEV; vaccine.
XX
OS   Hepatitis E virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             2. .103
FT                   /*tag=  a
XX
PN   US2003124510-A1.
XX
PD   03-JUL-2003.
XX
PF   07-MAY-2001; 2001US-00851410.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   25-JUL-1994;   94US-00279823.
PR   03-AUG-1998;   98US-00128275.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Reyes GR,  Yarbough PO,  Bradley DW,  Krawczynski KZ,  Tam AW;
PI   Fry KE;
XX
DR   WPI; 2003-810978/76.
DR   P-PSDB; ADD24382.
XX
PT   New proteins derived from an enterically transmitted non-A/non-B (ET-
PT   NANB) viral hepatitis agent, useful for diagnosing ET-NANB infection and
PT   producing vaccines for immunizing an individual against ET-NANB hepatitis
PT   viral agent.
XX
PS   Disclosure; SEQ ID NO 13; 81pp; English.
XX
CC   The invention relates to a protein derived from an enterically
CC   transmitted non-A/non-B viral hepatitis agent. The viral proteins are
CC   useful for detecting infection by the enterically transmitted non-A/non-B
CC   (ET-NANB/HEV) hepatitis viral agent. The proteins are also useful for
CC   producing vaccines for immunising an individual against HEV hepatitis
CC   viral agent. The DNA fragments are useful for identifying and sequencing
CC   the entire viral agent and for assaying the viral agent in an infected
CC   sample. The present sequence is used in the exemplification of the
CC   invention.
XX
SQ   Sequence 450 BP; 82 A; 165 C; 99 G; 104 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                29            Length:          450
Score:                    115.00        Matches:         115
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              20.95%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x ADD24381 (1-450)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 165

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 225

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 285

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 345

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 405

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsnSer 115
              |||||||||||||||||||||||||||||||||||||||||||||
Db        406 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAATTCC 450

RESULT 42
AAV66325
ID   AAV66325 standard; cDNA to mRNA; 449 BP.
XX
AC   AAV66325;
XX
DT   27-AUG-2003  (revised)
```

```
DT   25-MAR-2003  (revised)
DT   23-DEC-1998  (first entry)
XX
DE   ET-NANB (HEV) Mexico strain sequence encoding an epitope.
XX
KW   Enterically transmitted non A non B hepatitis virus; ET-NANB;
KW   Hepatitis E virus; HEV; Burma HEV isolate; vaccine; mexico strain;
KW   diagnostic probe; ds.
XX
OS   Non-A.
OS   non-B hepatitis virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             2. .103
FT                   /*tag=  a
XX
PN   US5824649-A.
XX
PD   20-OCT-1998.
XX
PF   07-JUN-1995;   95US-00475807.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   25-JUL-1994;   94US-00279823.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Bradley DW,  Reyes GR,  Krawczynski KZ,  Tam A,  Fry KE,  Yarbough PO;
XX
DR   WPI; 1998-582599/49.
DR   P-PSDB; AAW80199.
XX
PT   Hepatitis E virus proteins - useful for diagnosis or vaccine production
PT   the virus.
XX
PS   Disclosure; Col 79-82; 47pp; English.
XX
CC   The present sequence encodes an epitope of the Mexico strain sequence of
CC   enterically transmitted non A non B hepatitis virus (ET-NANB) (hepatitis
CC   E virus (HEV)). The specification describes an isolated protein which is
CC   specifically immunoreactive with antibodies present in individuals
CC   infected with HEV and encoded by a sequence contained in an open reading
CC   frame (ORF) of an HEV genome. The genome has a sequence that is more than
CC   70% identical to the ORF1 sequence from Burma HEV isolate (AAV66321). The
CC   protein is used as a vaccine and a diagnostic probe for ET-NANB. (Updated
CC   on 25-MAR-2003 to correct PR field.) (Updated on 27-AUG-2003 to correct
CC   OS field.)
XX
SQ   Sequence 449 BP; 82 A; 164 C; 99 G; 104 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              29.2          Length:        449
Score:                  114.00        Matches:       114
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            20.77%        Indels:        0
DB:                     1             Gaps:          0

US-09-769-066-16 (1-549) x AAV66325 (1-449)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 165

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 225

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 285

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 345

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 405

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsn 114
              ||||||||||||||||||||||||||||||||||||||||||
Db        406 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAAT 447

RESULT 43
AAV54733
ID   AAV54733 standard; cDNA to mRNA; 449 BP.
XX
AC   AAV54733;
XX
DT   25-MAR-2003  (revised)
DT   30-OCT-1998  (first entry)
XX
DE   Nucleic acid encoding an epitope of the Mexico strain of ET-NANB.
XX
KW   Enterically transmitted nonA/nonB hepatitis virus; identification; HEV;
KW   ET-NANB; detection; vaccine; ds.
XX
OS   Hepatitis virus.
XX
PN   US5789559-A.
XX
PD   04-AUG-1998.
XX
PF   25-JUL-1994;   94US-00279823.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   19-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Bradley DW,  Reyes GR,  Krawczynski KZ,  Tam A,  Fry KE,  Yarbough PO;
XX
DR   WPI; 1998-446186/38.
DR   P-PSDB; AAW71212.
XX
PT   Hepatitis E virus DNA - useful for e.g. virus detection and viral protein
PT   production.
XX
PS   Disclosure; Col 77-80; 45pp; English.
XX
CC   The present sequence encodes an epitope of the Mexico strain of an
CC   enterically transmitted nonA/nonB viral hepatitis agent (ET-NANB). The
CC   nucleic acid sequence may be used for identifying and sequencing the
CC   entire viral agent (also referred to as HEV), detecting ET-NANB in
CC   infected samples, e.g. by specific amplification of virus-derived DNA
CC   sequences and for producing recombinant viral proteins for use in
CC   vaccines. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 449 BP; 82 A; 164 C; 99 G; 104 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              29.2          Length:        449
Score:                  114.00        Matches:       114
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            20.77%        Indels:        0
DB:                     1             Gaps:          0
```

```
US-09-769-066-16 (1-549) x AAV54733 (1-449)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 165

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 225

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 285

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 345

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 405

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsn 114
              ||||||||||||||||||||||||||||||||||||||||||
Db        406 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAAT 447
```

```
RESULT 44
AAA99263
ID   AAA99263 standard; cDNA to mRNA; 449 BP.
XX
AC   AAA99263;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Hepatitis E virus clone 406.4-2 epitope cDNA sequence SEQ ID NO:13.
XX
KW   Hepatitis E virus; HEV; non-A/non-B viral hepatitis; viral protein;
KW   immunological; diagnosis; hepatitis; infection; identification;
KW   detection; immunoreactive; hepatotropic; antiinflammatory; virucide;
KW   vaccine; antiviral; antigenic; antibody; antigen; ds.
XX
OS   Hepatitis E virus.
XX
PN   US6120988-A.
XX
PD   19-SEP-2000.
XX
PF   07-JUN-1995;   95US-00478507.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   25-JUL-1994;   94US-00279823.
XX
PA   (GENE-) GENELABS TECHNOLOGIES INC.
PA   (USGO ) US GOVERNMENT.
XX
PI   Yarbough PO,  Krawczynski KZ,  Fry KE,  Bradley DW,  Tam A,  Reyes GR;
XX
DR   WPI; 2000-593712/56.
XX
PT   Identifying recombinant antigen immunoreactive with antibody induced by
PT   hepatitis E virus (HEV), for detecting HEV infection, comprises
PT   immunoreacting a polypeptide from an HEV genome with an HEV-positive
PT   antiserum.
XX
PS   Claim 5; Col 79-80; 46pp; English.
XX
CC   The present invention describes a method for identifying a recombinant
CC   antigen immunoreactive with a hepatitis E virus (HEV)-induced antibody.
CC   The method comprises producing a polypeptide derived from an HEV genome,
CC   immunoreacting the polypeptide with an HEV-positive antiserum and
CC   selecting the polypeptide as a recombinant antigen if the polypeptide
CC   reacts with the HEV-positive antiserum. The method is useful for
CC   identifying recombinant antigen immunoreactive with antibody induced by
CC   HEV. The enterically transmitted non-A/non-B hepatitis (ET-NANB (also
CC   known as HEV))-specific fragments are useful for identifying ET-NANB-
CC   derived cDNAs, which contain additional sequence information, as primers
CC   for detecting ET-NANB viral genomic material in a patient sample, for the
CC   synthesis of polypeptides for use in immunoassays, and for identifying
CC   similar antigenic regions encoded by related viral strains, e.g. Burmese
CC   strain. The antigens are especially useful in the preparation of vaccine
CC   against ET-NANB infection. These antigens may further be used to prepare
CC   antibodies to ET-NANB virus particles for use directly as antiviral
CC   agents, and to produce antiserum designed for pre- or post-exposure
CC   prophylaxis. The present sequence represents a specifically claimed HEV
CC   Mexican strain derived epitope encoding cDNA clone for use in the present
CC   invention
XX
SQ   Sequence 449 BP; 82 A; 164 C; 99 G; 104 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:                29.2          Length:          449
Score:                    114.00        Matches:         114
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              20.77%        Indels:          0
DB:                       1             Gaps:            0

US-09-769-066-16 (1-549) x AAA99263 (1-449)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 165

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 225

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 285

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 345

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 405

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsn 114
              ||||||||||||||||||||||||||||||||||||||||||
Db        406 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAAT 447
```

```
RESULT 45
AAF83499
ID   AAF83499 standard; cDNA; 449 BP.
XX
AC   AAF83499;
XX
DT   23-JUL-2001  (first entry)
XX
DE   HEV-Mexican strain derived epitope 406;4-2 cDNA.
XX
KW   HEV; enterically transmitted nonA/nonB viral hepatitis agent; viral;
KW   ET-NANB; infection; vaccine; epitope; ss.
XX
OS   Hepatitis E virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             2. .103
```

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FT                   /*tag=  a
XX
PN   US6229005-B1.
XX
PD   08-MAY-2001.
XX
PF   03-AUG-1998;   98US-00128275.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   05-APR-1991;   91US-00681078.
PR   25-JUL-1994;   94US-00279823.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Reyes GR,  Yarbough PO,  Bradley DW,  Krawczynski KZ,  Tam AW;
PI   Fry KE;
XX
DR   WPI; 2001-342705/36.
DR   P-PSDB; AAB62525.
XX
PT   New DNA sequences of enterically transmitted non-A/non-B (ET-NANB)
PT   hepatitis viral agent, useful in diagnosing infection by an enterically
PT   transmitted agent (e.g. ET-NANB virus), as well as in vaccine production.
XX
PS   Disclosure; Col 79-80; 45pp; English.
XX
CC   The invention relates to an isolated DNA comprising the genome of an
CC   enterically transmitted nonA/nonB (ET-NANB) viral hepatitis agent (also
CC   referred as HEV). The DNA sequences or their fragments are useful in
CC   preparing ET-NANB viral proteins and as probes for virus detection. These
CC   are particularly useful in diagnosing infection by an enterically
CC   transmitted agent (e.g. ET-NANB virus), as well as in vaccine production.
CC   The present sequence represents a cDNA encoding an epitope of HEV that is
CC   derived from the Mexican strain of ET-NANB (HEV). The epitope is
CC   specifically recognised by sera from patients with HEV infections
XX
SQ   Sequence 449 BP; 82 A; 164 C; 99 G; 104 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              29.2          Length:         449
Score:                  114.00        Matches:        114
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            20.77%        Indels:         0
DB:                     1             Gaps:           0

US-09-769-066-16 (1-549) x AAF83499 (1-449)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 165

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 225

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 285

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 345

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 405

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsn 114
              ||||||||||||||||||||||||||||||||||||||||||
Db        406 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAAT 447

RESULT 46
AAL50390
ID   AAL50390 standard; cDNA; 449 BP.
XX
AC   AAL50390;
XX
DT   08-NOV-2002  (first entry)
XX
DE   Hepatitis E virus (Mexican strain) epitopic peptide coding sequence.
XX
KW   HEV; enterically transmitted nonA/nonB hepatitis viral agent;
KW   Mexican strain; bile; ss; epitope.
XX
OS   Hepatitis E virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             2. .103
FT                   /*tag=  a
FT                   /partial
FT                   /product= "Hepatitis E virus (Mexican strain) epitopic
FT                   peptide"
FT                   /note= "No start codon is given"
XX
PN   US6379891-B1.
XX
PD   30-APR-2002.
XX
PF   19-APR-2000; 2000US-00553427.
XX
PR   17-JUN-1988;   88US-00208997.
PR   11-APR-1989;   89US-00336672.
PR   16-JUN-1989;   89US-00367486.
PR   13-OCT-1989;   89US-00420921.
PR   05-APR-1990;   90US-00505888.
PR   15-APR-1991;   91US-00681078.
PR   25-JUL-1994;   94US-00279823.
PR   07-JUN-1995;   95US-00478507.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA   (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI   Reyes GR,  Yarbough PO,  Bradley DW,  Krawczynski KZ,  Tam A,  Fry KE;
XX
DR   WPI; 2002-517277/55.
DR   P-PSDB; AAO15701.
XX
PT   Detecting the presence of enterically transmitted nonA/nonB hepatitis
PT   viral (HEV) agents in bile samples from infected humans and monkeys using
PT   polymerase chain reaction.
XX
PS   Disclosure; Col 51-52; 61pp; English.
XX
CC   The invention comprises a method for detecting the presence of
CC   enterically transmitted nonA/nonB hepatitis viral (HEV) agents in a
CC   sample and isolating HEV agents or nucleic acid fragments produced by the
CC   agent. The method utilises PCR - using bile from a human or cynomolgus
CC   monkey actively infected with HEV as a source of the agent. The method of
CC   the invention is used for detecting the presence of a viral agent in a
CC   sample of cultured cells infected with the agent and isolating
CC   enterically transmitted nonA/nonB HEV agents or nucleic acid fragments
CC   produced by the agent. The present DNA sequence was isolated from a
CC   Mexican strain of the Hepatitis E virus and encodes an epitopic peptide
XX
SQ   Sequence 449 BP; 82 A; 164 C; 99 G; 104 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              29.2          Length:         449
Score:                  114.00        Matches:        114
Percent Similarity:     100.00%       Conservative:   0
```

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Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            20.77%         Indels:        0
DB:                     1              Gaps:          0

US-09-769-066-16 (1-549) x AAL50390 (1-449)

Qy          1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaIle 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 GCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGACGTTGATTCTCGCGGTGCAATT 165

Qy         21 LeuArgArgGlnTyrAsnLeuSerThrSerProLeuThrSerSerValAlaSerGlyThr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 CTACGCCGCCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT 225

Qy         41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 AATTTAGTCCTGTATGCAGCCCCCCTTAATCCGCCTCTGCCGCTGCAGGACGGTACTAAT 285

Qy         61 ThrHisIleMetAlaThrGluAlaSerAsnTyrAlaGlnTyrArgValAlaArgAlaThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 345

Qy         81 IleArgTyrArgProLeuValProAsnAlaValGlyGlyTyrAlaIleSerIleSerPhe 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 ATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTC 405

Qy        101 TrpProGlnThrThrThrThrProThrSerValAspMetAsn 114
              ||||||||||||||||||||||||||||||||||||||||||
Db        406 TGGCCTCAAACAACCACAACCCCTACATCTGTTGACATGAAT 447

RESULT 47
AAZ00311
ID   AAZ00311 standard; DNA; 250 BP.
XX
AC   AAZ00311;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Conserved Nucleic acid sequence derived from HEV.
XX
KW   Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
KW   vaccine; passive immunisation; ss.
XX
OS   Hepatitis E virus.
XX
PN   WO9919732-A1.
XX
PD   22-APR-1999.
XX
PF   15-OCT-1998;   98WO-US021941.
XX
PR   15-OCT-1997;   97US-0061199P.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Schlauder GG,  Erker JC,  Desai SM,  Dawson GJ,  Mushahwar IK;
XX
DR   WPI; 1999-288017/24.
XX
PT   Detection of United States isolates of hepatitis E virus.
XX
PS   Example 11; Page 9B; 260pp; English.
XX
CC   The invention provides a method for detecting a US (sub)type hepatitis E
CC   virus (US-HEV), or its naturally occurring variants in a sample by
CC   treatment with a binding partner specific for a marker of the virus, and
CC   then detecting any complex formed. The method is used to diagnose
CC   infection with US-HEV. Polypeptides from US-HEV, antibodies specific for
CC   open reading frames (ORF) in US-HEV and host cells expressing these ORFs
CC   are useful in vaccines or for passive immunisation. The polypeptides are
CC   also used to raise specific antibodies (useful as immunoassay reagents).
CC   Fragments of nucleic acid from US-HEV are useful as primers and probes in
CC   usual hybridisation and amplification assays for detecting infection.
CC   Sequences AAZ00300-312 represent conserved nucleic acid sequences from
CC   various strains of HEV
XX
SQ   Sequence 250 BP; 53 A; 63 C; 60 G; 74 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              32.8           Length:        250
Score:                  65.00          Matches:       65
Percent Similarity:     78.31%         Conservative:  0
Best Local Similarity:  78.31%         Mismatches:    18
Query Match:            11.84%         Indels:        0
DB:                     1              Gaps:          0

US-09-769-066-16 (1-549) x AAZ00311 (1-250)

Qy        258 AlaLeuThrLeuLeuAsnLeuAlaAspThrLeuLeuGlyGlyLeuProThrGluLeuIle 277
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCCTGACTCTGTTTAATCTTGCTGATACGCTTCTTGGTGGTTTACCGACAGAATTGATT 61

Qy        278 SerSerAlaGlyGlyGlnLeuPheTyrSerArgProValValSerAlaAsnGlyGluPro 297
              ||||||||||||||||||||||||||||||||||||||
Db         62 TCGTCGGCTGGGGGTCAACTGTTTTACTCCCGCCCTGTTCAGAATTGATTTCGTCGGCTG 121

Qy        298 ThrValLysLeuTyrThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIlePro 317
              |||          |||  ||||||||||||||||||||      ||||||
Db        122 GGGGTCAACTGTTTTACTCCCGCCCTGTTTGCGCAGCAAGACAAGGGCATCACCATTCCA 181

Qy        318 HisAspIleAspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGlu 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CACGACATAGATTTAGGTGACTCCCGTGTGGTTATCCAGGATTATGATAACCAGCACGAA 241

Qy        338 GlnAspArg 340
              |||||||||
Db        242 CAAGATCGA 250


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